

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: March 28, 2005, 13:08:45 ; Search time 16 Seconds
(without alignments)
1942.376 Million cell updates/sec

Title: US-09-978-299a-330
Perfect score: 1694
Sequence: 1 MAAPKGSIMVTRQLGPLL.....EDHERAGPLPKVNLHSEI 323

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1500 summaries

Database :
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | length | DB ID | Description |
|------------|-------|-------------|--------|----------|---------------------|
| 1 | 423.5 | 25.0 | 342 | 2 UC7110 | brain-specific mem |
| 2 | 102 | 6.0 | 2380 | 2 T29551 | hypothetical prote |
| 3 | 95.5 | 5.6 | 741 | 2 T46488 | hypothetical prote |
| 4 | 92.5 | 5.5 | 858 | 2 A57513 | heat shock protein |
| 5 | 88.5 | 5.2 | 527 | 2 G71557 | probable glucanox |
| 6 | 88.5 | 5.2 | 817 | 2 T04697 | hypothetical prote |
| 7 | 87 | 5.1 | 736 | 2 UC7518 | subtilisin-like se |
| 8 | 86.5 | 5.1 | 327 | 2 AC0156 | probable cobalam |
| 9 | 85.5 | 5.0 | 859 | 2 S66666 | heat shock protein |
| 10 | 85.5 | 5.0 | 3225 | 2 T52300 | giantin - human |
| 11 | 85.5 | 5.0 | 3259 | 1 A56539 | giantin - human |
| 12 | 84.5 | 5.0 | 1021 | 2 T00361 | hypothetical prote |
| 13 | 84 | 5.0 | 1312 | 2 T39845 | hypothetical prote |
| 14 | 84 | 5.0 | 1350 | 2 T13254 | probable DNA repa |
| 15 | 83.5 | 4.9 | 486 | 2 S31805 | nitrile-oxide synth |
| 16 | 83 | 4.9 | 500 | 2 G72101 | VPS protein - porc |
| 17 | 83 | 4.9 | 500 | 2 C86522 | conserved hypothet |
| 18 | 83 | 4.9 | 503 | 2 A81571 | hypothetical prote |
| 19 | 83 | 4.9 | 1607 | 1 MMSB2 | conserved hypothet |
| 20 | 82 | 4.8 | 119 | 1 MSFG | laminin gamma-1 ch |
| 21 | 82 | 4.8 | 308 | 2 T31994 | motilin precursor |
| 22 | 82 | 4.8 | 626 | 2 A42891 | hypothetical prote |
| 23 | 81.5 | 4.8 | 264 | 2 JN0022 | beta-galactosidase |
| 24 | 81.5 | 4.8 | 566 | 2 S23477 | cil protein - sae |
| 25 | 81.5 | 4.8 | 778 | 2 H84678 | vicilin precursor |
| 26 | 81 | 4.8 | 485 | 1 S19677 | hypothetical prote |
| 27 | 81 | 4.8 | 848 | 1 C82712 | 1-aminocyclopropan |
| 28 | 81 | 4.8 | 1032 | 2 D95177 | ATP-dependent seri |
| 29 | 81 | 4.8 | 1032 | 2 F98043 | Snf2 family protei |

| | | | | | |
|-----|------|-----|------|----------|--------------------|
| 30 | 81 | 4.8 | 1609 | 1 MMRB2 | laminin gamma-1 ch |
| 31 | 80.5 | 4.8 | 277 | 2 T16134 | hypothetical prote |
| 32 | 80.5 | 4.8 | 282 | 2 JC4134 | ADP-ribosyl cyclas |
| 33 | 80.5 | 4.8 | 459 | 2 J00419 | coagulation factor |
| 34 | 80.5 | 4.8 | 661 | 2 B71447 | probable GLABRA2 |
| 35 | 80 | 4.7 | 491 | 1 MNXRBF | nonstructural prot |
| 36 | 80 | 4.7 | 614 | 2 A84152 | hypothetical prote |
| 37 | 79.5 | 4.7 | 264 | 1 GCBP4 | cil protein - sae |
| 38 | 79.5 | 4.7 | 600 | 2 T18593 | hypothetical prote |
| 39 | 79.5 | 4.7 | 827 | 2 T20492 | hypothetical prote |
| 40 | 79 | 4.7 | 399 | 2 B69642 | flavonemoglobin hm |
| 41 | 79 | 4.7 | 431 | 2 F97195 | foliopolyglutamate |
| 42 | 79 | 4.7 | 487 | 2 P0259 | hypothetical prote |
| 43 | 79 | 4.7 | 545 | 2 T09195 | secy protein homol |
| 44 | 79 | 4.7 | 959 | 2 T25704 | hypothetical prote |
| 45 | 79 | 4.7 | 1122 | 2 T54237 | hypothetical prote |
| 46 | 79 | 4.7 | 1123 | 1 UN0712 | protein-tyrosine k |
| 47 | 79 | 4.7 | 1124 | 2 S06856 | protein-tyrosine k |
| 48 | 79 | 4.7 | 1125 | 1 JH0771 | phytochrome - gard |
| 49 | 78.5 | 4.6 | 193 | 2 B83864 | protein-tyrosine k |
| 50 | 78.5 | 4.6 | 668 | 2 T26724 | thioredoxin BH1717 |
| 51 | 78.5 | 4.6 | 1449 | 2 T26724 | hypothetical prote |
| 52 | 78 | 4.6 | 564 | 2 T21017 | hypothetical prote |
| 53 | 78 | 4.6 | 624 | 2 T41341 | hypothetical prote |
| 54 | 77.5 | 4.6 | 166 | 2 AH2315 | probable serine-th |
| 55 | 77.5 | 4.6 | 287 | 2 T39197 | hypothetical prote |
| 56 | 77.5 | 4.6 | 462 | 2 A48933 | yeast atp12 protei |
| 57 | 77.5 | 4.6 | 464 | 2 B34130 | gamma-aminobutyric |
| 58 | 77.5 | 4.6 | 646 | 2 T27899 | gamma-aminobutyric |
| 59 | 77.5 | 4.6 | 669 | 2 T08960 | hypothetical prote |
| 60 | 77.5 | 4.6 | 696 | 2 B96831 | serine/threonine-s |
| 61 | 77.5 | 4.6 | 800 | 2 H83691 | hypothetical prote |
| 62 | 77.5 | 4.6 | 890 | 2 A40528 | hypothetical prote |
| 63 | 77.5 | 4.6 | 1259 | 2 S36126 | [protein-pil] urid |
| 64 | 77 | 4.5 | 330 | 2 B82063 | neural cell adhesi |
| 65 | 77 | 4.5 | 364 | 2 T08903 | thiamin ABC transp |
| 66 | 77 | 4.5 | 475 | 2 T46745 | hypothetical prote |
| 67 | 77 | 4.5 | 661 | 2 T42754 | arginine/ornithine |
| 68 | 77 | 4.5 | 714 | 2 T42754 | hypothetical prote |
| 69 | 77 | 4.5 | 719 | 2 S62466 | hypothetical prote |
| 70 | 77 | 4.5 | 747 | 2 S35546 | probable ATP-depen |
| 71 | 77 | 4.5 | 878 | 2 B71460 | ATP-dependent RNA |
| 72 | 76.5 | 4.5 | 363 | 2 P97899 | probable outer mem |
| 73 | 76.5 | 4.5 | 449 | 2 D86231 | hypothetical prote |
| 74 | 76.5 | 4.5 | 471 | 2 S45068 | hypothetical prote |
| 75 | 76.5 | 4.5 | 569 | 2 B50554 | 53k glycoprotein - |
| 76 | 76.5 | 4.5 | 657 | 2 S25184 | conserved hypothet |
| 77 | 76.5 | 4.5 | 1965 | 2 T33216 | cspl protein - Cor |
| 78 | 76.5 | 4.5 | 2895 | 2 T08437 | hypothetical prote |
| 79 | 76.5 | 4.5 | 3328 | 2 T30835 | hyperlaestic discs |
| 80 | 76 | 4.5 | 277 | 2 T33570 | breast cancer tumo |
| 81 | 76 | 4.5 | 375 | 2 AC1350 | heak protein (BC 1 |
| 82 | 76 | 4.5 | 390 | 2 T10378 | N-acetylmuramoyl-L |
| 83 | 76 | 4.5 | 464 | 2 S48329 | hypothetical prote |
| 84 | 76 | 4.5 | 572 | 2 T29880 | probable membrane |
| 85 | 76 | 4.5 | 662 | 2 T33271 | hypothetical prote |
| 86 | 76 | 4.5 | 811 | 2 S36109 | hypothetical prote |
| 87 | 76 | 4.5 | 930 | 2 T19283 | osteoblast-specifi |
| 88 | 76 | 4.5 | 942 | 2 JC7316 | hypothetical prote |
| 89 | 76 | 4.5 | 1299 | 2 T42989 | testicular zinc fi |
| 90 | 76 | 4.5 | 1471 | 2 T40117 | hypothetical prote |
| 91 | 76 | 4.5 | 1513 | 2 T33681 | myosin-2 isoform - |
| 92 | 76 | 4.5 | 1687 | 2 T30176 | hypothetical prote |
| 93 | 76 | 4.5 | 1828 | 2 B59254 | Bcf repeat transme |
| 94 | 76 | 4.5 | 1855 | 2 A59254 | myosin heavy chain |
| 95 | 76 | 4.5 | 2581 | 2 AF2545 | myosin heavy chain |
| 96 | 75.5 | 4.5 | 213 | 2 B81360 | hypothetical prote |
| 97 | 75.5 | 4.5 | 363 | 2 D95028 | probable protein d |
| 98 | 75.5 | 4.5 | 403 | 2 T02513 | ABC transporter. A |
| 99 | 75.5 | 4.5 | 414 | 2 B84546 | hypothetical prote |
| 100 | 75.5 | 4.5 | 453 | 2 T00284 | probable tetraacyl |
| 101 | 75.5 | 4.5 | 496 | 2 JC5261 | hypothetical prote |
| 102 | 75.5 | 4.5 | 754 | 2 S50601 | salt-tolerant prot |
| | | | | | hypothetical prote |

| | | | | | | |
|-----|------|-----|------|---|--------|---------------------|
| 103 | 75.5 | 4.5 | 988 | 2 | E96621 | hypothetical prote |
| 104 | 75.5 | 4.5 | 1284 | 2 | T40879 | probable helicase |
| 105 | 75 | 4.4 | 277 | 2 | B90843 | probable protoporp |
| 106 | 75 | 4.4 | 277 | 2 | B85701 | probable protoporp |
| 107 | 75 | 4.4 | 293 | 2 | C90032 | hypothetical prote |
| 108 | 75 | 4.4 | 357 | 2 | A12099 | WD-40 repeat prote |
| 109 | 75 | 4.4 | 426 | 2 | S16416 | gene R46 protein - |
| 110 | 75 | 4.4 | 461 | 2 | C86679 | transcription regu |
| 111 | 75 | 4.4 | 486 | 2 | S15470 | NS53 protein - hum |
| 112 | 75 | 4.4 | 507 | 2 | E71551 | probable monooxyge |
| 113 | 75 | 4.4 | 648 | 2 | UC4674 | SL1 protein - rat |
| 114 | 75 | 4.4 | 775 | 2 | T38352 | hypothetical prote |
| 115 | 75 | 4.4 | 893 | 2 | G88551 | protein M01A6.2 [1 |
| 116 | 75 | 4.4 | 1036 | 2 | S55984 | probable membrane |
| 117 | 75 | 4.4 | 1085 | 2 | T18369 | K-Cl cotransport p |
| 118 | 75 | 4.4 | 1173 | 1 | A53430 | 1-phosphatidylinos |
| 119 | 75 | 4.4 | 1216 | 2 | A28822 | 1-phosphatidylinos |
| 120 | 75 | 4.4 | 1276 | 2 | B96776 | hypothetical prote |
| 121 | 75 | 4.4 | 1334 | 2 | E86451 | probable copla-tyr |
| 122 | 75 | 4.4 | 1334 | 2 | E86451 | insecticidal toxin |
| 123 | 74.5 | 4.4 | 1496 | 2 | AH0447 | hypothetical prote |
| 124 | 74.5 | 4.4 | 357 | 2 | T19336 | argininosuccinate |
| 125 | 74.5 | 4.4 | 437 | 2 | C97020 | vitamin D-binding |
| 126 | 74.5 | 4.4 | 472 | 1 | A35327 | hypothetical prote |
| 127 | 74.5 | 4.4 | 500 | 2 | T44167 | hypothetical prote |
| 128 | 74.5 | 4.4 | 500 | 2 | T43981 | hypothetical prote |
| 129 | 74.5 | 4.4 | 555 | 1 | P1WLP | IL protein - human |
| 130 | 74.5 | 4.4 | 555 | 2 | T23531 | hypothetical prote |
| 131 | 74.5 | 4.4 | 673 | 2 | A71978 | hypothetical prote |
| 132 | 74.5 | 4.4 | 728 | 2 | D84647 | hypothetical prote |
| 133 | 74.5 | 4.4 | 761 | 2 | T09052 | hypothetical prote |
| 134 | 74.5 | 4.4 | 906 | 2 | T47340 | hypothetical prote |
| 135 | 74.5 | 4.4 | 1007 | 2 | T47430 | disease resistance |
| 136 | 74.5 | 4.4 | 1139 | 1 | E64234 | cytadherence-acces |
| 137 | 74.5 | 4.4 | 1342 | 2 | A36223 | kinase-related tra |
| 138 | 74.5 | 4.4 | 1630 | 2 | T00390 | KIA0614 protein - |
| 139 | 74 | 4.4 | 243 | 2 | AB1249 | 3-ketoacyl-acyl ca |
| 140 | 74 | 4.4 | 557 | 2 | T29655 | hypothetical prote |
| 141 | 74 | 4.4 | 818 | 2 | H83904 | hypothetical prote |
| 142 | 74 | 4.4 | 893 | 2 | T29621 | hypothetical prote |
| 143 | 74 | 4.4 | 907 | 2 | T01764 | hypothetical prote |
| 144 | 74 | 4.4 | 962 | 1 | JT0669 | helicase IT-like p |
| 145 | 74 | 4.4 | 1130 | 2 | T20288 | hypothetical prote |
| 146 | 74 | 4.4 | 1141 | 2 | A54962 | sterol regulatory |
| 147 | 74 | 4.4 | 1216 | 2 | A28821 | 1-phosphatidylinos |
| 148 | 74 | 4.4 | 1452 | 2 | T17157 | CL2AA protein - ra |
| 149 | 74 | 4.4 | 1463 | 2 | T17159 | CL2AA protein - ra |
| 150 | 74 | 4.4 | 1467 | 2 | T17160 | CL2BA protein - ra |
| 151 | 74 | 4.4 | 1479 | 2 | T17185 | alpha-latrotoxin r |
| 152 | 74 | 4.4 | 1487 | 2 | T14324 | myosin heavy chain |
| 153 | 74 | 4.4 | 1853 | 1 | A46761 | blmb protein - Eme |
| 154 | 74 | 4.4 | 2156 | 1 | BWASBE | genome polypeptid |
| 155 | 74 | 4.4 | 3924 | 2 | RRVUNE | anmyrin 2, neurona |
| 156 | 73.5 | 4.3 | 330 | 2 | T25169 | hypothetical prote |
| 157 | 73.5 | 4.3 | 386 | 2 | A39732 | H+-transporing tw |
| 158 | 73.5 | 4.3 | 417 | 2 | AH1170 | sugar ABC transpor |
| 159 | 73.5 | 4.3 | 561 | 2 | T27319 | hypothetical prote |
| 160 | 73.5 | 4.3 | 626 | 2 | T27318 | hypothetical prote |
| 161 | 73.5 | 4.3 | 673 | 1 | B64530 | methvl-accepting c |
| 162 | 73.5 | 4.3 | 711 | 2 | T30107 | hypothetical prote |
| 163 | 73.5 | 4.3 | 1204 | 2 | S62506 | alpha-glican synth |
| 164 | 73.5 | 4.3 | 1235 | 2 | S24109 | phosphorylase kina |
| 165 | 73.5 | 4.3 | 1414 | 2 | T33236 | hypothetical prote |
| 166 | 73.5 | 4.3 | 2845 | 2 | I49505 | adenomatous polypo |
| 167 | 73.5 | 4.3 | 3329 | 2 | T42205 | breast cancer susc |
| 168 | 73 | 4.3 | 298 | 2 | G98159 | probable transcrip |
| 169 | 73 | 4.3 | 298 | 2 | AB3128 | transcription regu |
| 170 | 73 | 4.3 | 366 | 2 | A64950 | membrane-bound pen |
| 171 | 73 | 4.3 | 446 | 2 | D64210 | replicative DNA he |
| 172 | 73 | 4.3 | 449 | 2 | I52630 | GABA receptor del |
| 173 | 73 | 4.3 | 472 | 2 | S39553 | tubulin gamma chai |
| 174 | 73 | 4.3 | 485 | 2 | G71239 | hypothetical prote |
| 175 | 73 | 4.3 | 485 | 2 | C64680 | hypothetical prote |
| 176 | 73 | 4.3 | 491 | 2 | A49597 | nonstructural prot |
| 177 | 73 | 4.3 | 491 | 2 | S31783 | V55 protein - bov1 |
| 178 | 73 | 4.3 | 494 | 2 | A89010 | protein R08F11.3 [|
| 179 | 73 | 4.3 | 668 | 1 | VCMVFP | env polypeptid pr |
| 180 | 73 | 4.3 | 671 | 1 | QRSCSN | two-component sens |
| 181 | 73 | 4.3 | 688 | 1 | T33709 | hypothetical prote |
| 182 | 73 | 4.3 | 814 | 2 | D82101 | oxidoreductase, ac |
| 183 | 73 | 4.3 | 1014 | 2 | S48235 | CINI protein - yea |
| 184 | 73 | 4.3 | 1039 | 2 | C64418 | isoleucine-CRMA 11 |
| 185 | 73 | 4.3 | 1548 | 2 | S34583 | serine proteinase |
| 186 | 73 | 4.3 | 1680 | 2 | A43434 | furin (EC 3.4.21.7 |
| 187 | 73 | 4.3 | 1776 | 2 | T30810 | chromatin structur |
| 188 | 72.5 | 4.3 | 1776 | 2 | T34665 | probable copper ho |
| 189 | 72.5 | 4.3 | 204 | 2 | E55183 | hypothetical prote |
| 190 | 72.5 | 4.3 | 242 | 2 | T26699 | hypothetical prote |
| 191 | 72.5 | 4.3 | 468 | 2 | T27746 | hypothetical prote |
| 192 | 72.5 | 4.3 | 484 | 2 | T04381 | NNS-LRR type reas |
| 193 | 72.5 | 4.3 | 504 | 2 | AC2628 | ABC transporter, m |
| 194 | 72.5 | 4.3 | 504 | 2 | B97410 | phosphate ABC tran |
| 195 | 72.5 | 4.3 | 531 | 2 | T29788 | hypothetical prote |
| 196 | 72.5 | 4.3 | 645 | 2 | S29849 | gene p74 protein - |
| 197 | 72.5 | 4.3 | 716 | 2 | S30687 | hypothetical prote |
| 198 | 72.5 | 4.3 | 769 | 2 | F81742 | conserved hypochet |
| 199 | 72.5 | 4.3 | 843 | 2 | S72375 | surface exclusion |
| 200 | 72.5 | 4.3 | 846 | 1 | A47299 | ror-related recept |
| 201 | 72.5 | 4.3 | 1036 | 2 | E84620 | hypothetical prote |
| 202 | 72.5 | 4.3 | 1188 | 2 | T41696 | probable C2-domain |
| 203 | 72.5 | 4.3 | 1223 | 2 | T17345 | hypothetical prote |
| 204 | 72.5 | 4.3 | 1451 | 1 | Q01719 | E2 glycoprotein pr |
| 205 | 72 | 4.3 | 222 | 2 | B55356 | urokinase-type pla |
| 206 | 72 | 4.3 | 310 | 2 | T46035 | ATMYB84 - Arabidop |
| 207 | 72 | 4.3 | 320 | 2 | C90536 | lipoprotein [limpor |
| 208 | 72 | 4.3 | 330 | 2 | F83955 | flagellar motor sw |
| 209 | 72 | 4.3 | 352 | 2 | A97069 | cobalamn biosynth |
| 210 | 72 | 4.3 | 360 | 2 | G64575 | conserved hypochet |
| 211 | 72 | 4.3 | 379 | 2 | AH1871 | two-component resp |
| 212 | 72 | 4.3 | 379 | 2 | A45267 | heterocyst pattern |
| 213 | 72 | 4.3 | 387 | 2 | C82545 | succinyl-CoA synth |
| 214 | 72 | 4.3 | 430 | 2 | C72014 | poly A polymerase |
| 215 | 72 | 4.3 | 430 | 2 | D86611 | poly A polymerase |
| 216 | 72 | 4.3 | 430 | 2 | C81526 | gamma-aminobutyric |
| 217 | 72 | 4.3 | 449 | 2 | A36303 | hypothetical prote |
| 218 | 72 | 4.3 | 454 | 2 | T05168 | hypothetical prote |
| 219 | 72 | 4.3 | 470 | 2 | T29380 | hypothetical prote |
| 220 | 72 | 4.3 | 477 | 2 | AC1923 | site-specific DNA- |
| 221 | 72 | 4.3 | 499 | 2 | F87373 | tyrptophan halogen |
| 222 | 72 | 4.3 | 600 | 1 | D65000 | NADH2 dehydrogenas |
| 223 | 72 | 4.3 | 654 | 1 | HMIVC8 | hemagglutinin prec |
| 224 | 72 | 4.3 | 655 | 2 | S07412 | hemagglutinin-este |
| 225 | 72 | 4.3 | 712 | 2 | E86660 | HYPOVERTICAL PROTEI |
| 226 | 72 | 4.3 | 768 | 2 | T17462 | disease resistance |
| 227 | 72 | 4.3 | 1069 | 2 | D85383 | hypothetical prote |
| 228 | 72 | 4.3 | 1166 | 2 | S33812 | myosin-like protei |
| 229 | 72 | 4.3 | 1199 | 2 | T33337 | hypothetical prote |
| 230 | 72 | 4.3 | 1411 | 2 | A84460 | probable retroelem |
| 231 | 72 | 4.3 | 1784 | 1 | E86921 | polyketide synthas |
| 232 | 72 | 4.3 | 3071 | 2 | T50345 | vacuolar protein s |
| 233 | 72 | 4.3 | 135 | 2 | T15610 | hypothetical prote |
| 234 | 71.5 | 4.2 | 173 | 2 | T18601 | hypothetical prote |
| 235 | 71.5 | 4.2 | 222 | 2 | B41643 | urokinase-type pla |
| 236 | 71.5 | 4.2 | 322 | 2 | C86112 | phosphatidylserine |
| 237 | 71.5 | 4.2 | 332 | 2 | C91271 | phosphatidylserine |
| 238 | 71.5 | 4.2 | 332 | 2 | A29234 | phosphatidylserine |
| 239 | 71.5 | 4.2 | 359 | 2 | F91219 | hypothetical prote |
| 240 | 71.5 | 4.2 | 359 | 2 | H86065 | hypothetical prote |
| 241 | 71.5 | 4.2 | 359 | 2 | H86065 | hypothetical prote |
| 242 | 71.5 | 4.2 | 359 | 2 | S48368 | probable membrane |
| 243 | 71.5 | 4.2 | 362 | 2 | T02057 | fructose-bisphosph |
| 244 | 71.5 | 4.2 | 400 | 2 | T32705 | hypothetical prote |
| 245 | 71.5 | 4.2 | 412 | 2 | C82522 | type I restrictio |
| 246 | 71.5 | 4.2 | 424 | 2 | D81739 | protoporphyrinogen |
| 247 | 71.5 | 4.2 | 428 | 2 | S07916 | RF4 protein - yeas |
| 248 | 71.5 | 4.2 | 453 | 2 | S59401 | hypothetical prote |
| 249 | 71.5 | 4.2 | 621 | 2 | H70334 | hypothetical prote |

| | | | | | | | | | | | | | |
|-----|------|-----|------|---|--------|---------------------|-----|------|-----|------|---|--------|-----------------------|
| 249 | 71.5 | 4.2 | 658 | 2 | D69431 | methionine-cRNA 1i | 322 | 70.5 | 4.2 | 1805 | 1 | A64224 | hypothetical prote |
| 250 | 71.5 | 4.2 | 691 | 2 | A34708 | vacuolar protein-8 | 323 | 70.5 | 4.2 | 1878 | 2 | B86189 | hypothetical prote |
| 251 | 71.5 | 4.2 | 745 | 2 | H96760 | unknown protein [i | 324 | 70.5 | 4.2 | 1942 | 2 | B71426 | hypothetical prote |
| 252 | 71.5 | 4.2 | 751 | 2 | F87789 | protein C34G6.2 [i | 325 | 70.5 | 4.2 | 1984 | 2 | T13171 | probable vitellog |
| 253 | 71.5 | 4.2 | 796 | 1 | UCL285 | protein-tyrosine-p | 326 | 70.5 | 4.2 | 2233 | 2 | T28669 | surfactant protein 5i |
| 254 | 71.5 | 4.2 | 861 | 2 | T27164 | hypothetical prote | 327 | 70.5 | 4.2 | 2843 | 1 | R8HUPP | adenomatous polyo |
| 255 | 71.5 | 4.2 | 1056 | 2 | S56039 | R1c1 protein - yea | 328 | 70.5 | 4.2 | 3329 | 2 | T30904 | breast cancer tumo |
| 256 | 71.5 | 4.2 | 1068 | 2 | S64015 | pliotropic drug r | 329 | 70 | 4.1 | 191 | 2 | AD0165 | probable lipoprote |
| 257 | 71.5 | 4.2 | 1086 | 2 | T33893 | hypothetical prote | 330 | 70 | 4.1 | 200 | 2 | T01335 | hypothetical prote |
| 258 | 71.5 | 4.2 | 1286 | 2 | T18734 | hypothetical prote | 331 | 70 | 4.1 | 247 | 2 | G82956 | hypothetical prote |
| 259 | 71.5 | 4.2 | 2867 | 2 | AG3481 | cellobiose-phospho | 332 | 70 | 4.1 | 256 | 2 | AB1277 | probable oxidoredu |
| 260 | 71 | 4.2 | 198 | 2 | AP1870 | hypothetical prote | 333 | 70 | 4.1 | 269 | 2 | S48978 | hypothetical prote |
| 261 | 71 | 4.2 | 220 | 2 | T21730 | hypothetical prote | 334 | 70 | 4.1 | 271 | 2 | T33013 | hypothetical prote |
| 262 | 71 | 4.2 | 234 | 2 | S17956 | lung protein - Pho | 335 | 70 | 4.1 | 275 | 2 | A82257 | oxidoreductase, sh |
| 263 | 71 | 4.2 | 256 | 1 | DPFG | beta-neoendorphin | 336 | 70 | 4.1 | 280 | 2 | H72593 | hypothetical prote |
| 264 | 71 | 4.2 | 257 | 1 | B96780 | chaumatin-like pro | 337 | 70 | 4.1 | 328 | 2 | C72386 | hypothetical prote |
| 265 | 71 | 4.2 | 307 | 2 | T14823 | probable glycoprot | 338 | 70 | 4.1 | 373 | 2 | B82697 | rod shape-determi |
| 266 | 71 | 4.2 | 327 | 2 | T09027 | hypothetical prote | 339 | 70 | 4.1 | 449 | 2 | A34625 | gamma-aminobutylic |
| 267 | 71 | 4.2 | 332 | 2 | C64073 | rbs repressor homo | 340 | 70 | 4.1 | 462 | 2 | S53084 | myel protein - Ara |
| 268 | 71 | 4.2 | 366 | 2 | C65800 | probable cytochrom | 341 | 70 | 4.1 | 521 | 2 | T01212 | hypothetical prote |
| 269 | 71 | 4.2 | 366 | 2 | G90951 | probable cytochrom | 342 | 70 | 4.1 | 578 | 2 | T41715 | hypothetical prote |
| 270 | 71 | 4.2 | 455 | 2 | S56695 | 1-aminocyclopropan | 343 | 70 | 4.1 | 585 | 2 | T47364 | hypothetical prote |
| 271 | 71 | 4.2 | 482 | 2 | A34924 | complement C3b/Cab | 344 | 70 | 4.1 | 608 | 2 | T47363 | hypothetical prote |
| 272 | 71 | 4.2 | 511 | 2 | B82228 | histidine ammonia- | 345 | 70 | 4.1 | 640 | 1 | HM1VEA | hemagglutinin prec |
| 273 | 71 | 4.2 | 566 | 2 | S19063 | hypothetical prote | 346 | 70 | 4.1 | 665 | 2 | H69101 | haemagglutinin r |
| 274 | 71 | 4.2 | 600 | 2 | C65869 | NADH dehydrogenase | 347 | 70 | 4.1 | 727 | 2 | T08920 | hypothetical prote |
| 275 | 71 | 4.2 | 600 | 2 | B91025 | NADH dehydrogenase | 348 | 70 | 4.1 | 790 | 2 | T19040 | hypothetical prote |
| 276 | 71 | 4.2 | 640 | 1 | HM1VEB | hemagglutinin prec | 349 | 70 | 4.1 | 835 | 2 | T15590 | hypothetical prote |
| 277 | 71 | 4.2 | 640 | 1 | HM1VEC | hemagglutinin prec | 350 | 70 | 4.1 | 888 | 2 | T01081 | hypothetical prote |
| 278 | 71 | 4.2 | 751 | 2 | AD2168 | phycocytrome-like p | 351 | 70 | 4.1 | 956 | 2 | T19046 | hypothetical prote |
| 279 | 71 | 4.2 | 765 | 2 | A11284 | cobalamin-independ | 352 | 70 | 4.1 | 1048 | 2 | T19045 | ras GTPase-activat |
| 280 | 71 | 4.2 | 776 | 2 | C96554 | unknown protein [i | 353 | 70 | 4.1 | 1085 | 2 | T31429 | ras GTPase-activat |
| 281 | 71 | 4.2 | 836 | 2 | S36110 | osteoblast-specifi | 354 | 70 | 4.1 | 1137 | 2 | D89610 | K-Cl cotransport p |
| 282 | 71 | 4.2 | 849 | 1 | S51527 | S-receptor Kinase | 355 | 70 | 4.1 | 1170 | 2 | T19042 | ras GTPase-activat |
| 283 | 71 | 4.2 | 943 | 2 | E91286 | probable ATP-depen | 356 | 70 | 4.1 | 1178 | 2 | S76370 | sensory transducti |
| 284 | 71 | 4.2 | 951 | 2 | G82965 | conserved hypotnet | 357 | 70 | 4.1 | 1207 | 2 | T19041 | ras GTPase-activat |
| 285 | 71 | 4.2 | 952 | 2 | A86128 | probable ATP-depen | 358 | 70 | 4.1 | 1259 | 2 | T19043 | ras GTPase-activat |
| 286 | 71 | 4.2 | 966 | 2 | B84481 | hypothetical prote | 359 | 70 | 4.1 | 1322 | 2 | T01842 | hypothetical prote |
| 287 | 71 | 4.2 | 1221 | 2 | T30529 | ubiquitin carboxyl | 360 | 70 | 4.1 | 1358 | 2 | A29360 | SIR4 protein - yea |
| 288 | 71 | 4.2 | 1240 | 2 | T04193 | hypothetical prote | 361 | 70 | 4.1 | 1409 | 1 | OFFFCP | copII polyprotein |
| 289 | 71 | 4.2 | 1453 | 2 | G96613 | hypothetical prote | 362 | 70 | 4.1 | 1420 | 2 | T17158 | CL2B8 protein - ra |
| 290 | 71 | 4.2 | 2490 | 1 | A54971 | protein-tyrosine-p | 363 | 70 | 4.1 | 1435 | 2 | T4611 | CL2B8 protein - ra |
| 291 | 71 | 4.2 | 4717 | 2 | T41581 | hypothetical colle | 364 | 70 | 4.1 | 1748 | 2 | S63127 | hypothetical prote |
| 292 | 70.5 | 4.2 | 152 | 2 | A81664 | hypothetical prote | 365 | 70 | 4.1 | 1810 | 2 | S65973 | probable membrane |
| 293 | 70.5 | 4.2 | 334 | 2 | T32256 | hypothetical prote | 366 | 70 | 4.1 | 1956 | 2 | T16416 | hypothetical prote |
| 294 | 70.5 | 4.2 | 411 | 2 | F87644 | transcription regu | 367 | 70 | 4.1 | 1966 | 2 | T08991 | hypothetical prote |
| 295 | 70.5 | 4.2 | 429 | 1 | S16043 | threonine synthase | 368 | 70 | 4.1 | 2052 | 2 | T37711 | probable n-end-rec |
| 296 | 70.5 | 4.2 | 469 | 2 | S44193 | tubulin gamma chai | 369 | 70 | 4.1 | 2052 | 2 | T18519 | myosin X - bovine |
| 297 | 70.5 | 4.2 | 472 | 1 | A53236 | transcription fact | 370 | 70 | 4.1 | 2493 | 2 | S45734 | probable membrane |
| 298 | 70.5 | 4.2 | 474 | 2 | T50558 | tubulin gamma-2 ch | 371 | 70 | 4.1 | 2531 | 2 | A46019 | notch-1 protein - |
| 299 | 70.5 | 4.2 | 496 | 2 | E72032 | general secretion p | 372 | 69.5 | 4.1 | 152 | 2 | A61282 | hypothetical prote |
| 300 | 70.5 | 4.2 | 496 | 2 | F86592 | sensor protein kin | 373 | 69.5 | 4.1 | 209 | 2 | T02394 | hypothetical prote |
| 301 | 70.5 | 4.2 | 517 | 2 | D86804 | insulin-like growt | 374 | 69.5 | 4.1 | 294 | 2 | AB0542 | hypothetical prote |
| 302 | 70.5 | 4.2 | 605 | 2 | A41915 | conserved hypotnet | 375 | 69.5 | 4.1 | 309 | 2 | B96566 | F6D8.20 [imported] |
| 303 | 70.5 | 4.2 | 634 | 2 | T41319 | hypothetical prote | 376 | 69.5 | 4.1 | 353 | 2 | T25775 | hypothetical prote |
| 304 | 70.5 | 4.2 | 654 | 2 | T30136 | hypothetical prote | 377 | 69.5 | 4.1 | 356 | 2 | T20656 | hypothetical prote |
| 305 | 70.5 | 4.2 | 662 | 2 | AG2420 | hypothetical prote | 378 | 69.5 | 4.1 | 358 | 2 | H81618 | arginine kinase-re |
| 306 | 70.5 | 4.2 | 665 | 2 | E86775 | ribonuclease [impo | 379 | 69.5 | 4.1 | 358 | 2 | B86578 | arginine kinase [i |
| 307 | 70.5 | 4.2 | 680 | 2 | S17982 | Kallmann syndrome | 380 | 69.5 | 4.1 | 358 | 2 | B72045 | cytoplasmic alpha- |
| 308 | 70.5 | 4.2 | 735 | 2 | D70174 | methyl-accepting c | 381 | 69.5 | 4.1 | 494 | 2 | AD0751 | hypothetical prote |
| 309 | 70.5 | 4.2 | 893 | 2 | B87244 | conserved hypotnet | 382 | 69.5 | 4.1 | 604 | 2 | T43014 | hypothetical prote |
| 310 | 70.5 | 4.2 | 909 | 1 | ORXIL2 | LDL receptor 2 pre | 383 | 69.5 | 4.1 | 626 | 2 | T00507 | polyprotein - deng |
| 311 | 70.5 | 4.2 | 944 | 2 | S56936 | vacuolar protein-s | 384 | 69.5 | 4.1 | 626 | 2 | T49110 | hypothetical prote |
| 312 | 70.5 | 4.2 | 1009 | 2 | T47327 | hypothetical prote | 385 | 69.5 | 4.1 | 652 | 2 | B84568 | probable calmoduli |
| 313 | 70.5 | 4.2 | 1086 | 2 | T14114 | K-cl cotransport p | 386 | 69.5 | 4.1 | 728 | 2 | T14472 | hypothetical prote |
| 314 | 70.5 | 4.2 | 1120 | 2 | JC7765 | mitotic spindle as | 387 | 69.5 | 4.1 | 850 | 2 | T14472 | S-receptor kinase |
| 315 | 70.5 | 4.2 | 1136 | 1 | USBS81 | paraaporal crystal | 388 | 69.5 | 4.1 | 851 | 2 | T47305 | hypothetical prote |
| 316 | 70.5 | 4.2 | 1142 | 2 | A45031 | cyasteine-rich fibr | 389 | 69.5 | 4.1 | 1001 | 2 | C66181 | hypothetical prote |
| 317 | 70.5 | 4.2 | 1180 | 2 | A26858 | paraaporal crystal | 390 | 69.5 | 4.1 | 1175 | 2 | S82417 | E-selectin ligand- |
| 318 | 70.5 | 4.2 | 1180 | 2 | I39870 | paraaporal crystal | 391 | 69.5 | 4.1 | 1264 | 2 | B84534 | probable polyprotein |
| 319 | 70.5 | 4.2 | 1279 | 2 | E64709 | type IIS restricti | 392 | 69.5 | 4.1 | 1358 | 2 | A03905 | genome polyprotein |
| 320 | 70.5 | 4.2 | 1553 | 2 | T31436 | DNA-directed RNA p | 393 | 69.5 | 4.1 | 2120 | 2 | T30243 | alpha tectorin - c |
| 321 | 70.5 | 4.2 | 1770 | 2 | S69953 | Tyb protein - yea | 394 | 69.5 | 4.1 | 2787 | 2 | S45416 | TEH1 protein - yea |

| | | | | | | |
|-----|------|-----|------|---|--------|--------------------|
| 395 | 69.5 | 4.1 | 3137 | 2 | A37797 | collagen alpha 3(V |
| 396 | 69 | 4.1 | 217 | 2 | AF1348 | competive negativ |
| 397 | 69 | 4.1 | 254 | 1 | DFHU | beta-neoendorphin |
| 398 | 69 | 4.1 | 402 | 2 | T29478 | hypothetical prote |
| 399 | 69 | 4.1 | 409 | 1 | D69280 | cell division cont |
| 400 | 69 | 4.1 | 421 | 2 | S75494 | hypothetical prote |
| 401 | 69 | 4.1 | 436 | 2 | B84071 | spore outer layer |
| 402 | 69 | 4.1 | 466 | 2 | B69842 | probable oxidoredu |
| 403 | 69 | 4.1 | 520 | 1 | S44099 | brain-derived neur |
| 404 | 69 | 4.1 | 523 | 2 | S68517 | nuclear hormone re |
| 405 | 69 | 4.1 | 538 | 1 | VGNZMU | cell fusion glycop |
| 406 | 69 | 4.1 | 538 | 2 | S52472 | cell fusion protei |
| 407 | 69 | 4.1 | 582 | 2 | D72075 | hypothetical prote |
| 408 | 69 | 4.1 | 600 | 2 | AD0797 | NADH2 dehydrogenas |
| 409 | 69 | 4.1 | 629 | 2 | F84207 | heat shock protein |
| 410 | 69 | 4.1 | 629 | 2 | G81592 | hypothetical prote |
| 411 | 69 | 4.1 | 629 | 2 | B86547 | hypothetical prote |
| 412 | 69 | 4.1 | 679 | 2 | A40351 | adhesion-type prot |
| 413 | 69 | 4.1 | 699 | 2 | T09483 | Cys-rich protein R |
| 414 | 69 | 4.1 | 713 | 2 | I50128 | fibroblast growth |
| 415 | 69 | 4.1 | 818 | 1 | S44098 | brain-derived neur |
| 416 | 69 | 4.1 | 1124 | 1 | I58388 | protein-tyrosine k |
| 417 | 69 | 4.1 | 1131 | 2 | U00382 | phytochrome A - ma |
| 418 | 69 | 4.1 | 1241 | 2 | U00466 | potassium transpor |
| 419 | 69 | 4.1 | 1260 | 1 | S05479 | neural cell adhesi |
| 420 | 69 | 4.1 | 1379 | 2 | T45119 | FIM protein (impor |
| 421 | 69 | 4.1 | 1446 | 2 | T13018 | hypothetical prote |
| 422 | 69 | 4.1 | 1770 | 2 | S45842 | Tyb protein - yeas |
| 423 | 69 | 4.1 | 1819 | 2 | B86410 | protein F3M18.14 f |
| 424 | 69 | 4.1 | 2026 | 1 | ORBY | adenylate cyclase |
| 425 | 69 | 4.1 | 2123 | 2 | S55089 | probable acetyl-Co |
| 426 | 69 | 4.1 | 2437 | 2 | S42612 | transmembrane prot |
| 427 | 69 | 4.1 | 2554 | 1 | TVEF7L | kinase-related pro |
| 428 | 69 | 4.1 | 2910 | 2 | T42214 | otogelin - mouse |
| 429 | 69 | 4.1 | 4919 | 2 | T31105 | hypothetical prote |
| 430 | 68.5 | 4.0 | 325 | 2 | A40084 | exogastrula-induct |
| 431 | 68.5 | 4.0 | 338 | 2 | B83806 | transcription regu |
| 432 | 68.5 | 4.0 | 347 | 2 | C64105 | o-succinylbenzoate |
| 433 | 68.5 | 4.0 | 355 | 2 | T23406 | hypothetical prote |
| 434 | 68.5 | 4.0 | 355 | 2 | F83914 | hypothetical prote |
| 435 | 68.5 | 4.0 | 360 | 2 | A81687 | histidinol-phospha |
| 436 | 68.5 | 4.0 | 370 | 2 | F75173 | hypothetical prote |
| 437 | 68.5 | 4.0 | 447 | 2 | T49777 | hypothetical prote |
| 438 | 68.5 | 4.0 | 486 | 2 | S31808 | probable beta-humc |
| 439 | 68.5 | 4.0 | 494 | 2 | A42170 | VPS protein - huma |
| 440 | 68.5 | 4.0 | 521 | 2 | H69317 | zinc finger protei |
| 441 | 68.5 | 4.0 | 531 | 2 | T01415 | conserved hypotet |
| 442 | 68.5 | 4.0 | 545 | 2 | H83342 | basic leucine zipp |
| 443 | 68.5 | 4.0 | 549 | 2 | G91178 | periplasmic trehal |
| 444 | 68.5 | 4.0 | 549 | 2 | H86024 | cytoplasmic trehal |
| 445 | 68.5 | 4.0 | 549 | 2 | S47739 | cytoplasmic trehal |
| 446 | 68.5 | 4.0 | 575 | 2 | T45668 | probable alpha,alp |
| 447 | 68.5 | 4.0 | 584 | 2 | S76210 | hypothetical prote |
| 448 | 68.5 | 4.0 | 593 | 2 | T04446 | hypothetical prote |
| 449 | 68.5 | 4.0 | 607 | 2 | S60658 | hypothetical prote |
| 450 | 68.5 | 4.0 | 622 | 2 | F71174 | legumin - Gnetum g |
| 451 | 68.5 | 4.0 | 636 | 2 | T10569 | hypothetical prote |
| 452 | 68.5 | 4.0 | 654 | 2 | T29247 | probable serine/th |
| 453 | 68.5 | 4.0 | 666 | 2 | DA2510 | hypothetical prote |
| 454 | 68.5 | 4.0 | 710 | 2 | T31197 | Oil protein - vacc |
| 455 | 68.5 | 4.0 | 717 | 2 | S47857 | transposon protei |
| 456 | 68.5 | 4.0 | 939 | 2 | S75908 | basic protein, cyt |
| 457 | 68.5 | 4.0 | 988 | 2 | T51054 | hypothetical prote |
| 458 | 68.5 | 4.0 | 1004 | 2 | T00795 | related to alpha-a |
| 459 | 68.5 | 4.0 | 1104 | 2 | T17367 | 266 proteasome reg |
| 460 | 68.5 | 4.0 | 1104 | 1 | SYBYVT | potassium channel |
| 461 | 68.5 | 4.0 | 1170 | 2 | S52525 | valine-tRNA ligase |
| 462 | 68.5 | 4.0 | 1246 | 2 | C36806 | probable membrane |
| 463 | 68.5 | 4.0 | 1461 | 2 | B84589 | hypothetical prote |
| 464 | 68.5 | 4.0 | 1570 | 2 | T18272 | probable retroelem |
| 465 | 68 | 4.0 | 127 | 1 | A46528 | 1-phosphatidylinos |
| 466 | 68 | 4.0 | 130 | 2 | I54553 | phosphatidylinosit |
| 467 | 68 | 4.0 | 167 | 1 | IERCAL | gene Tnb protein - |
| | | | | | | linB protein - Esc |
| 468 | 68 | 4.0 | 167 | 2 | AB0781 | insertion element |
| 469 | 68 | 4.0 | 167 | 2 | AD1041 | insertion element |
| 470 | 68 | 4.0 | 167 | 2 | AC0978 | insertion element |
| 471 | 68 | 4.0 | 197 | 2 | S28465 | quaternary amine t |
| 472 | 68 | 4.0 | 200 | 2 | B54022 | ADP-ribosylation f |
| 473 | 68 | 4.0 | 331 | 2 | B89759 | conserved hypotet |
| 474 | 68 | 4.0 | 371 | 2 | E71932 | probable outer mem |
| 475 | 68 | 4.0 | 396 | 2 | A40066 | corticosteroid-bin |
| 476 | 68 | 4.0 | 499 | 2 | T18639 | hypothetical prote |
| 477 | 68 | 4.0 | 501 | 2 | S75951 | hypothetical prote |
| 478 | 68 | 4.0 | 518 | 2 | A40942 | hypothetical prote |
| 479 | 68 | 4.0 | 522 | 2 | F97756 | phosphoprotein pho |
| 480 | 68 | 4.0 | 607 | 2 | A95970 | hypothetical prote |
| 481 | 68 | 4.0 | 621 | 2 | T39204 | conserved hypotet |
| 482 | 68 | 4.0 | 652 | 2 | B70785 | hypothetical prote |
| 483 | 68 | 4.0 | 683 | 2 | D71680 | probable asparagin |
| 484 | 68 | 4.0 | 693 | 2 | T25878 | ribonuclease E (rn |
| 485 | 68 | 4.0 | 734 | 2 | A82047 | hypothetical prote |
| 486 | 68 | 4.0 | 735 | 2 | AE1858 | primosomal replica |
| 487 | 68 | 4.0 | 802 | 1 | A36065 | anthranilate synth |
| 488 | 68 | 4.0 | 829 | 1 | A47373 | protein-tyrosine-p |
| 489 | 68 | 4.0 | 1003 | 2 | T24545 | protein-tyrosine-p |
| 490 | 68 | 4.0 | 1014 | 2 | T24412 | hypothetical prote |
| 491 | 68 | 4.0 | 1300 | 2 | A36502 | hypothetical prote |
| 492 | 68 | 4.0 | 1352 | 2 | F86246 | insulin receptor-x |
| 493 | 68 | 4.0 | 1352 | 2 | T47925 | hypothetical prote |
| 494 | 68 | 4.0 | 1526 | 2 | T19473 | copia-type polypro |
| 495 | 68 | 4.0 | 1697 | 2 | T00079 | hypothetical prote |
| 496 | 68 | 4.0 | 2338 | 2 | T25810 | hypothetical prote |
| 497 | 68 | 4.0 | 2820 | 2 | UC5196 | neurofibromin I - |
| 498 | 67.5 | 4.0 | 163 | 2 | B70854 | hypothetical prote |
| 499 | 67.5 | 4.0 | 196 | 2 | T26943 | hypothetical prote |
| 500 | 67.5 | 4.0 | 215 | 2 | C81731 | hypothetical prote |
| 501 | 67.5 | 4.0 | 228 | 2 | B69758 | hypothetical prote |
| 502 | 67.5 | 4.0 | 230 | 2 | B86139 | hypothetical prote |
| 503 | 67.5 | 4.0 | 248 | 2 | A25530 | hypothetical prote |
| 504 | 67.5 | 4.0 | 248 | 2 | S11390 | tropomyosin, fibro |
| 505 | 67.5 | 4.0 | 248 | 2 | S34124 | tropomyosin 5 - mo |
| 506 | 67.5 | 4.0 | 248 | 2 | S34124 | tropomyosin isofor |
| 507 | 67.5 | 4.0 | 264 | 2 | B71509 | tropomyosin - rat |
| 508 | 67.5 | 4.0 | 298 | 2 | B34791 | hypothetical prote |
| 509 | 67.5 | 4.0 | 303 | 2 | T21125 | interleukin-7 rece |
| 510 | 67.5 | 4.0 | 382 | 2 | I48190 | hypothetical prote |
| 511 | 67.5 | 4.0 | 450 | 2 | T30970 | surface antigen - |
| 512 | 67.5 | 4.0 | 478 | 2 | H82185 | hypothetical prote |
| 513 | 67.5 | 4.0 | 483 | 2 | B89364 | 6-phospho-beta-glu |
| 514 | 67.5 | 4.0 | 494 | 1 | B45738 | protein F26D2.3 [i |
| 515 | 67.5 | 4.0 | 494 | 2 | H91217 | alpha-amylase (EC |
| 516 | 67.5 | 4.0 | 494 | 2 | A86064 | guanosine pentapho |
| 517 | 67.5 | 4.0 | 544 | 2 | S46099 | guanosine pentapho |
| 518 | 67.5 | 4.0 | 554 | 2 | G82272 | hypothetical prote |
| 519 | 67.5 | 4.0 | 637 | 2 | B33785 | DNA repair protein |
| 520 | 67.5 | 4.0 | 671 | 2 | AF0042 | myelin-associated |
| 521 | 67.5 | 4.0 | 688 | 1 | UC1469 | probable oxidoredu |
| 522 | 67.5 | 4.0 | 696 | 2 | G81262 | beta-adrenergic-re |
| 523 | 67.5 | 4.0 | 809 | 2 | T16448 | probable integral |
| 524 | 67.5 | 4.0 | 860 | 2 | F86349 | hypothetical prote |
| 525 | 67.5 | 4.0 | 905 | 2 | S29329 | hypothetical prote |
| 526 | 67.5 | 4.0 | 1014 | 1 | DEBY | hypothetical prote |
| 527 | 67.5 | 4.0 | 1035 | 2 | F64114 | oxoglutarate dehyd |
| 528 | 67.5 | 4.0 | 1123 | 2 | AD0865 | type I site-specif |
| 529 | 67.5 | 4.0 | 1123 | 2 | T16388 | exonuclease V chat |
| 530 | 67.5 | 4.0 | 1451 | 2 | T18534 | hypothetical prote |
| 531 | 67.5 | 4.0 | 1477 | 2 | T18534 | protein-tyrosine k |
| 532 | 67.5 | 4.0 | 1570 | 2 | AC2012 | hypothetical prote |
| 533 | 67.5 | 4.0 | 1753 | 2 | S30855 | hypothetical prote |
| 534 | 67.5 | 4.0 | 1792 | 2 | T08878 | hypothetical prote |
| 535 | 67.5 | 4.0 | 1895 | 2 | S50240 | supervillin P205 - |
| 536 | 67.5 | 4.0 | 1932 | 2 | S53409 | 1,3-beta-glucan sy |
| 537 | 67.5 | 4.0 | 1951 | 2 | B43963 | probable membrane |
| 538 | 67.5 | 4.0 | 2227 | 1 | GNNYMK | RNA viral polymera |
| 539 | 67.5 | 4.0 | 3898 | 1 | GNNYHB | genome polypeptid |
| 540 | 67.5 | 4.0 | 4063 | 2 | T42993 | genome polypeptid |
| | | | 4101 | 2 | T23630 | probable spectrin |
| | | | | | | hypothetical prote |

| | | | | | | | | | | | | | |
|-----|----|-----|------|---|--------|----------------------|-----|------|-----|------|---|--------|--------------------|
| 541 | 67 | 4.0 | 163 | 2 | P96569 | hypothetical prote | 614 | 66.5 | 3.9 | 406 | 2 | AE2455 | hypothetical prote |
| 542 | 67 | 4.0 | 283 | 2 | H86547 | hypothetical prote | 615 | 66.5 | 3.9 | 408 | 2 | H84825 | hypothetical prote |
| 543 | 67 | 4.0 | 283 | 2 | G72075 | hypothetical prote | 616 | 66.5 | 3.9 | 431 | 2 | T47528 | hypothetical prote |
| 544 | 67 | 4.0 | 303 | 2 | D90694 | recombinatn asso | 617 | 66.5 | 3.9 | 431 | 2 | B86671 | hypothetical prote |
| 545 | 67 | 4.0 | 303 | 2 | H85534 | hypothetical prote | 618 | 66.5 | 3.9 | 448 | 2 | T39314 | hypothetical prote |
| 546 | 67 | 4.0 | 303 | 2 | S41303 | yaad protein - Bac | 619 | 66.5 | 3.9 | 472 | 2 | S39507 | glucuronosyl trans |
| 547 | 67 | 4.0 | 366 | 2 | S53898 | probable membrane | 620 | 66.5 | 3.9 | 474 | 2 | T47957 | tubulin gamma-1 ch |
| 548 | 67 | 4.0 | 366 | 2 | A71880 | probable outer mem | 621 | 66.5 | 3.9 | 478 | 2 | T33735 | hypothetical prote |
| 549 | 67 | 4.0 | 367 | 2 | T51455 | auxin transport pr | 622 | 66.5 | 3.9 | 483 | 2 | T39839 | hypothetical prote |
| 550 | 67 | 4.0 | 386 | 2 | F83958 | succinyl-CoA synth | 623 | 66.5 | 3.9 | 491 | 2 | F87793 | hypothetical prote |
| 551 | 67 | 4.0 | 451 | 2 | T40736 | probable pseudouri | 624 | 66.5 | 3.9 | 524 | 2 | S33640 | protein C27A12.6 l |
| 552 | 67 | 4.0 | 457 | 2 | E71614 | membrane transport | 625 | 66.5 | 3.9 | 537 | 1 | JQ1619 | cell fusion glycop |
| 553 | 67 | 4.0 | 481 | 2 | AE2327 | hypothetical prote | 626 | 66.5 | 3.9 | 633 | 2 | H96748 | unknown protein T1 |
| 554 | 67 | 4.0 | 483 | 2 | AC1811 | O-succinylbenzoyl- | 627 | 66.5 | 3.9 | 676 | 2 | B47232 | Kallmann syndrome |
| 555 | 67 | 4.0 | 493 | 2 | T10054 | pyruvate kinase (E | 628 | 66.5 | 3.9 | 714 | 2 | S66639 | hypothetical prote |
| 556 | 67 | 4.0 | 519 | 1 | A54549 | glycan 1,4-alpha-g | 629 | 66.5 | 3.9 | 772 | 2 | B82888 | phenylalanine-tRNA |
| 557 | 67 | 4.0 | 532 | 2 | B84657 | hypothetical prote | 630 | 66.5 | 3.9 | 787 | 2 | S47245 | ActA protein - Lis |
| 558 | 67 | 4.0 | 534 | 2 | A83420 | membrane-bound lye | 631 | 66.5 | 3.9 | 805 | 2 | T21957 | hypothetical prote |
| 559 | 67 | 4.0 | 538 | 1 | VGNZMM | cell fusion glycop | 632 | 66.5 | 3.9 | 821 | 2 | A12417 | hypothetical prote |
| 560 | 67 | 4.0 | 556 | 2 | T51501 | hypothetical prote | 633 | 66.5 | 3.9 | 846 | 2 | T38840 | hypothetical trp-a |
| 561 | 67 | 4.0 | 574 | 2 | T08434 | miato protein - f | 634 | 66.5 | 3.9 | 878 | 2 | F64425 | valine-tRNA ligase |
| 562 | 67 | 4.0 | 576 | 2 | T46385 | hypothetical prote | 635 | 66.5 | 3.9 | 890 | 2 | G64740 | [protein-Pil] urid |
| 563 | 67 | 4.0 | 583 | 2 | T10051 | pyruvate kinase (E | 636 | 66.5 | 3.9 | 890 | 2 | A85501 | protein Pil-uridy |
| 564 | 67 | 4.0 | 597 | 2 | T41062 | hypothetical prote | 637 | 66.5 | 3.9 | 890 | 2 | A90650 | protein Pil-uridy |
| 565 | 67 | 4.0 | 600 | 2 | B84948 | NADH2 dehydrogen | 638 | 66.5 | 3.9 | 928 | 2 | T24868 | hypothetical prote |
| 566 | 67 | 4.0 | 636 | 2 | G96717 | hypothetical prote | 639 | 66.5 | 3.9 | 1014 | 2 | T17275 | hypothetical prote |
| 567 | 67 | 4.0 | 640 | 2 | T19346 | hypothetical prote | 640 | 66.5 | 3.9 | 1047 | 2 | B17402 | hypothetical prote |
| 568 | 67 | 4.0 | 652 | 2 | A84461 | probable fibronin I | 641 | 66.5 | 3.9 | 1199 | 2 | T18348 | hypothetical prote |
| 569 | 67 | 4.0 | 653 | 2 | B82306 | probable lipoprote | 642 | 66.5 | 3.9 | 1426 | 2 | T00337 | probable pol polyp |
| 570 | 67 | 4.0 | 654 | 2 | B85802 | hypothetical prote | 643 | 66.5 | 3.9 | 1452 | 1 | VG1H79 | E2 glycoprotein pr |
| 571 | 67 | 4.0 | 654 | 2 | F90953 | sensory transducer | 644 | 66.5 | 3.9 | 1502 | 1 | RGBYH1 | CYC1/CYP3 transcri |
| 572 | 67 | 4.0 | 658 | 2 | T46984 | hypothetical prote | 645 | 66.5 | 3.9 | 1755 | 2 | S57045 | Yyb protein - yeas |
| 573 | 67 | 4.0 | 658 | 2 | A80241 | hypothetical prote | 646 | 66.5 | 3.9 | 1977 | 1 | S54771 | sodium channel alp |
| 574 | 67 | 4.0 | 662 | 2 | C91209 | hypothetical prote | 647 | 66.5 | 3.9 | 2109 | 1 | ZLVN | genome polyprotein |
| 575 | 67 | 4.0 | 662 | 2 | B86055 | hypothetical prote | 648 | 66.5 | 3.9 | 2262 | 2 | S16664 | large protein L - |
| 576 | 67 | 4.0 | 667 | 2 | S66017 | formate dehydrogen | 649 | 66.5 | 3.9 | 2297 | 2 | AB2494 | hypothetical prote |
| 577 | 67 | 4.0 | 675 | 2 | B96542 | unknown protein [i | 650 | 66.5 | 3.9 | 2311 | 1 | TVCHSR | kinase-related pro |
| 578 | 67 | 4.0 | 691 | 2 | T32748 | hypothetical prote | 651 | 66.5 | 3.9 | 2351 | 2 | A61208 | chondroitin sulfat |
| 579 | 67 | 4.0 | 781 | 2 | A13014 | methyl-accepting c | 652 | 66.5 | 3.9 | 2351 | 2 | G71415 | hypothetical prote |
| 580 | 67 | 4.0 | 788 | 2 | F98269 | hypothetical prote | 653 | 66.5 | 3.9 | 2894 | 2 | C64474 | hypothetical prote |
| 581 | 67 | 4.0 | 810 | 2 | T44430 | protein PV100 [lmp | 654 | 66.5 | 3.9 | 3898 | 1 | GNMVHC | genome polyprotein |
| 582 | 67 | 4.0 | 1042 | 2 | A57534 | protein 5AC (clone I | 655 | 66.5 | 3.9 | 4639 | 1 | A54794 | dynein heavy chain |
| 583 | 67 | 4.0 | 1139 | 2 | B54962 | sterol regulatory | 656 | 66.5 | 3.9 | 183 | 2 | T28711 | hypothetical prote |
| 584 | 67 | 4.0 | 1161 | 2 | B86368 | protein P28C11.9 l | 657 | 66.5 | 3.9 | 217 | 2 | AB1719 | competence negativ |
| 585 | 67 | 4.0 | 1173 | 2 | S48877 | Ca2+-transporting | 658 | 66.5 | 3.9 | 258 | 2 | B49597 | nonstructural prot |
| 586 | 67 | 4.0 | 1309 | 2 | F96509 | protein F27F5.19 l | 659 | 66.5 | 3.9 | 266 | 2 | T14345 | chitinase (Ec 3.2. |
| 587 | 67 | 4.0 | 1464 | 1 | S29159 | glutamate receptor | 660 | 66.5 | 3.9 | 308 | 2 | D89950 | porphobilinogen de |
| 588 | 67 | 4.0 | 1517 | 1 | F65112 | glutamate synthase | 661 | 66.5 | 3.9 | 339 | 2 | UC1442 | transcription fact |
| 589 | 67 | 4.0 | 1517 | 2 | C91140 | glutamate synthase | 662 | 66.5 | 3.9 | 367 | 2 | T10352 | protein gp41 - Org |
| 590 | 67 | 4.0 | 1518 | 2 | D96660 | protein P2K1.14 l | 663 | 66.5 | 3.9 | 373 | 2 | D89865 | hypothetical prote |
| 591 | 67 | 4.0 | 1569 | 2 | G02757 | clathrin heavy cha | 664 | 66.5 | 3.9 | 378 | 2 | B89588 | protein R09F10.7 l |
| 592 | 67 | 4.0 | 1577 | 2 | T15851 | hypothetical prote | 665 | 66.5 | 3.9 | 392 | 2 | B70777 | hypothetical prote |
| 593 | 67 | 4.0 | 1640 | 2 | T09522 | clathrin heavy cha | 666 | 66.5 | 3.9 | 412 | 2 | F81676 | heat shock gene re |
| 594 | 67 | 4.0 | 1755 | 2 | S69845 | TYB protein - yeas | 667 | 66.5 | 3.9 | 412 | 2 | I46421 | thyroxine-binding |
| 595 | 67 | 4.0 | 1755 | 2 | S61763 | TYB protein - yeas | 668 | 66.5 | 3.9 | 421 | 2 | AF0389 | exonuclease Shcd l |
| 596 | 67 | 4.0 | 1804 | 2 | S56247 | probable membrane | 669 | 66.5 | 3.9 | 421 | 2 | B90741 | hypothetical prote |
| 597 | 67 | 4.0 | 2278 | 1 | S56274 | FAB1 protein - yea | 670 | 66.5 | 3.9 | 421 | 2 | B85591 | hypothetical prote |
| 598 | 67 | 4.0 | 2535 | 2 | T04824 | hypothetical prote | 671 | 66.5 | 3.9 | 422 | 2 | C83869 | hypothetical prote |
| 599 | 67 | 4.0 | 2600 | 2 | D86161 | F1003.12 protein - | 672 | 66.5 | 3.9 | 427 | 2 | A12148 | proteasom protein |
| 600 | 67 | 4.0 | 4351 | 2 | T00252 | MEGF1 protein - ra | 673 | 66.5 | 3.9 | 447 | 1 | A42500 | alpha-1,3-mannosyl |
| 601 | 67 | 4.0 | 4563 | 1 | LPHUB | angiopoietin B-1 | 674 | 66.5 | 3.9 | 459 | 2 | G71619 | P1N7 domain protei |
| 602 | 67 | 3.9 | 186 | 2 | C71601 | probable integral | 675 | 66.5 | 3.9 | 532 | 2 | T05942 | cytochrome P450 82 |
| 603 | 67 | 3.9 | 225 | 2 | T67934 | neurofibromatosis | 676 | 66.5 | 3.9 | 566 | 2 | S39732 | arginine/orithine |
| 604 | 67 | 3.9 | 239 | 1 | Q4ECTD | hypothetical 26.3k | 677 | 66.5 | 3.9 | 584 | 2 | S55106 | probable membrane |
| 605 | 67 | 3.9 | 269 | 2 | S04124 | kafirin precursor | 678 | 66.5 | 3.9 | 595 | 2 | T41042 | hypothetical prote |
| 606 | 67 | 3.9 | 275 | 2 | T05595 | NAD glycohydrolase | 679 | 66.5 | 3.9 | 598 | 2 | AG0311 | NADH2 dehydrogen |
| 607 | 67 | 3.9 | 282 | 2 | S27769 | hypothetical prote | 680 | 66.5 | 3.9 | 610 | 1 | I46001 | Cab-binding protei |
| 608 | 67 | 3.9 | 296 | 2 | T31062 | hypothetical prote | 681 | 66.5 | 3.9 | 638 | 1 | YSBS72 | threonine-tRNA lig |
| 609 | 67 | 3.9 | 326 | 1 | VGXRM4 | glycoprotein VP7 p | 682 | 66.5 | 3.9 | 647 | 2 | AG2114 | hypothetical prote |
| 610 | 67 | 3.9 | 357 | 2 | A71938 | probable proline p | 683 | 66.5 | 3.9 | 679 | 2 | B96599 | protein F20N2.12 l |
| 611 | 67 | 3.9 | 362 | 2 | T29552 | hypothetical prote | 684 | 66.5 | 3.9 | 700 | 2 | B84125 | iron-sulphur-bindi |
| 612 | 67 | 3.9 | 378 | 1 | S17412 | ubiquinol-cytochro | 685 | 66.5 | 3.9 | 754 | 2 | D88734 | protein F32E10.1 l |
| 613 | 67 | 3.9 | 380 | 2 | S33720 | NS1 protein - deng | 686 | 66.5 | 3.9 | 779 | 2 | B81287 | hypothetical prote |

| | | | | | | |
|-----|------|-----|------|---|---------|-------------------------|
| 687 | 66 | 3.9 | 779 | 2 | 536111 | ostreoblast-specific |
| 688 | 66 | 3.9 | 795 | 2 | E86247 | receptor-like prot |
| 689 | 66 | 3.9 | 840 | 2 | A27832 | cell division cont |
| 690 | 66 | 3.9 | 858 | 2 | T08881 | prominin - mouse |
| 691 | 66 | 3.9 | 913 | 2 | T46339 | hypothetical prote |
| 692 | 66 | 3.9 | 921 | 2 | F81294 | probable helicase |
| 693 | 66 | 3.9 | 927 | 2 | T21772 | hypothetical prote |
| 694 | 66 | 3.9 | 937 | 2 | A45082 | neurotrophic recep |
| 695 | 66 | 3.9 | 1012 | 2 | T13712 | dof protein - frui |
| 696 | 66 | 3.9 | 1026 | 2 | T05882 | hypothetical prote |
| 697 | 66 | 3.9 | 1072 | 2 | T37876 | probable (Xeroderm |
| 698 | 66 | 3.9 | 1102 | 2 | T12681 | hypothetical prote |
| 699 | 66 | 3.9 | 1144 | 2 | T13749 | dof protein - frui |
| 700 | 66 | 3.9 | 1172 | 2 | S51623 | cut14 protein - fi |
| 701 | 66 | 3.9 | 1215 | 2 | A86593 | SM/SNF family hel |
| 702 | 66 | 3.9 | 1215 | 2 | B72029 | helicase, Smf2/Rad |
| 703 | 66 | 3.9 | 1252 | 2 | T00263 | hypothetical prote |
| 704 | 66 | 3.9 | 1260 | 1 | TVRTNU | protein-tyrosine k |
| 705 | 66 | 3.9 | 1348 | 2 | B23496 | TyB protein - yeas |
| 706 | 66 | 3.9 | 1384 | 2 | T18366 | latrophilin-2, spl |
| 707 | 66 | 3.9 | 1397 | 2 | T18377 | latrophilin-2, (spl |
| 708 | 66 | 3.9 | 1399 | 2 | T18370 | latrophilin-2 (spl |
| 709 | 66 | 3.9 | 1412 | 2 | T18380 | latrophilin-2 (spl |
| 710 | 66 | 3.9 | 1436 | 2 | A46496 | antigen WC1.1 prec |
| 711 | 66 | 3.9 | 1450 | 2 | T18382 | latrophilin-2 (spl |
| 712 | 66 | 3.9 | 1465 | 2 | T18386 | latrophilin-2 (spl |
| 713 | 66 | 3.9 | 1478 | 2 | T18384 | latrophilin-2 (spl |
| 714 | 66 | 3.9 | 1503 | 2 | T18389 | latrophilin-3, spl |
| 715 | 66 | 3.9 | 1510 | 2 | C84727 | probable glucan sy |
| 716 | 66 | 3.9 | 1512 | 2 | T18392 | latrophilin-3, spl |
| 717 | 66 | 3.9 | 1517 | 2 | F85985 | glutamate synthase |
| 718 | 66 | 3.9 | 1538 | 2 | AP0432 | glutamate synthase |
| 719 | 66 | 3.9 | 1538 | 2 | AP0432 | glutamate synthase |
| 720 | 66 | 3.9 | 1571 | 2 | T18395 | latrophilin-3, spl |
| 721 | 66 | 3.9 | 1580 | 2 | T18407 | latrophilin-3, spl |
| 722 | 66 | 3.9 | 1770 | 2 | S58651 | TyB protein - yeas |
| 723 | 66 | 3.9 | 1770 | 2 | S70233 | TyB protein - yeas |
| 724 | 66 | 3.9 | 1770 | 2 | S69948 | TyB protein - yeas |
| 725 | 66 | 3.9 | 1770 | 2 | S69966 | TyB protein - yeas |
| 726 | 66 | 3.9 | 1770 | 2 | S69950 | TyB protein - yeas |
| 727 | 66 | 3.9 | 1770 | 2 | S70230 | TyB protein - yeas |
| 728 | 66 | 3.9 | 1771 | 2 | S53592 | TyB protein - yeas |
| 729 | 66 | 3.9 | 2549 | 2 | S45340 | FKBP-rapamycin-aas |
| 730 | 66 | 3.9 | 2549 | 2 | A54837 | rapamycin/FKBP12 t |
| 731 | 66 | 3.9 | 2818 | 2 | B55282 | neurofibromatosis- |
| 732 | 66 | 3.9 | 3898 | 2 | S57437 | genome polyprotein |
| 733 | 66 | 3.9 | 3898 | 2 | S58295 | polyprotein - hog |
| 734 | 65.5 | 3.9 | 169 | 2 | T06062 | hypothetical prote |
| 735 | 65.5 | 3.9 | 169 | 2 | A97461 | glutathione S-tran |
| 736 | 65.5 | 3.9 | 235 | 2 | AC2679 | glutathione S-tran |
| 737 | 65.5 | 3.9 | 250 | 2 | T02392 | hypothetical prote |
| 738 | 65.5 | 3.9 | 262 | 2 | C83970 | cell-division init |
| 739 | 65.5 | 3.9 | 262 | 2 | D88930 | protein R11G1.10 |
| 740 | 65.5 | 3.9 | 268 | 2 | T15169 | hypothetical prote |
| 741 | 65.5 | 3.9 | 319 | 2 | H86218 | protein F22O13.12 |
| 742 | 65.5 | 3.9 | 319 | 2 | JC4926 | Xm1 endonuclease |
| 743 | 65.5 | 3.9 | 324 | 2 | T28331 | ORF MSV170 hypoth |
| 744 | 65.5 | 3.9 | 334 | 2 | B84432 | hypothetical prote |
| 745 | 65.5 | 3.9 | 336 | 2 | S52891 | probable membrane |
| 746 | 65.5 | 3.9 | 376 | 2 | S27976 | H+-transporting tw |
| 747 | 65.5 | 3.9 | 398 | 2 | T02484 | sugar ABC transp |
| 748 | 65.5 | 3.9 | 417 | 2 | AB1528 | probable signal tr |
| 749 | 65.5 | 3.9 | 422 | 2 | T39893 | malose/maltodextr |
| 750 | 65.5 | 3.9 | 429 | 2 | F84015 | hypothetical prote |
| 751 | 65.5 | 3.9 | 433 | 2 | T39745 | oligopeptide bind |
| 752 | 65.5 | 3.9 | 435 | 2 | E86515 | peptide ABC transp |
| 753 | 65.5 | 3.9 | 436 | 2 | A70923 | hypothetical prote |
| 754 | 65.5 | 3.9 | 437 | 2 | A31142 | gelolin, ovarian |
| 755 | 65.5 | 3.9 | 439 | 2 | G75314 | preprotein translo |
| 756 | 65.5 | 3.9 | 439 | 2 | G75314 | cell division prot |
| 757 | 65.5 | 3.9 | 452 | 2 | G97826 | cell division prot |
| 758 | 65.5 | 3.9 | 452 | 2 | F71672 | alpha-L-fucosidase |
| 759 | 65.5 | 3.9 | 462 | 2 | S10235 | |
| 760 | 65.5 | 3.9 | 468 | 2 | T33784 | hypothetical prote |
| 761 | 65.5 | 3.9 | 470 | 2 | B65175 | 6-phospho-beta-glu |
| 762 | 65.5 | 3.9 | 495 | 2 | F82123 | probable flagellar |
| 763 | 65.5 | 3.9 | 526 | 2 | T41944 | hypothetical prote |
| 764 | 65.5 | 3.9 | 528 | 2 | F70218 | GMP synthase (glut |
| 765 | 65.5 | 3.9 | 552 | 2 | A41035 | chitinase (EC 3.2. |
| 766 | 65.5 | 3.9 | 553 | 2 | T01416 | secy protein homol |
| 767 | 65.5 | 3.9 | 558 | 2 | A43667 | serine C-palmitoyl |
| 768 | 65.5 | 3.9 | 584 | 2 | E97303 | ABC-type multidrug |
| 769 | 65.5 | 3.9 | 589 | 2 | A71277 | arginine-tRNA lig |
| 770 | 65.5 | 3.9 | 589 | 2 | A71277 | ABC transporter (A |
| 771 | 65.5 | 3.9 | 609 | 2 | A96835 | probable receptor |
| 772 | 65.5 | 3.9 | 619 | 2 | B90141 | hypothetical prote |
| 773 | 65.5 | 3.9 | 653 | 2 | B86184 | hypothetical prote |
| 774 | 65.5 | 3.9 | 669 | 2 | T16626 | hypothetical prote |
| 775 | 65.5 | 3.9 | 684 | 2 | T37944 | Sertoli cell leuci |
| 776 | 65.5 | 3.9 | 745 | 2 | I57665 | hypothetical prote |
| 777 | 65.5 | 3.9 | 752 | 2 | G02273 | LIV-1 protein - hu |
| 778 | 65.5 | 3.9 | 757 | 2 | T34351 | hypothetical prote |
| 779 | 65.5 | 3.9 | 772 | 2 | A41860 | tetracycline resis |
| 780 | 65.5 | 3.9 | 784 | 2 | T45697 | hypothetical prote |
| 781 | 65.5 | 3.9 | 792 | 2 | T26050 | hypothetical prote |
| 782 | 65.5 | 3.9 | 794 | 2 | S59069 | Z13 protein - mous |
| 783 | 65.5 | 3.9 | 906 | 2 | G70767 | probable helicase |
| 784 | 65.5 | 3.9 | 954 | 2 | S46105 | glucan 1,4-alpha-g |
| 785 | 65.5 | 3.9 | 985 | 2 | A96777 | hypothetical prote |
| 786 | 65.5 | 3.9 | 994 | 1 | T0ECF5 | transposase - Esch |
| 787 | 65.5 | 3.9 | 1009 | 2 | T42925 | DNA-directed DNA p |
| 788 | 65.5 | 3.9 | 1014 | 2 | S32613 | HEX2 protein - Yea |
| 789 | 65.5 | 3.9 | 1017 | 2 | S67804 | LRG1 protein - Yea |
| 790 | 65.5 | 3.9 | 1061 | 2 | UC7116 | Xaa1-3 protein - A |
| 791 | 65.5 | 3.9 | 1078 | 2 | T30879 | dynein heavy chain |
| 792 | 65.5 | 3.9 | 1081 | 2 | JC5494 | hypothetical-tyrosine k |
| 793 | 65.5 | 3.9 | 1086 | 2 | AP1662 | cellulobiose-phospho |
| 794 | 65.5 | 3.9 | 1090 | 2 | T30576 | glucan synthase - |
| 795 | 65.5 | 3.9 | 1139 | 2 | S40932 | hypothetical prote |
| 796 | 65.5 | 3.9 | 1200 | 2 | T48194 | hypothetical prote |
| 797 | 65.5 | 3.9 | 1217 | 1 | T00059 | epidermal growth f |
| 798 | 65.5 | 3.9 | 1224 | 2 | B08154 | hypothetical prote |
| 799 | 65.5 | 3.9 | 1268 | 2 | B96805 | hypothetical prote |
| 800 | 65.5 | 3.9 | 1303 | 2 | B56395 | secretory phosphol |
| 801 | 65.5 | 3.9 | 1326 | 2 | B56395 | E2 glycoprotein pr |
| 802 | 65.5 | 3.9 | 1449 | 2 | A43573 | probable retroelem |
| 803 | 65.5 | 3.9 | 1454 | 2 | E84535 | secretory phosphol |
| 804 | 65.5 | 3.9 | 1465 | 2 | A56395 | hypothetical prote |
| 805 | 65.5 | 3.9 | 1576 | 2 | T21172 | hypothetical prote |
| 806 | 65.5 | 3.9 | 1584 | 2 | T226740 | hypothetical prote |
| 807 | 65.5 | 3.9 | 1646 | 2 | T20740 | hypothetical prote |
| 808 | 65.5 | 3.9 | 1974 | 2 | T16703 | hypothetical prote |
| 809 | 65.5 | 3.9 | 2338 | 2 | C69681 | kinase-related pro |
| 810 | 65.5 | 3.9 | 2555 | 2 | T73957 | peptide synthetase |
| 811 | 65.5 | 3.9 | 2561 | 1 | I40456 | genome polyprotein |
| 812 | 65.5 | 3.9 | 3388 | 2 | T19997 | hypothetical prote |
| 813 | 65.5 | 3.9 | 3944 | 2 | A43957 | dynein heavy chain |
| 814 | 65.5 | 3.9 | 4725 | 1 | AH2515 | hypothetical prote |
| 815 | 65.5 | 3.9 | 4936 | 2 | D88040 | protein F47F6.4 (l |
| 816 | 65.5 | 3.8 | 169 | 2 | S78046 | ribonuclease 6 (EC |
| 817 | 65 | 3.8 | 189 | 2 | F70574 | hypothetical prote |
| 818 | 65 | 3.8 | 219 | 2 | T21495 | hypothetical prote |
| 819 | 65 | 3.8 | 234 | 2 | U01695 | pathogenesis-relat |
| 820 | 65 | 3.8 | 239 | 2 | A16111 | 3-ketoacyl-acyl ca |
| 821 | 65 | 3.8 | 243 | 2 | T16792 | hypothetical prote |
| 822 | 65 | 3.8 | 298 | 2 | S75872 | hypothetical prote |
| 823 | 65 | 3.8 | 314 | 2 | AC0464 | cell division prot |
| 824 | 65 | 3.8 | 317 | 2 | AC0464 | MAH2 dehydrogenas |
| 825 | 65 | 3.8 | 344 | 2 | T12333 | gap junction prote |
| 826 | 65 | 3.8 | 356 | 1 | A42053 | conserved hypotet |
| 827 | 65 | 3.8 | 361 | 2 | F69798 | hypothetical prote |
| 828 | 65 | 3.8 | 375 | 2 | C81960 | hypothetical prote |
| 829 | 65 | 3.8 | 381 | 2 | T34015 | hypothetical prote |
| 830 | 65 | 3.8 | 387 | 2 | T23915 | xylose transport p |
| 831 | 65 | 3.8 | 393 | 2 | A86032 | |
| 832 | 65 | 3.8 | 393 | 2 | S47789 | |

| | | | | | | | | | | | | | |
|-----|------|-----|------|---|---------|---------------------|-----|------|-----|------|---|--------|---------------------|
| 833 | 65 | 3.8 | 393 | 2 | C91185 | xylose transport p | 906 | 64.5 | 3.8 | 416 | 2 | A56486 | perinuclear bindin |
| 834 | 65 | 3.8 | 393 | 2 | T04957 | hypothetical prote | 907 | 64.5 | 3.8 | 424 | 2 | T31862 | hypothetical prote |
| 835 | 65 | 3.8 | 399 | 1 | S73883 | yeB protein homol | 908 | 64.5 | 3.8 | 439 | 2 | T36432 | probable DEAD-box |
| 836 | 65 | 3.8 | 402 | 2 | T40066 | probable vacuolar | 909 | 64.5 | 3.8 | 456 | 2 | P84472 | probable replicasi |
| 837 | 65 | 3.8 | 411 | 2 | T29475 | hypothetical prote | 910 | 64.5 | 3.8 | 458 | 2 | C67620 | cytochrome P450 Ea |
| 838 | 65 | 3.8 | 433 | 2 | H86178 | hypothetical prote | 911 | 64.5 | 3.8 | 477 | 2 | A47236 | zinc-finger protei |
| 839 | 65 | 3.8 | 435 | 2 | D72023 | protoporphyrinogen | 912 | 64.5 | 3.8 | 482 | 2 | AB1421 | beta-glucosidase h |
| 840 | 65 | 3.8 | 440 | 2 | A43519 | complement recepto | 913 | 64.5 | 3.8 | 490 | 2 | T15097 | hypothetical prote |
| 841 | 65 | 3.8 | 467 | 2 | S16915 | gamma-aminobutyric | 914 | 64.5 | 3.8 | 494 | 2 | A48285 | exopolysphatase |
| 842 | 65 | 3.8 | 467 | 2 | S19317 | gamma-aminobutyric | 915 | 64.5 | 3.8 | 516 | 2 | B81684 | exodeoxyribonuclea |
| 843 | 65 | 3.8 | 469 | 2 | D86144 | protein probable U | 916 | 64.5 | 3.8 | 522 | 2 | H84671 | hypothetical prote |
| 844 | 65 | 3.8 | 475 | 2 | T08753 | hypothetical prote | 917 | 64.5 | 3.8 | 523 | 2 | T26740 | hypothetical prote |
| 845 | 65 | 3.8 | 479 | 2 | F70965 | hypothetical prote | 918 | 64.5 | 3.8 | 534 | 2 | G97703 | hypothetical prote |
| 846 | 65 | 3.8 | 480 | 2 | A31589 | carboxypeptidase C | 919 | 64.5 | 3.8 | 551 | 2 | T15127 | hypothetical prote |
| 847 | 65 | 3.8 | 497 | 2 | JC5076 | myc-associated zin | 920 | 64.5 | 3.8 | 554 | 2 | T28062 | hypothetical prote |
| 848 | 65 | 3.8 | 508 | 2 | S74977 | hypothetical prote | 921 | 64.5 | 3.8 | 558 | 2 | S57953 | CADP protein alpha |
| 849 | 65 | 3.8 | 528 | 2 | B42560 | 4-chlorobenzoate-C | 922 | 64.5 | 3.8 | 584 | 2 | T09113 | response regulator |
| 850 | 65 | 3.8 | 530 | 2 | G02091 | pancreatic zymogen | 923 | 64.5 | 3.8 | 618 | 2 | S33044 | hypothetical prote |
| 851 | 65 | 3.8 | 535 | 2 | E87656 | hypothetical prote | 924 | 64.5 | 3.8 | 628 | 1 | BWBSGA | glucose-inhibited |
| 852 | 65 | 3.8 | 561 | 2 | S62788 | carboxylesterase (| 925 | 64.5 | 3.8 | 632 | 2 | C70386 | dnak-type molecula |
| 853 | 65 | 3.8 | 578 | 2 | B71431 | hypothetical prote | 926 | 64.5 | 3.8 | 636 | 2 | A84903 | hypothetical prote |
| 854 | 65 | 3.8 | 592 | 2 | S51371 | transforming growt | 927 | 64.5 | 3.8 | 640 | 2 | T08758 | hypothetical prote |
| 855 | 65 | 3.8 | 613 | 2 | T28952 | hypothetical prote | 928 | 64.5 | 3.8 | 667 | 2 | B97012 | methy1-accepting c |
| 856 | 65 | 3.8 | 697 | 2 | H86457 | 78.1k hypothetica | 929 | 64.5 | 3.8 | 674 | 2 | T23235 | hypothetical prote |
| 857 | 65 | 3.8 | 705 | 2 | S55420 | conserved hypothet | 930 | 64.5 | 3.8 | 692 | 2 | B86635 | exonuclease ABC s |
| 858 | 65 | 3.8 | 809 | 2 | S33533 | heat shock protein | 931 | 64.5 | 3.8 | 704 | 1 | S33704 | transforming prote |
| 859 | 65 | 3.8 | 810 | 2 | T33323 | hypothetical prote | 932 | 64.5 | 3.8 | 725 | 2 | T17732 | helicase-like prot |
| 860 | 65 | 3.8 | 818 | 2 | S64251 | SAP4 protein - yea | 933 | 64.5 | 3.8 | 734 | 2 | T13674 | hypothetical prote |
| 861 | 65 | 3.8 | 836 | 2 | D82177 | conserved hypothet | 934 | 64.5 | 3.8 | 743 | 2 | T13673 | hypothetical prote |
| 862 | 65 | 3.8 | 856 | 2 | A44339 | protein kinase (EC | 935 | 64.5 | 3.8 | 774 | 2 | P96639 | protein T1P9.8 (Im |
| 863 | 65 | 3.8 | 880 | 2 | S49627 | regulatory protein | 936 | 64.5 | 3.8 | 829 | 2 | D71485 | probable adenylate |
| 864 | 65 | 3.8 | 887 | 2 | T25358 | hypothetical prote | 937 | 64.5 | 3.8 | 832 | 2 | T31792 | hypothetical prote |
| 865 | 65 | 3.8 | 976 | 2 | B84659 | probable receptor- | 938 | 64.5 | 3.8 | 838 | 2 | D71492 | hypothetical prote |
| 866 | 65 | 3.8 | 1048 | 1 | BVBCSC | exonuclease (EC 3. | 939 | 64.5 | 3.8 | 888 | 2 | T51593 | GTP-binding regula |
| 867 | 65 | 3.8 | 1091 | 2 | C95133 | second chain of ma | 940 | 64.5 | 3.8 | 901 | 1 | FAMU03 | alpha-actinin 3 - |
| 868 | 65 | 3.8 | 1091 | 2 | G98001 | hypothetical prote | 941 | 64.5 | 3.8 | 901 | 1 | T01135 | probable GTP-bind1 |
| 869 | 65 | 3.8 | 1111 | 2 | G96693 | hypothetical prote | 942 | 64.5 | 3.8 | 913 | 1 | VG8BPS | glycoprotein gII p |
| 870 | 65 | 3.8 | 1189 | 2 | T52346 | disease resistance | 943 | 64.5 | 3.8 | 935 | 2 | S57080 | hypothetical prote |
| 871 | 65 | 3.8 | 1225 | 1 | S24284 | E2 glycoprotein pr | 944 | 64.5 | 3.8 | 938 | 2 | T01809 | hypothetical prote |
| 872 | 65 | 3.8 | 1248 | 2 | A53588 | adenylate cyclase | 945 | 64.5 | 3.8 | 973 | 2 | U00971 | transposase cnpA - |
| 873 | 65 | 3.8 | 1253 | 2 | T21065 | hypothetical prote | 946 | 64.5 | 3.8 | 980 | 1 | TVCTMD | macrophage colony- |
| 874 | 65 | 3.8 | 1320 | 2 | P96614 | probable copia-tyr | 947 | 64.5 | 3.8 | 1031 | 2 | C81302 | probable type I si |
| 875 | 65 | 3.8 | 1321 | 2 | T23476 | hypothetical prote | 948 | 64.5 | 3.8 | 1052 | 1 | A44937 | kinecioplast-associ |
| 876 | 65 | 3.8 | 1321 | 2 | S27337 | multidrug resistan | 949 | 64.5 | 3.8 | 1052 | 2 | A46166 | protein-tyrosine k |
| 877 | 65 | 3.8 | 1372 | 2 | S18921 | genome polyprotein | 950 | 64.5 | 3.8 | 1124 | 2 | JH0588 | calmodulin-binding |
| 878 | 65 | 3.8 | 1616 | 2 | G64242 | cyadherence-acces | 951 | 64.5 | 3.8 | 1265 | 2 | F71429 | hypothetical prote |
| 879 | 65 | 3.8 | 1744 | 2 | JH0720 | tarabin - African | 952 | 64.5 | 3.8 | 1350 | 2 | T30341 | hypothetical prote |
| 880 | 65 | 3.8 | 2077 | 2 | T43991 | large tegument pro | 953 | 64.5 | 3.8 | 1531 | 2 | T42218 | silt-1 protein hom |
| 881 | 65 | 3.8 | 2098 | 2 | T25888 | hypothetical prote | 954 | 64.5 | 3.8 | 1616 | 2 | S62504 | conserved hypothet |
| 882 | 65 | 3.8 | 2133 | 2 | T30637 | hypothetical prote | 955 | 64.5 | 3.8 | 1755 | 2 | S69963 | TYB protein - yeas |
| 883 | 65 | 3.8 | 2253 | 2 | T30336 | nuclear/mitotic ap | 956 | 64.5 | 3.8 | 1755 | 2 | S69839 | TYB protein - yeas |
| 884 | 65 | 3.8 | 2354 | 2 | T13288 | met-41 protein - f | 957 | 64.5 | 3.8 | 1755 | 2 | S69960 | TYB protein - yeas |
| 885 | 65 | 3.8 | 4543 | 1 | A53102 | alpha-2-macroglobu | 958 | 64.5 | 3.8 | 2139 | 2 | A35672 | glutamate synthase |
| 886 | 65 | 3.8 | 159 | 2 | T10363 | hypothetical prote | 959 | 64.5 | 3.8 | 2194 | 1 | JQ1977 | ADP-ribosylation f |
| 887 | 64.5 | 3.8 | 170 | 2 | S67318 | hypothetical prote | 960 | 64.5 | 3.8 | 2227 | 1 | GNMYHM | genome polyprotein |
| 888 | 64.5 | 3.8 | 176 | 2 | A59136 | hypothetical prote | 961 | 64.5 | 3.8 | 2334 | 2 | S32920 | cell wall-associat |
| 889 | 64.5 | 3.8 | 176 | 2 | AB3152 | outer membrane lip | 962 | 64.5 | 3.8 | 3449 | 2 | T01083 | hypothetical prote |
| 890 | 64.5 | 3.8 | 197 | 2 | T21030 | hypothetical prote | 963 | 64.5 | 3.8 | 3766 | 2 | T29165 | hypothetical prote |
| 891 | 64.5 | 3.8 | 216 | 1 | S58576 | endopeptidase C1p | 964 | 64 | 3.8 | 179 | 2 | JH0260 | hypothetical prote |
| 892 | 64.5 | 3.8 | 245 | 2 | A41858 | hypothetical prote | 965 | 64 | 3.8 | 246 | 2 | T00541 | ADP-ribosylation f |
| 893 | 64.5 | 3.8 | 272 | 2 | B90544 | hypothetical prote | 966 | 64.5 | 3.8 | 263 | 2 | A55122 | hypothetical prote |
| 894 | 64.5 | 3.8 | 285 | 2 | T298738 | hypothetical prote | 967 | 64 | 3.8 | 260 | 2 | A82059 | deoxytyridine kina |
| 895 | 64.5 | 3.8 | 322 | 2 | T29490 | hypothetical prote | 968 | 64 | 3.8 | 266 | 2 | T14348 | probable chitinase |
| 896 | 64.5 | 3.8 | 326 | 2 | T08849 | alternative respei | 969 | 64 | 3.8 | 326 | 1 | JQ1444 | glycoprotein VP7 p |
| 897 | 64.5 | 3.8 | 331 | 2 | B47236 | zinc-finger protei | 970 | 64 | 3.8 | 340 | 2 | VGXK37 | anthranilate dioxy |
| 898 | 64.5 | 3.8 | 336 | 1 | MMWZP1 | FI protein - fowli | 971 | 64 | 3.8 | 352 | 2 | AB3332 | hypothetical prote |
| 899 | 64.5 | 3.8 | 374 | 2 | S32604 | collagen alpha 2(Iv | 972 | 64 | 3.8 | 358 | 2 | T05106 | hypothetical prote |
| 900 | 64.5 | 3.8 | 374 | 2 | T02315 | hypothetical prote | 973 | 64 | 3.8 | 361 | 2 | G89196 | hypothetical prote |
| 901 | 64.5 | 3.8 | 386 | 1 | JH0610 | acid phosphatase (| 974 | 64 | 3.8 | 361 | 2 | B81360 | hypothetical prote |
| 902 | 64.5 | 3.8 | 390 | 2 | A86065 | UDP-N-acetyl gluc | 975 | 64 | 3.8 | 395 | 2 | H96513 | hypothetical prote |
| 903 | 64.5 | 3.8 | 390 | 2 | G91218 | UDP-N-acetyl gluc | 976 | 64 | 3.8 | 418 | 2 | S29506 | neurotensin recept |
| 904 | 64.5 | 3.8 | 397 | 2 | C84904 | hypothetical prote | 977 | 64 | 3.8 | | | | |
| 905 | 64.5 | 3.8 | 397 | 2 | | | 978 | 64 | 3.8 | | | | |

| | | | | | | | | | | | | |
|------|----|-----|------|---|--------|------|------|-----|-----|---|--------|---------------------|
| 979 | 64 | 3.8 | 418 | 2 | T25092 | 1052 | 63.5 | 3.7 | 188 | 2 | D6952 | transcription repr |
| 980 | 64 | 3.8 | 447 | 2 | JC7153 | 1053 | 63.5 | 3.7 | 189 | 2 | AR0560 | conserved hypothet |
| 981 | 64 | 3.8 | 447 | 2 | S6586 | 1054 | 63.5 | 3.7 | 190 | 2 | G85542 | glycoprotein/poly |
| 982 | 64 | 3.8 | 447 | 2 | A55836 | 1055 | 63.5 | 3.7 | 190 | 2 | C90692 | glycoprotein/poly |
| 983 | 64 | 3.8 | 452 | 2 | C85024 | 1056 | 63.5 | 3.7 | 190 | 2 | E64775 | probable lipoprote |
| 984 | 64 | 3.8 | 467 | 2 | A71431 | 1057 | 63.5 | 3.7 | 199 | 2 | U50430 | prolactin - elepha |
| 985 | 64 | 3.8 | 468 | 2 | T25475 | 1058 | 63.5 | 3.7 | 215 | 2 | S64696 | a2-mating type pro |
| 986 | 64 | 3.8 | 472 | 2 | A33312 | 1059 | 63.5 | 3.7 | 216 | 2 | C90956 | probable membrane |
| 987 | 64 | 3.8 | 472 | 2 | H96607 | 1060 | 63.5 | 3.7 | 216 | 2 | H85804 | unknown protein en |
| 988 | 64 | 3.8 | 474 | 1 | OMH1B | 1061 | 63.5 | 3.7 | 217 | 2 | HA0561 | potential acraB op |
| 989 | 64 | 3.8 | 483 | 2 | T40801 | 1062 | 63.5 | 3.7 | 228 | 2 | H83867 | hypothetical prote |
| 990 | 64 | 3.8 | 492 | 2 | T02458 | 1063 | 63.5 | 3.7 | 246 | 2 | C96780 | trnauctin-like pro |
| 991 | 64 | 3.8 | 504 | 2 | T50270 | 1064 | 63.5 | 3.7 | 260 | 2 | AF0915 | hypothetical prote |
| 992 | 64 | 3.8 | 507 | 1 | A30828 | 1065 | 63.5 | 3.7 | 262 | 2 | G02476 | lysosomal-aasocia |
| 993 | 64 | 3.8 | 523 | 1 | A53196 | 1066 | 63.5 | 3.7 | 285 | 2 | T22616 | hypothetical prote |
| 994 | 64 | 3.8 | 525 | 2 | A70157 | 1067 | 63.5 | 3.7 | 305 | 2 | E84848 | probable RING zinc |
| 995 | 64 | 3.8 | 527 | 2 | T01019 | 1068 | 63.5 | 3.7 | 312 | 2 | HA2389 | hypothetical prote |
| 996 | 64 | 3.8 | 572 | 2 | F96755 | 1069 | 63.5 | 3.7 | 315 | 2 | T47181 | glycoprotein VP7 p |
| 997 | 64 | 3.8 | 594 | 2 | A49804 | 1070 | 63.5 | 3.7 | 326 | 1 | VGXRA8 | hypothetical prote |
| 998 | 64 | 3.8 | 598 | 2 | T25207 | 1071 | 63.5 | 3.7 | 351 | 2 | T29369 | hypothetical prote |
| 999 | 64 | 3.8 | 604 | 2 | T37870 | 1072 | 63.5 | 3.7 | 355 | 2 | AF0454 | utroporphyrinogen d |
| 1000 | 64 | 3.8 | 605 | 2 | T31690 | 1073 | 63.5 | 3.7 | 366 | 2 | JC7690 | Gfi-1-like protein |
| 1001 | 64 | 3.8 | 620 | 2 | AP2174 | 1074 | 63.5 | 3.7 | 369 | 2 | F87422 | hypothetical prote |
| 1002 | 64 | 3.8 | 630 | 2 | D86391 | 1075 | 63.5 | 3.7 | 369 | 2 | T40279 | hypothetical prote |
| 1003 | 64 | 3.8 | 632 | 2 | T00108 | 1076 | 63.5 | 3.7 | 370 | 2 | H90675 | probable ATP bindi |
| 1004 | 64 | 3.8 | 643 | 2 | S36017 | 1077 | 63.5 | 3.7 | 371 | 2 | AF2396 | two-component sens |
| 1005 | 64 | 3.8 | 648 | 2 | S16866 | 1078 | 63.5 | 3.7 | 373 | 2 | B39732 | H+-transporting tw |
| 1006 | 64 | 3.8 | 651 | 2 | P64457 | 1079 | 63.5 | 3.7 | 379 | 2 | T24814 | hypothetical prote |
| 1007 | 64 | 3.8 | 654 | 1 | ORECCS | 1080 | 63.5 | 3.7 | 383 | 2 | T39854 | hypothetical prote |
| 1008 | 64 | 3.8 | 655 | 2 | AS7681 | 1081 | 63.5 | 3.7 | 388 | 2 | T31887 | hypothetical prote |
| 1009 | 64 | 3.8 | 716 | 2 | G82627 | 1082 | 63.5 | 3.7 | 388 | 2 | A88949 | protein R09B5.5 [i |
| 1010 | 64 | 3.8 | 767 | 2 | T41344 | 1083 | 63.5 | 3.7 | 388 | 2 | T31888 | hypothetical prote |
| 1011 | 64 | 3.8 | 769 | 2 | S55554 | 1084 | 63.5 | 3.7 | 392 | 2 | C85526 | hypothetical prote |
| 1012 | 64 | 3.8 | 773 | 2 | T39513 | 1085 | 63.5 | 3.7 | 395 | 2 | A48661 | hypothetical prote |
| 1013 | 64 | 3.8 | 774 | 2 | JC7265 | 1086 | 63.5 | 3.7 | 396 | 2 | T22097 | hypothetical prote |
| 1014 | 64 | 3.8 | 794 | 2 | T46073 | 1087 | 63.5 | 3.7 | 398 | 2 | S77230 | hypothetical prote |
| 1015 | 64 | 3.8 | 808 | 2 | T22363 | 1088 | 63.5 | 3.7 | 398 | 2 | T19421 | hypothetical prote |
| 1016 | 64 | 3.8 | 820 | 2 | G86246 | 1089 | 63.5 | 3.7 | 404 | 2 | E82012 | sodium/glutamate s |
| 1017 | 64 | 3.8 | 857 | 2 | T04208 | 1090 | 63.5 | 3.7 | 404 | 2 | F81240 | sodium/glutamate s |
| 1018 | 64 | 3.8 | 908 | 2 | A33280 | 1091 | 63.5 | 3.7 | 420 | 2 | F83494 | hypothetical prote |
| 1019 | 64 | 3.8 | 916 | 2 | F71962 | 1092 | 63.5 | 3.7 | 432 | 2 | T20536 | hypothetical prote |
| 1020 | 64 | 3.8 | 931 | 2 | A49737 | 1093 | 63.5 | 3.7 | 434 | 2 | T20539 | hypothetical prote |
| 1021 | 64 | 3.8 | 937 | 2 | T41400 | 1094 | 63.5 | 3.7 | 435 | 2 | T43749 | cytochrome oxidase |
| 1022 | 64 | 3.8 | 976 | 1 | URRTAP | 1095 | 63.5 | 3.7 | 439 | 2 | T28196 | hypothetical prote |
| 1023 | 64 | 3.8 | 976 | 2 | PC4208 | 1096 | 63.5 | 3.7 | 459 | 2 | A34791 | interleukin-7 rece |
| 1024 | 64 | 3.8 | 987 | 2 | A54092 | 1097 | 63.5 | 3.7 | 459 | 2 | A75097 | hypothetical prote |
| 1025 | 64 | 3.8 | 1002 | 2 | B54145 | 1098 | 63.5 | 3.7 | 463 | 2 | F81194 | hypothetical prote |
| 1026 | 64 | 3.8 | 1002 | 2 | T04462 | 1099 | 63.5 | 3.7 | 463 | 2 | E81830 | hypothetical prote |
| 1027 | 64 | 3.8 | 1012 | 2 | T41940 | 1100 | 63.5 | 3.7 | 468 | 2 | S61864 | probable membrane |
| 1028 | 64 | 3.8 | 1017 | 2 | G85055 | 1101 | 63.5 | 3.7 | 470 | 2 | S68964 | legumin precursor |
| 1029 | 64 | 3.8 | 1029 | 2 | C72363 | 1102 | 63.5 | 3.7 | 474 | 2 | H84210 | hypothetical prote |
| 1030 | 64 | 3.8 | 1133 | 1 | S41478 | 1103 | 63.5 | 3.7 | 475 | 2 | T38597 | zinc finger protei |
| 1031 | 64 | 3.8 | 1146 | 2 | P84487 | 1104 | 63.5 | 3.7 | 481 | 2 | AB1890 | hypothetical prote |
| 1032 | 64 | 3.8 | 1242 | 2 | T39453 | 1105 | 63.5 | 3.7 | 481 | 2 | S74934 | pled-1 protein - s |
| 1033 | 64 | 3.8 | 1272 | 2 | T49313 | 1106 | 63.5 | 3.7 | 488 | 2 | D70614 | 1-aminocyclopropan |
| 1034 | 64 | 3.8 | 1284 | 2 | T50993 | 1107 | 63.5 | 3.7 | 491 | 2 | T03978 | type I serine-thre |
| 1035 | 64 | 3.8 | 1299 | 1 | MMB5HS | 1108 | 63.5 | 3.7 | 505 | 2 | T53417 | hypothetical prote |
| 1036 | 64 | 3.8 | 1335 | 2 | H75511 | 1109 | 63.5 | 3.7 | 514 | 2 | T25534 | lamin B2 - human |
| 1037 | 64 | 3.8 | 1389 | 2 | T41230 | 1110 | 63.5 | 3.7 | 515 | 2 | A45023 | probable adenylyl- |
| 1038 | 64 | 3.8 | 1518 | 2 | E75199 | 1111 | 63.5 | 3.7 | 539 | 2 | C96758 | ABC transporter, A |
| 1039 | 64 | 3.8 | 1518 | 2 | T28880 | 1112 | 63.5 | 3.7 | 547 | 1 | C70393 | L2TR-1 - human |
| 1040 | 64 | 3.8 | 1588 | 2 | T38660 | 1113 | 63.5 | 3.7 | 547 | 2 | E81017 | cell fusion glycop |
| 1041 | 64 | 3.8 | 1672 | 2 | T46237 | 1114 | 63.5 | 3.7 | 552 | 2 | T24694 | hypothetical prote |
| 1042 | 64 | 3.8 | 1684 | 2 | T02632 | 1115 | 63.5 | 3.7 | 552 | 2 | T54388 | transporter bindin |
| 1043 | 64 | 3.8 | 1733 | 2 | D70887 | 1116 | 63.5 | 3.7 | 572 | 1 | VGNZBA | beta-glucosidase h |
| 1044 | 64 | 3.8 | 1756 | 2 | S45867 | 1117 | 63.5 | 3.7 | 575 | 2 | QJ1583 | hypothetical prote |
| 1045 | 64 | 3.8 | 1783 | 2 | T37258 | 1118 | 63.5 | 3.7 | 575 | 2 | D96585 | hypothetical prote |
| 1046 | 64 | 3.8 | 1917 | 2 | C88728 | 1119 | 63.5 | 3.7 | 591 | 2 | T02402 | transporter bindin |
| 1047 | 64 | 3.8 | 2121 | 2 | A59233 | 1120 | 63.5 | 3.7 | 601 | 2 | T24694 | hypothetical prote |
| 1048 | 64 | 3.8 | 2124 | 2 | T01526 | 1121 | 63.5 | 3.7 | 601 | 1 | K18BTE | thymidine kinase |
| 1049 | 64 | 3.8 | 2261 | 1 | A42548 | 1122 | 63.5 | 3.7 | 608 | 2 | SS1790 | centromere protein |
| 1050 | 64 | 3.8 | 2319 | 1 | T18414 | 1123 | 63.5 | 3.7 | 633 | 2 | G89836 | ABC transporter pe |
| 1051 | 64 | 3.8 | 4273 | 2 | C69679 | 1124 | 63.5 | 3.7 | 689 | 2 | T25202 | hypothetical prote |

| | | | | | | | | | | | | | |
|------|------|-----|------|---|--------|--------------------|------|----|-----|------|---|--------|----------------------|
| 1125 | 63.5 | 3.7 | 693 | 2 | F86156 | hypothetical prote | 1198 | 63 | 3.7 | 316 | 2 | S35516 | type II site-speci |
| 1126 | 63.5 | 3.7 | 704 | 1 | S25820 | dynamn-related pr | 1199 | 63 | 3.7 | 320 | 2 | T19358 | hypothetical prote |
| 1127 | 63.5 | 3.7 | 706 | 1 | Q08B6L | glycoprotein H - h | 1200 | 63 | 3.7 | 326 | 1 | VGXRB7 | glycoprotein VP7 p |
| 1128 | 63.5 | 3.7 | 765 | 2 | A01656 | cobalamin-independ | 1201 | 63 | 3.7 | 335 | 2 | A39743 | u-plasminogen acti |
| 1129 | 63.5 | 3.7 | 799 | 2 | S18209 | fibroblast growth | 1202 | 63 | 3.7 | 335 | 2 | UC1441 | transcription fact |
| 1130 | 63.5 | 3.7 | 851 | 2 | A59284 | unconventional myo | 1203 | 63 | 3.7 | 336 | 2 | A42040 | porphobilinogen de |
| 1131 | 63.5 | 3.7 | 858 | 2 | AD2272 | protein serine-thr | 1204 | 63 | 3.7 | 336 | 2 | T50560 | SIN4A protein (im |
| 1132 | 63.5 | 3.7 | 882 | 2 | F86164 | hypothetical prote | 1205 | 63 | 3.7 | 346 | 2 | T48496 | membrane protein - |
| 1133 | 63.5 | 3.7 | 888 | 2 | E71608 | ATP-dept. acyl-CoA | 1206 | 63 | 3.7 | 348 | 2 | A41764 | tumor necrosis fac |
| 1134 | 63.5 | 3.7 | 903 | 2 | T20804 | hypothetical prote | 1207 | 63 | 3.7 | 357 | 2 | T03557 | ribose transport s |
| 1135 | 63.5 | 3.7 | 903 | 2 | G87372 | Tomb-dependent rec | 1208 | 63 | 3.7 | 358 | 2 | C96036 | probable ferredoxi |
| 1136 | 63.5 | 3.7 | 922 | 2 | T21573 | hypothetical prote | 1209 | 63 | 3.7 | 385 | 2 | B86603 | cell division prot |
| 1137 | 63.5 | 3.7 | 926 | 2 | S39344 | deubiquinating enz | 1210 | 63 | 3.7 | 385 | 2 | B72022 | probable Nreb prot |
| 1138 | 63.5 | 3.7 | 928 | 2 | S40745 | hypothetical prote | 1211 | 63 | 3.7 | 391 | 2 | B64994 | 2-hydroxyglutaryl-d |
| 1139 | 63.5 | 3.7 | 935 | 2 | T48778 | hypothetical prote | 1212 | 63 | 3.7 | 398 | 2 | JC4146 | protoporphyrinogen |
| 1140 | 63.5 | 3.7 | 956 | 1 | Q08EK2 | UHL05 protein - hu | 1213 | 63 | 3.7 | 403 | 2 | T02290 | hypothetical prote |
| 1141 | 63.5 | 3.7 | 974 | 2 | A90140 | conserved hypotet | 1214 | 63 | 3.7 | 405 | 2 | T16836 | hypothetical prote |
| 1142 | 63.5 | 3.7 | 1011 | 2 | T29806 | hypothetical prote | 1215 | 63 | 3.7 | 410 | 2 | B85617 | hypothetical prote |
| 1143 | 63.5 | 3.7 | 1011 | 2 | A12046 | ABC transporter AT | 1216 | 63 | 3.7 | 410 | 2 | G90753 | hypothetical prote |
| 1144 | 63.5 | 3.7 | 1029 | 1 | S21369 | collagen alpha 2(V | 1217 | 63 | 3.7 | 416 | 2 | A70110 | conserved hypotet |
| 1145 | 63.5 | 3.7 | 1036 | 2 | F71565 | probable isoleucin | 1218 | 63 | 3.7 | 421 | 2 | D81374 | probable oxidoredu |
| 1146 | 63.5 | 3.7 | 1061 | 2 | D69799 | cytochrome P450 / | 1219 | 63 | 3.7 | 427 | 2 | A53964 | carboxyl-terminal |
| 1147 | 63.5 | 3.7 | 1080 | 2 | T43164 | lacta protein - Li | 1220 | 63 | 3.7 | 433 | 2 | T08938 | hypothetical prote |
| 1148 | 63.5 | 3.7 | 1100 | 2 | G84534 | probable retroelem | 1221 | 63 | 3.7 | 440 | 2 | H95373 | probable Nreb prot |
| 1149 | 63.5 | 3.7 | 1122 | 2 | S64443 | probable membrane | 1222 | 63 | 3.7 | 465 | 2 | T00982 | En/Spm-like transp |
| 1150 | 63.5 | 3.7 | 1131 | 2 | T07137 | phytochrome A - so | 1223 | 63 | 3.7 | 471 | 2 | S46739 | hypothetical prote |
| 1151 | 63.5 | 3.7 | 1133 | 1 | EGRT | epidermal growth f | 1224 | 63 | 3.7 | 473 | 2 | B84143 | Na+/H+ antiporter |
| 1152 | 63.5 | 3.7 | 1177 | 2 | A00438 | probable exported | 1225 | 63 | 3.7 | 476 | 2 | T46067 | hypothetical prote |
| 1153 | 63.5 | 3.7 | 1328 | 2 | S52481 | TYB protein - yeas | 1226 | 63 | 3.7 | 479 | 2 | S52705 | probable membrane |
| 1154 | 63.5 | 3.7 | 1328 | 2 | A49634 | aldehyde oxidase (| 1227 | 63 | 3.7 | 482 | 2 | T30983 | hypothetical prote |
| 1155 | 63.5 | 3.7 | 1391 | 2 | S50608 | hypothetical prote | 1228 | 63 | 3.7 | 505 | 2 | T50815 | cdcd2-like protein |
| 1156 | 63.5 | 3.7 | 1418 | 2 | T15232 | hypothetical prote | 1229 | 63 | 3.7 | 518 | 2 | T50175 | dan-directed rna p |
| 1157 | 63.5 | 3.7 | 1463 | 2 | A53144 | phospholipase A2 r | 1230 | 63 | 3.7 | 532 | 2 | T47335 | hypothetical prote |
| 1158 | 63.5 | 3.7 | 1616 | 1 | U02144 | 183K protein - tom | 1231 | 63 | 3.7 | 533 | 2 | A42574 | hypothetical prote |
| 1159 | 63.5 | 3.7 | 1628 | 2 | T43682 | nucleoporin - f188 | 1232 | 63 | 3.7 | 535 | 2 | F83949 | hypothetical prote |
| 1160 | 63.5 | 3.7 | 1652 | 2 | T16799 | hypothetical prote | 1233 | 63 | 3.7 | 555 | 2 | H84476 | probable Athlia re |
| 1161 | 63.5 | 3.7 | 1661 | 2 | T21986 | hypothetical prote | 1234 | 63 | 3.7 | 561 | 2 | T34083 | hypothetical prote |
| 1162 | 63.5 | 3.7 | 1663 | 2 | T21993 | hypothetical prote | 1235 | 63 | 3.7 | 562 | 2 | B41035 | chitinase (EC 3.2. |
| 1163 | 63.5 | 3.7 | 1711 | 2 | T21432 | hypothetical prote | 1236 | 63 | 3.7 | 586 | 2 | S58713 | probable membrane |
| 1164 | 63.5 | 3.7 | 1751 | 2 | T50002 | hypothetical prote | 1237 | 63 | 3.7 | 586 | 2 | B83790 | hypothetical prote |
| 1165 | 63.5 | 3.7 | 1755 | 2 | S69979 | TYB protein - yeas | 1238 | 63 | 3.7 | 590 | 2 | T45916 | interleukin 1 rece |
| 1166 | 63.5 | 3.7 | 1755 | 2 | S69975 | TYB protein - yeas | 1239 | 63 | 3.7 | 590 | 2 | B84898 | hypothetical prote |
| 1167 | 63.5 | 3.7 | 1755 | 2 | S50641 | TYB protein YER138 | 1240 | 63 | 3.7 | 592 | 2 | A42100 | transforming grow |
| 1168 | 63.5 | 3.7 | 1755 | 2 | S69960 | TYB protein - yeas | 1241 | 63 | 3.7 | 622 | 2 | T37257 | hypothetical prote |
| 1169 | 63.5 | 3.7 | 1957 | 2 | S68453 | sodium channel pro | 1242 | 63 | 3.7 | 634 | 2 | S31925 | beta-fructofuranos |
| 1170 | 63.5 | 3.7 | 2017 | 1 | A46014 | myosin heavy chain | 1243 | 63 | 3.7 | 647 | 2 | S70592 | NADH2 dehydrogenas |
| 1171 | 63.5 | 3.7 | 2057 | 2 | S61477 | myosin II heavy ch | 1244 | 63 | 3.7 | 647 | 2 | J50337 | frizzled-1 protein |
| 1172 | 63.5 | 3.7 | 2227 | 1 | GNNYHR | genome polyprotein | 1245 | 63 | 3.7 | 674 | 2 | S18670 | dnax-c-type molecula |
| 1173 | 63.5 | 3.7 | 2340 | 2 | I48310 | kinase-related pro | 1246 | 63 | 3.7 | 677 | 2 | B82870 | DNA topoisomerase |
| 1174 | 63.5 | 3.7 | 2692 | 2 | T23768 | alpha-fetoprotein | 1247 | 63 | 3.7 | 686 | 2 | J55708 | villin-like protei |
| 1175 | 63.5 | 3.7 | 2783 | 1 | A41948 | mucin MUC5B, trach | 1248 | 63 | 3.7 | 710 | 2 | T25734 | hypothetical prote |
| 1176 | 63.5 | 3.7 | 3570 | 2 | T45025 | lipid transfer pro | 1249 | 63 | 3.7 | 728 | 2 | T20561 | hypothetical prote |
| 1177 | 63 | 3.7 | 117 | 2 | S37202 | probable RAV2-like | 1250 | 63 | 3.7 | 738 | 2 | T45916 | hypothetical prote |
| 1178 | 63 | 3.7 | 117 | 2 | T44655 | AcNMPV orf93 - Bom | 1251 | 63 | 3.7 | 764 | 2 | JC4736 | methy1-accepting c |
| 1179 | 63 | 3.7 | 158 | 2 | F84776 | hypothetical prote | 1252 | 63 | 3.7 | 767 | 2 | S63220 | probable membrane |
| 1180 | 63 | 3.7 | 161 | 2 | T41833 | hypothetical prote | 1253 | 63 | 3.7 | 790 | 2 | S27458 | SMW2 protein - Yea |
| 1181 | 63 | 3.7 | 168 | 2 | B71486 | hypothetical prote | 1254 | 63 | 3.7 | 851 | 2 | A46160 | interferon alpha-i |
| 1182 | 63 | 3.7 | 175 | 2 | S37649 | high-sulfur kerati | 1255 | 63 | 3.7 | 870 | 2 | A46637 | hypothetical prote |
| 1183 | 63 | 3.7 | 197 | 2 | S74851 | hypothetical prote | 1256 | 63 | 3.7 | 874 | 2 | T15570 | hypothetical prote |
| 1184 | 63 | 3.7 | 204 | 1 | WZVZ83 | 24K HindIII-C prot | 1257 | 63 | 3.7 | 876 | 2 | D70971 | 3',5'-cyclic nucle |
| 1185 | 63 | 3.7 | 204 | 2 | I42503 | CSL protein - vacc | 1258 | 63 | 3.7 | 885 | 2 | JC7898 | gene boss protein |
| 1186 | 63 | 3.7 | 207 | 2 | B83523 | hypothetical prote | 1259 | 63 | 3.7 | 896 | 2 | S26740 | protein TIF9.20 [i |
| 1187 | 63 | 3.7 | 215 | 2 | D41681 | S-erythralin 4 - g | 1260 | 63 | 3.7 | 925 | 2 | H86638 | probable family 31 |
| 1188 | 63 | 3.7 | 227 | 2 | H82449 | hypothetical prote | 1261 | 63 | 3.7 | 993 | 2 | T38558 | type III restrictio |
| 1189 | 63 | 3.7 | 249 | 2 | S09868 | probable prp1aeni | 1262 | 63 | 3.7 | 1001 | 2 | H64593 | glutamate receptor |
| 1190 | 63 | 3.7 | 280 | 2 | AC0411 | hypothetical prote | 1263 | 63 | 3.7 | 1009 | 2 | S28857 | receptor-kinase 1i |
| 1191 | 63 | 3.7 | 284 | 2 | T25938 | hypothetical prote | 1264 | 63 | 3.7 | 1011 | 2 | T45718 | hypothetical prote |
| 1192 | 63 | 3.7 | 295 | 2 | A81566 | probable UDP-gluc | 1265 | 63 | 3.7 | 1027 | 2 | T46296 | myosin-like protei |
| 1193 | 63 | 3.7 | 297 | 2 | F68145 | hypothetical prote | 1266 | 63 | 3.7 | 1054 | 2 | D96519 | actosomal protein |
| 1194 | 63 | 3.7 | 301 | 2 | S20081 | surface virulence | 1267 | 63 | 3.7 | 1060 | 2 | S63953 | dynein heavy chain |
| 1195 | 63 | 3.7 | 309 | 2 | T27426 | hypothetical prote | 1268 | 63 | 3.7 | 1060 | 2 | T30297 | hypothetical prote |
| 1196 | 63 | 3.7 | 309 | 2 | T16660 | hypothetical prote | 1269 | 63 | 3.7 | 1165 | 2 | T21636 | thrombospondin 2 p |
| 1197 | 63 | 3.7 | 313 | 2 | A81142 | crRNA delta(2)-iso | 1270 | 63 | 3.7 | 1172 | 1 | TSHUP2 | |

| | | | | | | |
|------|------|-----|------|---|--------|---------------------|
| 1271 | 63 | 3.7 | 1209 | 2 | T16663 | hypothetical prote |
| 1272 | 63 | 3.7 | 1210 | 2 | S35548 | DNA-directed RNA p |
| 1273 | 63 | 3.7 | 1286 | 1 | S35845 | DNA-directed RNA p |
| 1274 | 63 | 3.7 | 1286 | 2 | T28521 | DNA-directed RNA p |
| 1275 | 63 | 3.7 | 1286 | 2 | A72161 | MeR protein - vari |
| 1276 | 63 | 3.7 | 1289 | 2 | T43251 | furin (EC 3.4.21.7 |
| 1277 | 63 | 3.7 | 1299 | 2 | T33136 | hypothetical prote |
| 1278 | 63 | 3.7 | 1426 | 2 | A99580 | hypothetical prote |
| 1279 | 63 | 3.7 | 1460 | 2 | T00095 | hypothetical prote |
| 1280 | 63 | 3.7 | 1464 | 2 | A43274 | N-methyl D-asparta |
| 1281 | 63 | 3.7 | 1486 | 2 | A10906 | glutamate synthase |
| 1282 | 63 | 3.7 | 1513 | 2 | A54895 | mucin 2, intestinal |
| 1283 | 63 | 3.7 | 1535 | 2 | S46224 | peroxidase - frui |
| 1284 | 63 | 3.7 | 1624 | 2 | T25592 | hypothetical prote |
| 1285 | 63 | 3.7 | 1624 | 2 | T08880 | NMDA receptor-bind |
| 1286 | 63 | 3.7 | 1662 | 1 | H71402 | probable kinesin - |
| 1287 | 63 | 3.7 | 1818 | 1 | S73852 | hypothetical prote |
| 1288 | 63 | 3.7 | 1839 | 1 | RRWPEM | genome polyprotein |
| 1289 | 63 | 3.7 | 2274 | 2 | T21052 | hypothetical prote |
| 1290 | 63 | 3.7 | 2748 | 2 | S57976 | nuclear migration |
| 1291 | 63 | 3.7 | 4544 | 1 | S02392 | alpha-2-macroglobu |
| 1292 | 62.5 | 3.7 | 135 | 2 | A13164 | hypothetical prote |
| 1293 | 62.5 | 3.7 | 151 | 2 | A47667 | VPS homolog - bovi |
| 1294 | 62.5 | 3.7 | 169 | 2 | A25652 | protein kinase (EC |
| 1295 | 62.5 | 3.7 | 184 | 2 | E71504 | hypothetical prote |
| 1296 | 62.5 | 3.7 | 206 | 2 | H71531 | superoxide dismuta |
| 1297 | 62.5 | 3.7 | 225 | 2 | F87528 | hypothetical prote |
| 1298 | 62.5 | 3.7 | 226 | 2 | A64152 | probable thiamine- |
| 1299 | 62.5 | 3.7 | 235 | 2 | S15655 | zein, 19K - maize |
| 1300 | 62.5 | 3.7 | 253 | 2 | F89790 | conserved hypochet |
| 1301 | 62.5 | 3.7 | 259 | 2 | H81159 | ycf1 protein - red |
| 1302 | 62.5 | 3.7 | 261 | 2 | T11948 | 22K zein precursor |
| 1303 | 62.5 | 3.7 | 267 | 2 | T02983 | enkephalin precurs |
| 1304 | 62.5 | 3.7 | 269 | 2 | B35678 | probable senescenc |
| 1305 | 62.5 | 3.7 | 270 | 2 | B84578 | hypothetical prote |
| 1306 | 62.5 | 3.7 | 274 | 2 | T42648 | short-chain alcoh |
| 1307 | 62.5 | 3.7 | 291 | 2 | G97327 | hypothetical prote |
| 1308 | 62.5 | 3.7 | 306 | 2 | E70190 | ATP-binding protei |
| 1309 | 62.5 | 3.7 | 323 | 2 | E88930 | protein R1611.11 |
| 1310 | 62.5 | 3.7 | 328 | 2 | G89152 | protein C24B5.5 [i |
| 1311 | 62.5 | 3.7 | 332 | 2 | B85588 | probable membrane |
| 1312 | 62.5 | 3.7 | 332 | 2 | A99738 | hypothetical prote |
| 1313 | 62.5 | 3.7 | 332 | 2 | C64816 | hypothetical prote |
| 1314 | 62.5 | 3.7 | 332 | 2 | B84245 | DNA topoisomerase |
| 1315 | 62.5 | 3.7 | 366 | 2 | G97321 | alpha/beta superfa |
| 1316 | 62.5 | 3.7 | 371 | 2 | S50228 | PAB1 protein - yea |
| 1317 | 62.5 | 3.7 | 375 | 2 | S77053 | magnesium/cobalt t |
| 1318 | 62.5 | 3.7 | 380 | 2 | A10260 | probable aminotran |
| 1319 | 62.5 | 3.7 | 399 | 2 | S58222 | PO-rich protein - |
| 1320 | 62.5 | 3.7 | 400 | 2 | AG1238 | hypothetical prote |
| 1321 | 62.5 | 3.7 | 401 | 2 | AG2415 | two-component hybr |
| 1322 | 62.5 | 3.7 | 407 | 2 | S49643 | hypothetical prote |
| 1323 | 62.5 | 3.7 | 418 | 2 | T10652 | hypothetical prote |
| 1324 | 62.5 | 3.7 | 419 | 2 | S49643 | hypothetical prote |
| 1325 | 62.5 | 3.7 | 427 | 2 | S41087 | inward rectifier p |
| 1326 | 62.5 | 3.7 | 427 | 2 | S52846 | potassium channel, |
| 1327 | 62.5 | 3.7 | 453 | 2 | S11087 | gamma-aminobutyric |
| 1328 | 62.5 | 3.7 | 475 | 2 | A12439 | hypothetical prote |
| 1329 | 62.5 | 3.7 | 479 | 2 | S73770 | NADH oxidase nox - |
| 1330 | 62.5 | 3.7 | 481 | 2 | A8E911 | TLID protein (limp |
| 1331 | 62.5 | 3.7 | 485 | 2 | E72115 | hypothetical prote |
| 1332 | 62.5 | 3.7 | 488 | 2 | T05313 | hypothetical prote |
| 1333 | 62.5 | 3.7 | 493 | 2 | C71903 | D-lamyl-D-alanine |
| 1334 | 62.5 | 3.7 | 495 | 1 | A45738 | alpha-amylose (EC |
| 1335 | 62.5 | 3.7 | 495 | 2 | B85810 | cytoplasmic alpha- |
| 1336 | 62.5 | 3.7 | 495 | 2 | B90962 | cytochrome-c oxida |
| 1337 | 62.5 | 3.7 | 508 | 2 | S74200 | hypothetical prote |
| 1338 | 62.5 | 3.7 | 517 | 2 | T07704 | hypothetical prote |
| 1339 | 62.5 | 3.7 | 519 | 2 | T44269 | probable photomorp |
| 1340 | 62.5 | 3.7 | 532 | 2 | F84901 | lens fiber cell be |
| 1341 | 62.5 | 3.7 | 533 | 2 | JC1103 | methy1-accepting c |
| 1342 | 62.5 | 3.7 | 534 | 2 | B69896 | acetyl choline rec |
| 1343 | 62.5 | 3.7 | 548 | 2 | T23270 | |

| | | | | | | |
|------|------|-----|------|---|--------|---------------------|
| 1344 | 62.5 | 3.7 | 551 | 2 | A57189 | secy protein homol |
| 1345 | 62.5 | 3.7 | 551 | 2 | P84557 | probable preprotei |
| 1346 | 62.5 | 3.7 | 554 | 2 | T45137 | phosphoprotein pho |
| 1347 | 62.5 | 3.7 | 554 | 2 | T50310 | phosphoprotein pho |
| 1348 | 62.5 | 3.7 | 568 | 1 | PIWL18 | L1 protein - huma |
| 1349 | 62.5 | 3.7 | 574 | 1 | VGNZR2 | cell fusion glycop |
| 1350 | 62.5 | 3.7 | 574 | 1 | VGNZR2 | cell fusion glycop |
| 1351 | 62.5 | 3.7 | 574 | 1 | VGNZR2 | cell fusion glycop |
| 1352 | 62.5 | 3.7 | 574 | 2 | B28929 | cell fusion glycop |
| 1353 | 62.5 | 3.7 | 574 | 2 | S37254 | cell fusion protei |
| 1354 | 62.5 | 3.7 | 578 | 2 | T38775 | hypothetical prote |
| 1355 | 62.5 | 3.7 | 599 | 2 | G86204 | hydrogenase (EC 1. |
| 1356 | 62.5 | 3.7 | 601 | 1 | S11777 | hypothetical prote |
| 1357 | 62.5 | 3.7 | 603 | 2 | T24315 | myelin-associated |
| 1358 | 62.5 | 3.7 | 626 | 2 | A61084 | endopeptidase O (E |
| 1359 | 62.5 | 3.7 | 630 | 2 | B98058 | TVI protein - huma |
| 1360 | 62.5 | 3.7 | 645 | 2 | G01205 | hypothetical prote |
| 1361 | 62.5 | 3.7 | 652 | 2 | T20046 | hypothetical prote |
| 1362 | 62.5 | 3.7 | 663 | 2 | T26835 | mitosis initiation |
| 1363 | 62.5 | 3.7 | 708 | 2 | A38436 | hypothetical prote |
| 1364 | 62.5 | 3.7 | 721 | 2 | A95144 | phenylalanine-tRNA |
| 1365 | 62.5 | 3.7 | 721 | 2 | G98011 | primosomal replica |
| 1366 | 62.5 | 3.7 | 748 | 2 | T04774 | hypothetical prote |
| 1367 | 62.5 | 3.7 | 759 | 2 | T41357 | hypothetical prote |
| 1368 | 62.5 | 3.7 | 769 | 2 | T49911 | anthranilate phosp |
| 1369 | 62.5 | 3.7 | 785 | 2 | T01025 | hypothetical prote |
| 1370 | 62.5 | 3.7 | 795 | 2 | I64115 | hypothetical prote |
| 1371 | 62.5 | 3.7 | 797 | 2 | AH1302 | 3',5'-cyclic-GMP p |
| 1372 | 62.5 | 3.7 | 804 | 2 | B83963 | hypothetical prote |
| 1373 | 62.5 | 3.7 | 809 | 2 | E70692 | protein ZC53.4 [im |
| 1374 | 62.5 | 3.7 | 819 | 2 | E70105 | protein Tf9.14 [i |
| 1375 | 62.5 | 3.7 | 828 | 2 | C96639 | protein tyrosine p |
| 1376 | 62.5 | 3.7 | 832 | 2 | JC8051 | hypothetical prote |
| 1377 | 62.5 | 3.7 | 849 | 2 | T20422 | 3',5'-cyclic-GMP p |
| 1378 | 62.5 | 3.7 | 853 | 2 | A36617 | hypothetical prote |
| 1379 | 62.5 | 3.7 | 854 | 2 | A42828 | bone morphogenetic |
| 1380 | 62.5 | 3.7 | 855 | 2 | B89472 | focal adhesion kin |
| 1381 | 62.5 | 3.7 | 895 | 2 | T49010 | hypothetical prote |
| 1382 | 62.5 | 3.7 | 921 | 2 | T51804 | respiratory burst |
| 1383 | 62.5 | 3.7 | 932 | 2 | E69552 | leucyl-tRNA synthe |
| 1384 | 62.5 | 3.7 | 932 | 2 | S76501 | preprotein translo |
| 1385 | 62.5 | 3.7 | 976 | 2 | T51137 | ionotropic glutama |
| 1386 | 62.5 | 3.7 | 1038 | 2 | JC5527 | bone morphogenetic |
| 1387 | 62.5 | 3.7 | 1052 | 2 | I53012 | hypothetical prote |
| 1388 | 62.5 | 3.7 | 1060 | 2 | S63252 | hypothetical prote |
| 1389 | 62.5 | 3.7 | 1196 | 2 | S40908 | hypothetical prote |
| 1390 | 62.5 | 3.7 | 1279 | 2 | T18312 | tyb protein - yea |
| 1391 | 62.5 | 3.7 | 1328 | 2 | B28097 | tyb protein - yea |
| 1392 | 62.5 | 3.7 | 1353 | 2 | T19691 | hypothetical prote |
| 1393 | 62.5 | 3.7 | 1366 | 2 | B86292 | F7H2.12 protein - |
| 1394 | 62.5 | 3.7 | 1447 | 1 | VGIHE3 | E2 glycoprotein pr |
| 1395 | 62.5 | 3.7 | 1447 | 1 | VGIHE2 | E2 glycoprotein pr |
| 1396 | 62.5 | 3.7 | 1449 | 1 | VGIHE5 | E2 glycoprotein pr |
| 1397 | 62.5 | 3.7 | 1449 | 2 | S47423 | E2 glycoprotein pr |
| 1398 | 62.5 | 3.7 | 1453 | 2 | S41453 | spike protein - ca |
| 1399 | 62.5 | 3.7 | 1475 | 2 | T33318 | hypothetical prote |
| 1400 | 62.5 | 3.7 | 1528 | 2 | J50703 | DNA topoisomerase |
| 1401 | 62.5 | 3.7 | 1548 | 2 | T25080 | hypothetical prote |
| 1402 | 62.5 | 3.7 | 1663 | 2 | T28923 | hypothetical prote |
| 1403 | 62.5 | 3.7 | 1827 | 1 | UUHU | sucrose alpha-gluc |
| 1404 | 62.5 | 3.7 | 1899 | 2 | T49273 | hypothetical prote |
| 1405 | 62.5 | 3.7 | 1979 | 2 | JM0059 | mcpd protein - mo |
| 1406 | 62.5 | 3.7 | 2167 | 2 | AF1489 | cell wall-associat |
| 1407 | 62.5 | 3.7 | 2183 | 2 | S47307 | genome polyprotein |
| 1408 | 62.5 | 3.7 | 2492 | 1 | C44213 | nonstructural poly |
| 1409 | 62.5 | 3.7 | 2492 | 1 | MNWVTD | toxlin A - Clostrid |
| 1410 | 62.5 | 3.7 | 2710 | 2 | A37052 | giant protein p619 |
| 1411 | 62.5 | 3.7 | 4861 | 2 | S37152 | hypothetical prote |
| 1412 | 62.5 | 3.7 | 5105 | 2 | T32650 | hypothetical prote |
| 1413 | 62.5 | 3.7 | 5138 | 2 | B96695 | hypothetical prote |
| 1414 | 62 | 3.7 | 117 | 2 | T07861 | germination-specif |
| 1415 | 62 | 3.7 | 144 | 2 | AF3156 | hypothetical prote |
| 1416 | 62 | 3.7 | 144 | 2 | C98131 | |

| | | | | | |
|------|----|-----|-----|---|--------|
| 1417 | 62 | 3.7 | 156 | 2 | T44233 |
| 1418 | 62 | 3.7 | 161 | 2 | F72861 |
| 1419 | 62 | 3.7 | 161 | 2 | F72861 |
| 1420 | 62 | 3.7 | 227 | 2 | H95231 |
| 1421 | 62 | 3.7 | 232 | 2 | D71432 |
| 1422 | 62 | 3.7 | 258 | 2 | T38373 |
| 1423 | 62 | 3.7 | 264 | 2 | A81668 |
| 1424 | 62 | 3.7 | 282 | 2 | A35084 |
| 1425 | 62 | 3.7 | 290 | 2 | H81832 |
| 1426 | 62 | 3.7 | 294 | 2 | T21474 |
| 1427 | 62 | 3.7 | 309 | 2 | B82460 |
| 1428 | 62 | 3.7 | 326 | 1 | VGK7H |
| 1429 | 62 | 3.7 | 326 | 1 | VGK7H |
| 1430 | 62 | 3.7 | 326 | 1 | VGK7H |
| 1431 | 62 | 3.7 | 334 | 2 | T29672 |
| 1432 | 62 | 3.7 | 339 | 2 | B34895 |
| 1433 | 62 | 3.7 | 341 | 2 | SE4079 |
| 1434 | 62 | 3.7 | 342 | 1 | F64141 |
| 1435 | 62 | 3.7 | 344 | 2 | T28729 |
| 1436 | 62 | 3.7 | 349 | 2 | G81697 |
| 1437 | 62 | 3.7 | 350 | 2 | G01950 |
| 1438 | 62 | 3.7 | 352 | 2 | H43763 |
| 1439 | 62 | 3.7 | 353 | 2 | C70502 |
| 1440 | 62 | 3.7 | 354 | 1 | S17953 |
| 1441 | 62 | 3.7 | 358 | 2 | T23802 |
| 1442 | 62 | 3.7 | 359 | 2 | H85823 |
| 1443 | 62 | 3.7 | 359 | 2 | B90977 |
| 1444 | 62 | 3.7 | 359 | 2 | B90977 |
| 1445 | 62 | 3.7 | 363 | 2 | T33527 |
| 1446 | 62 | 3.7 | 374 | 2 | AG3337 |
| 1447 | 62 | 3.7 | 385 | 2 | T18821 |
| 1448 | 62 | 3.7 | 387 | 2 | D75417 |
| 1449 | 62 | 3.7 | 389 | 2 | B65182 |
| 1450 | 62 | 3.7 | 394 | 2 | T21759 |
| 1451 | 62 | 3.7 | 394 | 2 | T21759 |
| 1452 | 62 | 3.7 | 398 | 2 | AF0529 |
| 1453 | 62 | 3.7 | 402 | 2 | G83289 |
| 1454 | 62 | 3.7 | 406 | 2 | C81017 |
| 1455 | 62 | 3.7 | 407 | 2 | T37865 |
| 1456 | 62 | 3.7 | 410 | 2 | C64831 |
| 1457 | 62 | 3.7 | 416 | 1 | K8FO |
| 1458 | 62 | 3.7 | 420 | 2 | H86331 |
| 1459 | 62 | 3.7 | 421 | 2 | B64819 |
| 1460 | 62 | 3.7 | 424 | 2 | T26997 |
| 1461 | 62 | 3.7 | 433 | 2 | T27538 |
| 1462 | 62 | 3.7 | 443 | 2 | T44643 |
| 1463 | 62 | 3.7 | 463 | 2 | T41390 |
| 1464 | 62 | 3.7 | 464 | 2 | T20238 |
| 1465 | 62 | 3.7 | 476 | 2 | G84634 |
| 1466 | 62 | 3.7 | 483 | 2 | AD1223 |
| 1467 | 62 | 3.7 | 497 | 2 | B81987 |
| 1468 | 62 | 3.7 | 509 | 2 | F81041 |
| 1469 | 62 | 3.7 | 515 | 2 | T00510 |
| 1470 | 62 | 3.7 | 517 | 2 | T43358 |
| 1471 | 62 | 3.7 | 521 | 2 | AB0269 |
| 1472 | 62 | 3.7 | 527 | 2 | AE2932 |
| 1473 | 62 | 3.7 | 543 | 2 | T16015 |
| 1474 | 62 | 3.7 | 549 | 2 | T16016 |
| 1475 | 62 | 3.7 | 550 | 2 | B98350 |
| 1476 | 62 | 3.7 | 570 | 2 | AC2356 |
| 1477 | 62 | 3.7 | 575 | 2 | AD0453 |
| 1478 | 62 | 3.7 | 575 | 2 | B64174 |
| 1479 | 62 | 3.7 | 580 | 2 | C81352 |
| 1480 | 62 | 3.7 | 593 | 1 | DTCHPH |
| 1481 | 62 | 3.7 | 600 | 2 | T04267 |
| 1482 | 62 | 3.7 | 604 | 2 | S57065 |
| 1483 | 62 | 3.7 | 605 | 2 | D82434 |
| 1484 | 62 | 3.7 | 689 | 2 | T33785 |
| 1485 | 62 | 3.7 | 689 | 2 | S60306 |
| 1486 | 62 | 3.7 | 699 | 1 | S38982 |
| 1487 | 62 | 3.7 | 721 | 2 | T05815 |
| 1488 | 62 | 3.7 | 731 | 2 | T09172 |
| 1489 | 62 | 3.7 | 736 | 2 | S59136 |

hypothetical prote
Acotf-93 protein -
Coq family protei
conserved hypothet
hypothetical prote
hypothetical prote
conserved hypothet
fibinogen-related
hypothetical prote
hypothetical prote
glycoprotein VP7 p
glycoprotein VP7 p
hypothetical prote
transcription fact
snRNP-associated p
probable L-iditol
hypothetical prote
fructose-bisphosph
hypothetical prote
nonstructural prot
hypothetical prote
alkanal monooxygen
connexin 40 - mous
hypothetical prote
hypothetical prote
hypothetical prote
transcription regu
hypothetical prote
acyl-CoA dehydroge
hypothetical prote
bacteriophage M4 a
hypothetical prote
1-deoxy-D-xylulose
conserved hypothet
amino-acid N-acety
probable MYST-fami
yeoQ protein - Ebc
cosglutination fact
Fef9.9 protein - A
yblu protein - Ebc
hypothetical prote
hypothetical prote
galactosyl transfe
zinc finger protei
hypothetical prote
probable prollycar
hypothetical prote
hypothetical prote
cytoplasmic axial
probable cytochrom
hmf-3/forhead tra
anthranilate synth
Na+/H+ antiporter
hypothetical prote
hypothetical prote
hypothetical prote
hypothetical prote
lysocitrinate dehydr
hypothetical prote
lipid export ABC t
puri bfunctional
Npr1 protein homol
probable membrane
probable conserved
hypothetical prote
Bp1 protein - pa
kinesin-related pr
hypothetical prote
probable calcium-a
estradiol 17beta-d

| | | | | | |
|------|----|-----|-----|---|--------|
| 1490 | 62 | 3.7 | 762 | 2 | C69657 |
| 1491 | 62 | 3.7 | 789 | 2 | T45762 |
| 1492 | 62 | 3.7 | 799 | 2 | T00052 |
| 1493 | 62 | 3.7 | 819 | 1 | TWCHRG |
| 1494 | 62 | 3.7 | 819 | 2 | A96567 |
| 1495 | 62 | 3.7 | 837 | 2 | B82932 |
| 1496 | 62 | 3.7 | 838 | 2 | JC7363 |
| 1497 | 62 | 3.7 | 844 | 2 | S61104 |
| 1498 | 62 | 3.7 | 859 | 2 | F44981 |
| 1499 | 62 | 3.7 | 906 | 2 | B84948 |
| 1500 | 62 | 3.7 | 937 | 2 | I53282 |

ALIGNMENTS

RESULT 1
JC7110
brain-specific membrane anchor protein - human
C:Species: Homo sapiens (man)
C:Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
C:Accession: JC7110
R:Elson, G.C.A.; de Coignac, A.B.; Aubry, J.P.; Delneste, Y.; Magistrelli, G.; Holzwarth
Biochem. Biophys. Res. Commun. 264, 55-62, 1999
A>Title: BSMAP, a novel protein expressed specifically in the brain whose gene is local
A:Reference number: JC7110; MUID:994548621; PMID:10527841
A:Accession: JC7110
A:Molecule type: mRNA
A:Residues: 1-342 <EUS>
A:Cross-references: UNIPROT:O9UK28; GB:AF186264; NID:g6003653; PIDN:AAFO0529.1; PID:g600
C:Gene: bsmad
A:Map position: 19p12
C:Superfamily: human brain-specific membrane anchor protein
C:Keywords: brain; glycoprotein; membrane bound; transmembrane protein
Query Match 25.0%; Score 423.5; DB 2; Length 342;
Best Local Similarity 33.5%; Pred. No. 3.7e-29;
Matches 107; Conservative 56; Mismatches 115; Indels 41; Gaps 8;
QY 16 LPLLLTLTALA---GSGTASAEAFDSVLGDTASCHRAQGLTYPLATYPRBEEL----- 67
DB 7 MPPLLILLILASPASAPAPADPAFQLDGTQNCQRCH-DRDLGPOQAQLEGASE 65
QY 68 -----YACQRCRIFSCQFVDDGIDARKTKLEBSACTEYSGSDQYACHLCCQ 118
DB 66 SPYRAVLISACERCRIFSCRFYARSSKKNATQTECEAAVEAYVEAQOACSHGCW 125
QY 119 NOLPFAELROBOLMSLMKMLPLPLTLVRSFWSMDMSAQSFTSSWTFYLOADDGKIV 178
DB 126 SQAPRPPEQKRVLEAPSGALSL-LDLFSLCNDLVNAGGFVSSWTYLLQDNGKVV 184
QY 179 IFQSKPEIQ---YAPHLEQEPNLRSE-----SLSKM--SYLOMRNSQAKR 219
DB 185 VFQQPIYVLSIGFOGGRQVRVETWGRSHPALRVHDPVGRDLKVRKAKIRVKTSSAK 244
QY 220 NPLDESDGFLRCLISLNSG---WILTTVLVSWTLMTCATATVAVQYVSEKSI 276
DB 245 VESERPQNDPLSCMSRRSGLPRIWLACCLFSLVLMILMSCSLVTPAGHLKRPULT 304
QY 277 YGDLEFPMNEQKLNRYPASS 295
DB 305 EQHKGFMMEDPWPPLYPPS 323
RESULT 2
T29551
hypothetical protein C16D9.2 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C:Accession: T29551
R:Gatung, S.; Le, T.T.
Submitted to the EMBL Data Library, July 1996

A:Description: The sequence of C. elegans cosmid C16D9.
A:Reference number: Z20640
A:Accession: J29551
A:Status: Preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-2380 <GAT>
A:Cross-references: EMBL:U64858; PIDN:AA18281.1; GSPDB:GN00023; CESP:C16D9.2
A:Experimental source: strain Bristol N2; clone C16D9
C:Genetics:
A:Gene: CESP:C16D9.2
A:Map position: 5
A:Introns: 45/3; 70/3; 116/1; 252/3; 316/1; 365/1; 473/2; 508/1; 531/1; 596/2; 681/3; 721

Query Match 6.0%; Score 102; DB 2; Length 2380;
Best Local Similarity 21.7%; Pred. No. 3.6;
Matches 65; Conservative 38; Mismatches 97; Indels 100; Gaps 16;

34 SAEAPSVLGDPTASCHRAQ---LTYPPLH-----YKREBELYACQRCRLFSIC 80
25 SATVSSSL---KTQSQCEKRLNAYPLDGSVHTGLAEVYSRISCRGCE----- 76
81 QFVDDGIDLNTKLECESACTEAYSQSDQYACHLGCQNL-PPAELRQEQOLMSLMPKQH 139
77 -----DVDERESKCDVKSCSEBIVSN---ACKQCRVAVISFLAQOALLIQVHVNME 126
140 LL-----PRLTVAS-----FMSMDMSASFTSSWTFYLQADDKIVLFO 181
127 VLETSMKLKEPPELTAELEKIANADIWFPSQTRPLNGILGWRT----- 172
182 SKPEIQVAPHLQEPTNLRESLSLQ-----SYLQMRNSQARNFLEDSGDFLRC 233
173 SLPO-----NSFRNSLSSEVAVPEPHGHVRLALSTRNVIVSRITTYHLR 221
234 LSLNSGWLITTLTVLSVWL---LWICCAVAVAVEQYVSEKLSIYDLEFMNEQKLN 289
222 LS-KSG---TTLLEVIGQLSDPDRVAVCYRT---NQPTPKKLTIM---TLNDNTIN 268

RESULT 3
T46488
Hypoetical protein DKFPZ434J065.1 - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 04-Feb-2000 #sequence_revision 04-Feb-2000 #text_change 09-Jul-2004
A:Accession: T46488
R:Duesterhoef, A.; Lauber, J.; Mewes, H.W.; Gassenhuber, J.; Wiemann, S.
Submitted to the Protein Sequence Database, January 2000
A:Reference number: Z23035
A:Accession: T46488
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-741 <AAA>
A:Cross-references: UNIPROT:Q8NDE6; EMBL:AL137638
A:Experimental source: adult testis; clone DKFPZ434J065
C:Genetics:
A:Note: DKFPZ434J065.1

Query Match 5.6%; Score 95.5; DB 2; Length 741;
Best Local Similarity 18.0%; Pred. No. 3.3;
Matches 65; Conservative 47; Mismatches 118; Indels 131; Gaps 15;

31 GRASAEAPSVLGDPTASCHRAQOLYPLHTYKREBELYACQ-----RGCRLSFI 79
305 GKTCKMLDSGALGD---HGCE---HSCVSSSDSFVCCQFEGYILREDKTKRKADV 354
80 CQFVDDGIDLNTKLECESACTEAYSQSDQYAC-----HL 115
355 COAIDHG-----CHICV---NSDDSYTCCLBGFRLAEDGKRCKRKADVCKSTH 401
116 GCQN-----QLPPAELRQEQOLMSLMPKQHLPLTLTVNSFMSDMDMSAS 160
402 GCEHICVNNNGNSYICKCSGFLAEDGRCKCTEGPDLVIVIDGSKSLGSENFENVQ 461

161 FITSWTFYLOADDGKIVIFQSKPE-----IQVAPHLQEPTNLRESLSKMSYLOMRN 214
462 FVT-----GIIDSLTSPKARVGLQSTQVHTFEFT-LRPNFSKAK-----DMK 505
215 SQAHNPLEDESGD-----FLRCLSLNSGWLITTLTVLSVWLWICCATVATAVEQY 268
506 AVAHMKYMGKSMWGLAKHMFERSFTQGE-----ARPISTR 543
269 VPSRKLTIYGD-----LERNQKLNRYPASSLVVRSKTEPDEEAGPLPTKVLNLAHS 321
544 VPRALVFTDGRADVDVSEWASAKANGITTVAVGVKALEELQELIASEPTKHLFYA 602
322 E 322
603 E 603

RESULT 4
A57513
heat shock protein 110k - Chinese hamster
C:Species: Crictetus griseus (Chinese hamster)
C:Date: 08-Dec-1995 #sequence_revision 08-Dec-1995 #text_change 09-Jul-2004
A:Accession: A57513; S51311
R:Lee-Yoon, D.; Easton, D.; Murawski, M.; Burd, R.; Subjeck, J.R.
J. Biol. Chem. 270, 15725-15733, 1995
A:Title: Identification of a major subfamily of large hep70-like proteins through the c1
A:Reference number: A57513; MUID:95318163; PMID:7797574
A:Accession: A57513
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-858 <LEB>
A:Cross-references: UNIPROT:Q60446; GB:Z47807; NID:9633180; PIDN:CAA87768.1; PID:9633181
R:Yoon, D.; Murawski, M.J.; Burd, R.; Easton, D.P.; Subjeck, J.R.
Submitted to the EMBL Data Library, January 1995
A:Description: Identification of a major subfamily of large hep70-like proteins through
A:Reference number: S51311
A:Accession: S51311
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-858 <YOO>
A:Cross-references: EMBL:Z47807; NID:9633180; PIDN:CAA87768.1; PID:9633181
C:Superfamily: heat shock protein 91
C:Keywords: heat shock; stress-induced protein

Query Match 5.5%; Score 92.5; DB 2; Length 858;
Best Local Similarity 21.3%; Pred. No. 7.2;
Matches 62; Conservative 47; Mismatches 89; Indels 93; Gaps 14;

53 QLTYPPLH-----TYKREBELYAC-----QRGRLSFSICQFVDDGIDLNTKTL 94
316 KIEVPLHSLMGQTHLKTEDVAIEIVGATRIPAVKERIAKF-----GKDVST-- 365
95 ECESACTEAYSQSDQYV---CHLGCQNLPPAELRQEQOLMSLMPKQHLPLTLTVRSFWS 152
366 -----LNADEAVARGCALQCALISPAKRVESVTDVAP-----FISLVNHD 410
153 DMDMSASGFT-----SWTFYLOADDGKIVIFQSKPEIQVAPHLQEPTNLRESLS 205
411 EETBVEHVEFRNMAAPRSKVLTLRKGFLEAFYSP--QGVPIYP-----A 457
206 KMSYLQMRNSQAHNPLEDESGDGLRCLSLNSGWLITTLTVLSVWLWICCATVATAV 265
458 KIIGRVVGNVAOK---DGKSKVKVAVRVNTGIGF-----ISTASMV 498
266 EGYVPSER---LSYIGDLEFMNEQKLNRYPASSLVVRSKTEPDEEAGPLP 313
499 EK-VPTEDDGSVEADMECPNOK-----PSSSDVDNKSQODNSEAGTOP 543

RESULT 5
G7157
probable glucanotransferase - Chlamydia trachomatis (serotype D, strain UW3/Cx)
C:Species: Chlamydia trachomatis

QY 182 SKPEI-----QYA-----PHLEOE--PTNLRSSLSK---MSYLQMNQGAHNN 220
 Db 170 QKQPLSRPLHYSEYKGLDVALDQPHSNKDELPSCGHHHGTQPKGLALRLKGAEPMKR 229
 QY 221 FLEDGSDGFLRLCLSLNSGMLTTTLVLSVWVL--WICCATVATAVEQYVPSSEKLSIYGD 279
 Db 230 ALNRQCG--GYLSC-----GWFDPANVTVPDTPLELVN-----RLNPAERV----- 267
 QY 280 LEFPMNQKLNRYRPASSLVYRKTE---DHERAGPLPTKVL 318
 Db 268 -----KGWRLPEGLTMVNRQGNLDQIDTRQIPPLDSRIEL 303

RESULT 9

S66666
 heat shock protein (clone E71) - mouse
 C:Species: Mus musculus (house mouse)
 C:Date: 15-Feb-1997 #sequence_revision 13-Mar-1997 #text_change 09-Jul-2004
 C:Accession: S66666; S72507
 R:Morozov, A.; Subjeck, J.; Raychaudhuri, P.
 FBS Lett. 371, 214-218, 1995
 A:Title: HPV16 E7 oncoprotein induces expression of a 110 kDa heat shock protein.
 A:Reference number: S66666; MUID:96013135; PMID:7556594
 A:Accession: S66666
 A:Status: nucleic acid sequence not shown
 A:Molecule type: mRNA
 A:Residues: 1-859 <MOR>
 A:Cross-references: UNIPROT:Q61699, EMBL:L40406
 R:Morozov, A.; Subjeck, J.; Raychaudhuri, P.
 submitted to the EMBL Data Library, June 1995
 A:Reference number: S72507
 A:Accession: S72507
 A:Molecule type: mRNA
 A:Residues: 1-182, 'I', 184-450, 'G', 452-493, 'T', 495-575, 'NE', 578-615, 'Y', 617-629, 'E', 631-7
 A:Cross-references: EMBL:L40406; NID:9840651; PIDN:AAA9485.1; PID:9840652
 C:Genetics:
 A:Gene: hsp-E71
 C:Superfamily: heat shock protein 91
 C:Keywords: heat shock; molecular chaperone; stress-induced protein

Query Match 5.0%; Score 85.5; DB 2; Length 859;
 Best Local Similarity 20.2%; Pred. No. 29;
 Matches 63; Conservative 51; Mismatches 105; Indels 93; Gaps 15;
 QY 30 SGTASAEAFDSVLDGTASCHRAQCLTYPLH-----TYKREELVAC-----Q 71
 Db 298 SGRNRSGPBEICAEILQ-----KIEVPLHSIMAQTLKAEDVSAIETVGATRIPAVKE 352
 QY 72 RGRPLFSICQFVDDGIDLNRTKLCEESACTEAYSSQDEQYACHLGCQNLFPALRLQ 131
 Db 353 RLAKRF-----GKDVSTLTNDEAV-----RRCALQCALISPAFKRESV 394
 QY 132 MSLMKMKHLFPPLTVRSFWSMDMSAQSFT-----SSWTFYLQADGDKIVFQSKP 184
 Db 395 TDVAV-----FPISLVNMHDSSEETGVAHVFSRNHAPFSKLTPLRGRPELBAFYSDP 449
 QY 185 EIOYAPHLEQEPPTNLRSSLSKMSYLOMNQGAHNFLEDGSDGFLRLCLSLNSGMLTT 244
 Db 450 ---QDVPE-----AKIGRFVQNVSAQK---DGKSRVKKVKNVNTHTGIFT- 491
 QY 245 TLVLSVWVLWICCATVATAVEQYVPSSEK---LSIYGDLEFPMNQKLNRYRPASSLVYRS 301
 Db 492 -----ISISMWER-VPTREBSSSLEAMMECFQRNR-----PTESSDVVKN 532
 QY 302 KTEDEHEKGPDP 313
 Db 533 IQDNSEAGTOP 544

RESULT 10

152300
 giantin - human

N:Alternate names: GCP372
 C:Species: Homo sapiens (man)
 C:Date: 01-Nov-1996 #sequence_revision 01-Nov-1996 #text_change 09-Jul-2004
 C:Accession: 152300
 R:Solda, M.; Matsu, Y.; Fujiwara, T.; Nishio, M.; Ikehara, Y.
 Biochem. Biophys. Res. Commun. 205, 1399-1408, 1994
 A:Title: Molecular cloning and sequence analysis of a human 372-kDa protein localized in
 A:Reference number: 152300; MUID:95100974; PMID:7802676
 A:Accession: 152300
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-3225 <RES>
 A:Cross-references: UNIPROT:Q14789; GB:D25542; NID:9662389; PIDN:BA05025.1; PID:9808869
 C:Superfamily: giantin

Query Match 5.0%; Score 85.5; DB 2; Length 3225;
 Best Local Similarity 22.2%; Pred. No. 1,4e+02;
 Matches 76; Conservative 45; Mismatches 110; Indels 111; Gaps 17;

QY 25 ALAGSGTASAE-----FDSVLDGTASCHRAQCLTYPLHYPKEEELVACORG 73
 Db 1263 ALQGGTVAAQIKAQKLEIEKVELEKVSSTTS-----ELT-----KSEEVFQJQE- 1310
 QY 74 CRLFSICQFVDDGIDLNRTKLCEESACT-----EAYSQSDQYACHLGCQNLFPALRLQ 128
 Db 1311 -----QINKQGLEISLKTVSHAEVHAESIQKQ-----ESSQQLIAGL-- 1350
 QY 129 EQLMSLMKMKHLFPPLTVR---SFWSDMDASQSTTSWTFYLOADGDKIVFQSKP 184
 Db 1351 EHLRELQPKDELQKLSKKEEDVSYLSQISEKEALTYQTEIRIQED-LIKALHTQL 1409
 QY 185 EIOYAPH-----LEQEPPTNLRSSLSKMSYLOMNQGA-----HNRNLEDGES 227
 Db 1410 EMQKHEDEKRIKQVLECEKQKPEBIGESRRKQOI--QKQLQALLSKRKALKENKS 1467
 QY 228 DGPLRLCLSLNSGML--LTTTLVLSVWVLWICCATVATAVEQYVPS--EKLSTYGDLEF 282
 Db 1468 --LQEBLSIARGTIERITKSL-----ADVBQSQAQNKEDVYLGRLAL 1509
 QY 283 MNE-----QKLNRYRPASSLVYRSKTEDEHE 308
 Db 1510 LQEBRDKLITEMDRSLLENQSLSSCSRLKLALEGLTEDEK 1551

RESULT 11

156539
 giantin - human
 N:Alternate names: macrogolglin
 C:Species: Homo sapiens (man)
 C:Date: 19-Oct-1995 #sequence_revision 26-Jan-1996 #text_change 09-Jul-2004
 C:Accession: A56539; S37536
 R:Seelig, H.P.; Schranz, P.; Schroefer, H.; Wiemann, C.; Grifflths, G.; Renz, M.
 Mol. Cell. Biol. 14, 2564-2576, 1994
 A:Title: Molecular genetic analyses of a 376-kilodalton Golgi complex membrane protein (
 A:Reference number: A56539; MUID:94187728; PMID:7511208
 A:Accession: A56539
 A:Molecule type: mRNA
 A:Residues: 1-3259 <SEB>
 A:Cross-references: UNIPROT:Q14789; EMBL:X75304; NID:9405714; PIDN:CA053052.1; PID:94057
 C:Genetics:
 A:Gene: GDB:GOLGB1; GCP; GCP371
 A:Cross-references: GDB:454958
 A:Map position: 3q13.31-3q13.31
 C:Superfamily: giantin
 C:Keywords: coiled coil; Golgi apparatus; transmembrane protein
 F:3238-3254/Domain: transmembrane predicted <TM>

Query Match 5.0%; Score 85.5; DB 1; Length 3259;
 Best Local Similarity 22.2%; Pred. No. 1,4e+02;
 Matches 76; Conservative 45; Mismatches 110; Indels 111; Gaps 17;

QY 25 ALAGSGTASAE-----FDSVLDGTASCHRAQCLTYPLHYPKEEELVACORG 73

Db 1297 ALGGTSVAQIKAKLKEIEAKVELELVKSSSTS-----ELT-----KKSBEVFOLOE- 1344
 Qy 74 CRLPSICQFVDDGIDINRTKLECEBACT-----EAYSOSDEQVACHGCONOLPFAELRQ 128
 Db 1345 -----QINKGIEIEBLKTVSHBAEVHNASLQOKL-----ESSOLOIAGI-- 1384
 Qy 129 EQLMSLMPKMLLPPLTLVR-----SFWSMDMSAQSFITSSWTFYLQADGKIVIFQSKP 184
 Db 1385 EHLNELQPKLDELQKLSKEEDVYSLSGQSEKKAALTKIQTIELIEQED-LIKALHTQL 1443
 Qy 185 EIQYAPH-----LEQETNLRESLSKMSYLQMRNSQA-----HKNFLEDGES 227
 Db 1444 EMQAKHEDEKIKOQVELCEMKQKPEEIGESRAKOQI--ORKIQAALISRKKALENKENS 1501
 Qy 228 DGFRLCLSLNSGWI--LTTTLVLSVMVLWICATVATVAVGQYPS---EKLSIYGDEL 282
 Db 1502 --LQEBLSLANGTIERLTKSL-----ADVSQVSAQNKKEQDTVGLRLAL 1543
 Qy 283 MNE-----QKLNRYPASSLVVRSKTEDEER 308
 Db 1544 LQEBRDKLITEMDRSLLENQSLSSCESLKLALBGLTETDEK 1585

RESULT 12
 T00361
 hypothetical protein KIAA0678 - human (fragment)
 C:Species: Homo sapiens (man)
 C:Date: 01-Feb-1999 #sequence_revision 01-Feb-1999 #text_change 09-Jul-2004
 C:Accession: T00361
 R:Hitkawa, K.; Nagase, T.; Suyama, M.; Miyajima, N.; Tanaka, A.; Kotani, H.; Nomura, N.
 DNA Res. 5, 169-176, 1998
 A:Title: Prediction of the coding sequences of unidentified human genes. X. The complete
 A:Reference number: Z14142; MUID:98403880; PMID:9734811
 A:Accession: T00361
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-1021 <ISH>
 A:Cross-references: UNIPROT:O75165; EMBL:AB014578; NID:G3327169; PIDN:BA031653.1; PID:93
 A:Experimental source: brain; clone HK02710
 C:Genetics:
 A>Note: KIAA0678

Query Match 5.0%; Score 84.5; DB 2; Length 1021;
 Best Local Similarity 18.8%; Pred. No. 44;
 Matches 68; Conservative 51; Mismatches 133; Indels 109; Gaps 16;
 Qy 20 LLLTALAGSGGTASAEAFDSV-----LGDGTASGACQQLTYPLHTPKR-----E 65
 Db 554 LIFSLIRVHGAGQVQQLALBVVNIVTNSQDCVNNIABSMVLSLLALHSLPSSRQLVLE 613
 Qy 66 ELVACQCGCRFSLICQFVDDGIDINRTKLECEBACTEYVSQSDQYACHGCONOLPFAE 125
 Db 614 TLVYLTSSSTKLIK-----EKMAAGALITLLDMFCNSTHPQVR 650
 Qy 126 LROQLMSLMPKMLLP-----LTVRSFWSMDMSAQSFITSSWTFYLQADGKIVIFQ- 181
 Db 651 AQTAELEPAKTRADLTGKRVITLTKPLSPVPMAMR-----DNEBAVHIFEG 699
 Qy 182 --SKPEIQYAPH-LEQETNLRESLSKMSYLQMRNSQAHPNLED-----GESDG----- 229
 Db 700 THENPELIMNDNSDKVSTVREMWLEHFKN--QODNPEANMKLPEDFAVVGGEAEGELAV 758
 Qy 230 ---FLRCLSLNSGWI-----TTTLV-----LSVMVLMIICATVATA 264
 Db 759 GGVFLRFIAQPAVLRKREFLLALLEKLEKKNPHGETJETLTMTATVCFPSAOPQ 818
 Qy 265 VEQVYPSKLSIYDGL-----EFMNEQKLNRYPASSLVVRSKTEBDH-----EAGP 311
 Db 819 LADQVPP-----LGHLPKVIQAMNHRN--NALPKAIRIVYHALSERVELCVRAMASLETIGP 872
 Qy 312 L 312
 Db 873 L 873

RESULT 13
 T30845
 probable DNA repair protein RAD50 - mouse
 C:Species: Mus musculus (house mouse)
 C:Date: 22-Oct-1999 #sequence_revision 22-Oct-1999 #text_change 09-Jul-2004
 C:Accession: T30845
 R:Klim, K.K.; Daud, A.I.; Wong, S.C.; Pajak, L.; Tsai, S.C.; Wang, H.; Henzel, W.J.; Fiel
 J. Biol. Chem. 271, 29255-29264, 1996
 A:Title: Mouse RAD50 has limited epitoic homology to p53 and is expressed in the adult
 A:Reference number: Z20899; MUID:97067183; PMID:8910585
 A:Accession: T30845
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-1312 <KIM>
 A:Cross-references: UNIPROT:P70388; EMBL:U66887; NID:g1575574; PID:g1575575; PIDN:AAC528
 C:Genetics:
 A:Gene: RAD50
 A:Map position: 11
 C:Superfamily: RAD50 protein
 C:Keywords: DNA repair

Query Match 5.0%; Score 84; DB 2; Length 1312;
 Best Local Similarity 21.7%; Pred. No. 65;
 Matches 65; Conservative 46; Mismatches 106; Indels 82; Gaps 15;

Qy 63 KEELVACQCGCRFSLICQFVDDGIDINRTKLECE-----SACTEAYSQ-----SD 108
 Db 618 KEELDSYED--KLFDVCGSQDLSDLGRLKEIEKSKORAMLAGATVAVSQFITYQLTD 675
 Qy 109 EQVCHGCONQLPFAELROQLMSLMPKMLLPPLTVRSFWSMDMSAQSFITSSWTF 168
 Db 676 ENQSCCPVCQRFVFTAELEQVSDLSKALA-----PKLKSIESEKKK--- 722
 Qy 169 YLQADD--GKIVFQSPKEIQYAPHLEQETNLRESLSKMSYLQMRNSQAHPNLEDGE 226
 Db 723 ERRDENMGLVPVAGSIIDLK-----EKIEPELR--NLQSVN-----RDQLKNDIEQE 772
 Qy 227 SDGFLRCLSLNSGWI--LTTTLVLSVMVLWICATVATVAVGQY-----VSEKLSI 276
 Db 773 T-----LQGTIMEEBSAKV---CLTDVTIMERFQWELKDVERKIKQAAXL 816
 Qy 277 YG-----DLERNQKLNRYPASSLVVRSKTE-----DHGAGPLPKVLAHSE 322
 Db 817 QGVLDRTVQQVNOEKQK--QHRLDVTYSKIELRKLIQDQSQIQIHLASKTINLASE 873

RESULT 14
 T13254
 nitric-oxide synthase (EC 1.14.13.39) - fruit fly (Drosophila melanogaster)
 C:Species: Drosophila melanogaster
 C:Date: 13-Aug-1999 #sequence_revision 13-Aug-1999 #text_change 09-Jul-2004
 C:Accession: T13254
 R:Reguleki, M.; Tully, T.
 Proc. Natl. Acad. Sci. U.S.A. 92, 9072-9076, 1995
 A:Title: Molecular and biochemical characterization of dNOS: A Drosophila Ca/calmodulin-
 A:Reference number: Z17642; MUID:9601611; PMID:7568075
 A:Accession: T13254
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-1350 <REG>
 A:Cross-references: UNIPROT:Q27571; EMBL:U25117; NID:g1000081; PID:g1000082; PIDN:AAC468
 C:Genetics:
 A:Gene: NOS
 A:Cross-references: FlyBase:FBgn0011676
 A:Map position: 2
 C:Function:
 A:Description: catalyzes the oxidation of an L-arginine guanidino nitrogen and of NADPH;
 C:Superfamily: nitric-oxide synthase; flavodoxin homology; NADPH-ferritinoprotein reduct
 C:Keywords: calmodulin binding; chromoprotein; FAD; flavoprotein; FMN; heme; iron; metal
 F/329/Binding site: heme iron (Cys) (axial ligand) #status predicted

Query Match 5.0%; Score 84; DB 2; Length 1350;
Best Local Similarity 22.6%; Pred. No. 68;
Matches 76; Conservative 42; Mismatches 133; Indels 86; Gaps 16;

Search completed: March 28, 2005, 13:11:03
Job time : 40 secs

QY 14 LGPLPILLITVALAG-GSGTASAEAFDSVLGDTASCHRAQOLTYPLATYPKEEELVACQR 72
DB 1031 LTTPEPSRQLTLTLGFCEDTADKERLELVNDSSAYEDMRHRLP-HLLDVLEFPSCRP 1089
QY 73 GC-----RLEFIC--QPVVDGIDLN--RTLCECSACTEAYSOSDEQYACHL 115
DB 1090 PAPILLAQLTPLQPFYFISSPRRVSDIHLVAIVKRCED-----GQDERYGV-- 1141
QY 116 GCONQLPFAELROEQLMSLMPHLLF-----PLTLV-----RSFWS----- 152
DB 1142 -CSNVL--SGRADDELPMFARSALGFHLPSDRSRPITLIGPGICIAFRSFQOEFOYLR 1198
QY 153 DMMDSAQSFITSSWTFYLQADGKIVIFOSKPEIQYAPHLFOEPTNL-RESSLSRMSYLO 211
DB 1199 DLDPTAK--LPEMWLFCGRNRDVLVAEKAELQKQILDRVFLALSREQAIPK-TYVQ 1255
QY 212 MRNSQAHNRFLEDGSDGFLRCLSLNSGMILTTTLVLSVMVLWICATVATAVQYVPS 271
DB 1256 -----DLIEQFDSLXYQLIVQERGHIV-----CGDVTMAEHVYQTI 1292
QY 272 EKLSTYGDLEFMNEOKLRNRYPASLWVVRSKTEDHEE 308
DB 1293 RK-CIAG-----KEOKSEAEVETFLTLRDESRVYHD 1323

RESULT 15

S31805

VPS protein - porcine rotavirus

C.Species: porcine rotavirus

C.Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 09-Jul-2004

C.Accession: S31805

R.Xu, L.; Tian, Y.; Tarlow, O.; McCrae, M.A.

submitted to the EMBL Data Library, May 1992

A.Reference number: S31783

A.Accession: S31805

A.Status: preliminary

A.Molecule type: genomic RNA

A.Residues: 1-486 <XUL>

A.Cross-references: UNIPROT:085037; EMBL:Z12107; NID:961354; PIDN:CAA78092.1; PID:961355

A.Experimental source: strain OSY

C.Superfamily: bovine rotavirus nonstructural protein NcVP2

Query Match 4.9%; Score 83.5; DB 2; Length 486;

Best Local Similarity 20.8%; Pred. No. 22;

Matches 65; Conservative 37; Mismatches 114; Indels 97; Gaps 15;

QY 48 CHRAQOLTYPLATYPKEEELVACQGRGRLFSICQ-----FVDDG----- 86
DB 42 CLDCCQ-----HT-----DLTYC-RGCTWYHVCOWCSQYGRCEFLDNEPHILMRTPKNEV 90
QY 87 -----IDLNRKLECSACTEAYSOSDEQYACHLGCNQLPFAELROEQLMSLMPKM 138
DB 91 TTDDLMNLVDMPTLEPMNQKIVDKFINNTRQHKCRNECVNQW-----YN 135
QY 139 HLLFPLTL-----VRSFWSMDMSAQ--SFTSSWTF-YIQADDGKIVIFQ 181
DB 136 HLLMPTTLQSLIELDGDVYIFGYDDNNVNGQTFPSFVNLVDIYDKLLLDVNFT--- 192
QY 182 SKPEIQYAPHLFOEPTNLRESSLSRMSYQMR--NSQAHNRFLEDGESDGF-----LRC 233
DB 193 ---RMSFLPVTLQOEVALRYFSKSRPISQRKCVSDSRPSINVLENLHNPSSFRMOTTNRC 249
QY 234 LSLNSGMILTTTLVLSVMVLWICATVATAVQYVSEKLSIYGDLEFMNEOKLRNRYPA 293
DB 250 NELSSPMNAGKLVADTSAVFN---LKTSHVEFYISITRCRVF-----TQRKLK--IA 298
QY 294 SSLVVRSKTEDH 306
DB 299 SKLIKPNYITSNH 311

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: March 28, 2005, 13:08:45 ; Search time 58 Seconds
(without alignments)
2851.751 Million cell updates/sec

Title: US-09-978-299a-330

Perfect score: 1694

Sequence: 1 MAAPKSGSLMWRQLGLPPL.....EDHEAGPLPTKMLAHSEI 323

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1500 summaries

Database : UniProt 03.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|--------|-------------|--------|---------------|--------------------|
| 1 | 1694 | 100.0 | 323 | 1 CA08_HUMAN | Q9PXS4 homo sapien |
| 2 | 1674.5 | 98.8 | 324 | 1 Q96KX7 | Q96KX7 mus sapien |
| 3 | 1611 | 95.1 | 323 | 1 CA08_MOUSE | Q9G773 mus musculu |
| 4 | 1234 | 72.8 | 239 | 2 Q6P5R1 | Q6P5R1 mus sapien |
| 5 | 993.5 | 58.6 | 324 | 2 Q6P5R1 | Q6P5R1 xenopus lae |
| 6 | 957.5 | 56.5 | 318 | 2 Q8QF83 | Q8QF83 tetradon n |
| 7 | 905 | 53.4 | 309 | 2 Q8UW68 | Q8UW68 tetradon n |
| 8 | 595.5 | 35.2 | 339 | 2 Q7T2E2 | Q7T2E2 brachydano |
| 9 | 423.5 | 25.0 | 342 | 1 BMAP_HUMAN | Q9UK28 homo sapien |
| 10 | 415.5 | 24.5 | 337 | 2 Q7TN12 | Q7TN12 mus musculu |
| 11 | 104 | 6.1 | 832 | 2 Q81Y26 | Q81Y26 mus musculu |
| 12 | 102 | 6.0 | 1250 | 2 Q81713 | Q81713 caenorhabdi |
| 13 | 102 | 6.0 | 2456 | 2 Q81715 | Q81715 caenorhabdi |
| 14 | 100 | 5.9 | 808 | 2 Q6ZQ08 | Q6ZQ08 mus musculu |
| 15 | 100 | 5.7 | 768 | 2 Q97215 | Q97215 leishmania |
| 16 | 96.5 | 5.7 | 858 | 2 Q66HA8 | Q66HA8 rattus norv |
| 17 | 96 | 5.7 | 937 | 2 Q66FT5 | Q66FT5 homo sapien |
| 18 | 95.5 | 5.6 | 537 | 2 Q96AA0 | Q96AA0 homo sapien |
| 19 | 95.5 | 5.6 | 715 | 2 Q6UWAS | Q6UWAS homo sapien |
| 20 | 95.5 | 5.6 | 915 | 2 Q6UWAS | Q6UWAS homo sapien |
| 21 | 95.5 | 5.6 | 1016 | 2 Q8HDE6 | Q8HDE6 homo sapien |
| 22 | 94 | 5.5 | 517 | 2 Q8H883 | Q8H883 oryza sativ |
| 23 | 94 | 5.5 | 1312 | 2 Q9J1I8 | Q9J1I8 rattus norv |
| 24 | 93.5 | 5.5 | 956 | 1 QMTM2_HUMAN | Q00339 homo sapien |
| 25 | 92.5 | 5.5 | 858 | 1 H105_CRIGR | Q60446 cricetus |
| 26 | 91 | 5.4 | 407 | 2 Q6C994 | Q6C994 yarrowia li |
| 27 | 90 | 5.3 | 616 | 2 Q9W1F4 | Q9W1F4 dirosophila |
| 28 | 89 | 5.3 | 971 | 2 Q7YS79 | Q7YS79 canis famli |
| 29 | 89 | 5.3 | 1124 | 1 PHYA_LATSA | P93673 lachnus sa |
| 30 | 88.5 | 5.2 | 527 | 1 MALO_CHLTR | Q84089 chlamydia t |
| 31 | 88.5 | 5.2 | 527 | 2 Q6YW20 | Q6YW20 oryza sativ |

| | | | | | |
|-----|------|-----|------|--------------|----------------------|
| 32 | 88.5 | 5.2 | 703 | 2 Q7S872 | Q7S872 neurospora |
| 33 | 88.5 | 5.2 | 817 | 2 Q9S2T4 | Q9S2T4 arabidopsis |
| 34 | 88 | 5.2 | 1349 | 2 Q7YU33 | Q7YU33 dirosophila |
| 35 | 87.5 | 5.2 | 142 | 2 Q9H1H9 | Q9H1H9 thermoplas |
| 36 | 87.5 | 5.2 | 523 | 2 Q7T5A5 | Q7T5A5 onion yello |
| 37 | 87.5 | 5.2 | 662 | 2 Q9F7S3 | Q9F7S3 gamma-prote |
| 38 | 87.5 | 5.2 | 937 | 1 YW92_CABRL | P34531 caenorhabdi |
| 39 | 87 | 5.1 | 693 | 2 Q9D6Z0 | Q9D6Z0 gallus galli |
| 40 | 87 | 5.1 | 736 | 2 Q9FCV7 | Q9FCV7 oryza sativ |
| 41 | 86.5 | 5.1 | 327 | 2 Q66CU1 | Q66CU1 yersinia ps |
| 42 | 86.5 | 5.1 | 327 | 2 Q8ZG12 | Q8ZG12 yersinia pe |
| 43 | 86.5 | 5.1 | 535 | 2 Q9MT44 | Q9MT44 dirosophila |
| 44 | 86.5 | 5.1 | 535 | 2 Q9VD23 | Q9VD23 dirosophila |
| 45 | 86.5 | 5.1 | 1030 | 2 Q6L168 | Q6L168 photobacter |
| 46 | 86 | 5.1 | 389 | 1 SUCC_XANCP | Q8P676 xanthomonas |
| 47 | 86 | 5.1 | 429 | 2 Q7ACB2 | Q7ACB2 geobacter s |
| 48 | 86 | 5.1 | 641 | 2 Q7Y0Y5 | Q7Y0Y5 geosyrium h |
| 49 | 86 | 5.1 | 850 | 2 Q6AJR1 | Q6AJR1 desulfofatale |
| 50 | 86 | 5.1 | 894 | 2 Q8XSV3 | Q8XSV3 ralsionia s |
| 51 | 85.5 | 5.0 | 330 | 2 Q87SV6 | Q87SV6 vibrio para |
| 52 | 85.5 | 5.0 | 398 | 1 DXR_PHOLL | Q7R8P3 photorhabd |
| 53 | 85.5 | 5.0 | 558 | 2 Q6NDX0 | Q6NDX0 brachydano |
| 54 | 85.5 | 5.0 | 579 | 2 Q8NFG4 | Q8NFG4 homo sapien |
| 55 | 85.5 | 5.0 | 717 | 2 Q6L217 | Q6L217 methanococc |
| 56 | 85.5 | 5.0 | 1212 | 2 Q7Q9W7 | Q7Q9W7 anopheles g |
| 57 | 85.5 | 5.0 | 1389 | 2 Q6DRM6 | Q6DRM6 brachydano |
| 58 | 85.5 | 5.0 | 3259 | 1 G0B1_HUMAN | Q14789 homo sapien |
| 59 | 85 | 5.0 | 337 | 2 Q6MPT1 | Q6MPT1 bdellovibri |
| 60 | 85 | 5.0 | 356 | 1 GBA3_NEUCR | Q9H1W7 neurospora |
| 61 | 85 | 5.0 | 467 | 2 Q9EXY5 | Q9EXY5 escherichia |
| 62 | 85 | 5.0 | 678 | 1 LGP2_MOUSE | Q9J187 mus musculu |
| 63 | 84.5 | 5.0 | 450 | 2 Q6C655 | Q6C655 yarrowia li |
| 64 | 84.5 | 5.0 | 486 | 2 Q84940 | Q84940 porcine rot |
| 65 | 84.5 | 5.0 | 1021 | 2 Q7SEK3 | Q7SEK3 ashbya goe |
| 66 | 84.5 | 5.0 | 858 | 1 DUCD_HUMAN | Q7S165 homo sapien |
| 67 | 84.5 | 5.0 | 1375 | 2 Q6ZUT5 | Q6ZUT5 homo sapien |
| 68 | 84 | 5.0 | 395 | 2 Q7PJ24 | Q7PJ24 anopheles g |
| 69 | 84 | 5.0 | 445 | 2 Q8XZF5 | Q8XZF5 ralsionia s |
| 70 | 84 | 5.0 | 476 | 2 Q94F80 | Q94F80 zea mays (m |
| 71 | 84 | 5.0 | 570 | 2 Q6A0A5 | Q6A0A5 mus musculu |
| 72 | 84 | 5.0 | 858 | 1 H105_MOUSE | Q61699 mus musculu |
| 73 | 84 | 5.0 | 858 | 2 Q8C430 | Q8C430 mus musculu |
| 74 | 84 | 5.0 | 858 | 2 Q8VCW6 | Q8VCW6 mus musculu |
| 75 | 84 | 5.0 | 869 | 2 Q6S2C5 | Q6S2C5 caenorhabdi |
| 76 | 84 | 5.0 | 1312 | 2 P70388 | P70388 mus musculu |
| 77 | 84 | 5.0 | 1349 | 1 NOS_DROME | Q27571 dirosophila |
| 78 | 84 | 5.0 | 5729 | 2 Q81622 | Q81622 plasmodium |
| 79 | 83.5 | 4.9 | 376 | 2 Q9B5B5 | Q9B5B5 rapanus sa |
| 80 | 83.5 | 4.9 | 486 | 1 VNS3_ROTUM | Q6BX81 debaryomyce |
| 81 | 83.5 | 4.9 | 486 | 2 Q85037 | Q85037 porcine rot |
| 82 | 83.5 | 4.9 | 623 | 2 Q6ZU80 | Q6ZU80 homo sapien |
| 83 | 83.5 | 4.9 | 678 | 2 Q64ZJ4 | Q64ZJ4 bacteroides |
| 84 | 83.5 | 4.9 | 700 | 2 Q9F8S5 | Q9F8S5 rapanus sa |
| 85 | 83.5 | 4.9 | 1020 | 2 Q6BX81 | Q6BX81 debaryomyce |
| 86 | 83.5 | 4.9 | 1318 | 2 Q43254 | Q43254 homo sapien |
| 87 | 83.5 | 4.9 | 1397 | 2 Q6CXX5 | Q6CXX5 kluyveromyc |
| 88 | 83.5 | 4.9 | 3056 | 2 Q6P0D5 | Q6P0D5 sus scrofa |
| 89 | 83.5 | 4.9 | 3622 | 2 Q6B685 | Q6B685 paramedum |
| 90 | 83 | 4.9 | 278 | 2 Q6DF00 | Q6DF00 xenopus tro |
| 91 | 83 | 4.9 | 412 | 2 Q9ZVZ5 | Q9ZVZ5 dirosophila |
| 92 | 83 | 4.9 | 421 | 2 Q61603 | Q61603 oryza sativ |
| 93 | 83 | 4.9 | 433 | 2 Q6DCN1 | Q6DCN1 xenopus lae |
| 94 | 83 | 4.9 | 461 | 2 Q9J5L5 | Q9J5L5 macaca faec |
| 95 | 83 | 4.9 | 500 | 2 Q9JSH1 | Q9JSH1 chlamydia p |
| 96 | 83 | 4.9 | 503 | 2 Q9Z8T3 | Q9Z8T3 chlamydia p |
| 97 | 83 | 4.9 | 503 | 2 Q9K258 | Q9K258 chlamydia p |
| 98 | 83 | 4.9 | 735 | 2 Q7OK26 | Q7OK26 anopheles g |
| 99 | 83 | 4.9 | 1607 | 1 LMGI_MOUSE | P02468 mus musculu |
| 100 | 82.5 | 4.9 | 326 | 2 Q8V708 | Q8V708 bovine roca |
| 101 | 82.5 | 4.9 | 566 | 2 Q8CAC0 | Q8CAC0 mus musculu |
| 102 | 82.5 | 4.9 | 579 | 2 Q8QZS3 | Q8QZS3 mus musculu |
| 103 | 82.5 | 4.9 | 1703 | 2 Q7R677 | Q7R677 giardia lam |
| 104 | 82 | 4.8 | 308 | 2 Q9UAX8 | Q9UAX8 caenorhabdi |

| | | | | | | | | | | | | | |
|-----|------|-----|------|---|-------------|---------------------|-----|------|-----|------|---|------------|--------------------|
| 105 | 82 | 4.8 | 389 | 1 | SUCC_XANAC | 08ph15 xanthomonas | 178 | 79.5 | 4.7 | 600 | 2 | 017401 | 017401 caenorhabdi |
| 106 | 82 | 4.8 | 469 | 2 | 06CT13 | 06ct13 kluyveromyc | 179 | 79.5 | 4.7 | 632 | 2 | 06CN05 | 06cn05 xenopus lae |
| 107 | 82 | 4.8 | 621 | 2 | 06LMP4 | 06lmp4 methanococc | 180 | 79.5 | 4.7 | 682 | 2 | 06ZMN9 | 06zmn9 homo sapien |
| 108 | 82 | 4.8 | 626 | 1 | BGAL_LEUTIA | 002603 leuconostoc | 181 | 79.5 | 4.7 | 702 | 2 | 08TEJ1 | 08tej1 homo sapien |
| 109 | 82 | 4.8 | 1299 | 2 | 0847C8 | 0847c8 nobilaria s | 182 | 79.5 | 4.7 | 793 | 2 | 07RDJ3 | 07rdj3 plasmodium |
| 110 | 82 | 4.8 | 1349 | 2 | 0964G1 | 0964g1 pseudocenter | 183 | 79.5 | 4.7 | 837 | 2 | 06P4A6 | 06p4a6 homo sapien |
| 111 | 82 | 4.8 | 1564 | 2 | 06BP7 | 06bp7 homo sapien | 184 | 79.5 | 4.7 | 838 | 1 | POSN_MOUSE | 062009 mus musculu |
| 112 | 82 | 4.8 | 1568 | 2 | 015077 | 015077 homo sapien | 185 | 79.5 | 4.7 | 848 | 2 | 075AF5 | 075af5 aebhya goss |
| 113 | 82 | 4.8 | 2804 | 1 | NPBL_HUMAN | 06k79 homo sapien | 186 | 79.5 | 4.7 | 971 | 2 | 06CT54 | 06ct54 kluyveromyc |
| 114 | 82 | 4.8 | 2804 | 2 | 06TEH8 | 06teh8 homo sapien | 187 | 79.5 | 4.7 | 971 | 2 | 06ZWI1 | 06zwi1 homo sapien |
| 115 | 81.5 | 4.8 | 247 | 2 | 06HKX3 | 06hcx3 bacillus th | 188 | 79.5 | 4.7 | 999 | 2 | 09NO36 | 09nq36 homo sapien |
| 116 | 81.5 | 4.8 | 264 | 1 | RCII_BPP4 | 06hcx3 bacillus th | 189 | 79.5 | 4.7 | 1136 | 2 | P87224 | 067224 neurospora |
| 117 | 81.5 | 4.8 | 381 | 2 | 08DK45 | 08dk45 synechococc | 190 | 79.5 | 4.7 | 1866 | 2 | 086W13 | 086w13 homo sapien |
| 118 | 81.5 | 4.8 | 438 | 2 | 06MTB4 | 06mtb4 mycoplasma | 191 | 79.5 | 4.7 | 1984 | 2 | 09QBH1 | 09qbh1 viral hemor |
| 119 | 81.5 | 4.8 | 525 | 2 | VCL_THIECC | 043358 theobroma c | 192 | 79.5 | 4.7 | 1984 | 2 | 09QJW0 | 09qjw0 viral hemor |
| 120 | 81.5 | 4.8 | 775 | 2 | 07SD99 | 07sd99 neurospora | 193 | 79.5 | 4.7 | 1984 | 2 | 09WME7 | 09wme7 viral hemor |
| 121 | 81.5 | 4.8 | 778 | 2 | 09SUJ6 | 09suj6 arabidopsis | 194 | 79.5 | 4.7 | 2330 | 1 | EFLA_MOUSE | 060882 mus musculu |
| 122 | 81.5 | 4.8 | 937 | 2 | 07XRN6 | 07xrn6 oryza sativ | 195 | 79.5 | 4.7 | 193 | 2 | 06UBI9 | 06ubi9 nostoc sp. |
| 123 | 81.5 | 4.8 | 996 | 2 | VGNM_RCMV | 06fk73 candida gla | 196 | 79.5 | 4.7 | 301 | 2 | 08CT27 | 08ct27 mus musculu |
| 124 | 81.5 | 4.8 | 1020 | 2 | 06FK73 | 06fk73 anopheles g | 197 | 79.5 | 4.7 | 305 | 2 | 09DG31 | 09dg31 gallus gall |
| 125 | 81.5 | 4.8 | 1173 | 2 | 070548 | 09up86 homo sapien | 198 | 79.5 | 4.7 | 399 | 1 | HMP_BACSU | 098852 bacillus su |
| 126 | 81.5 | 4.8 | 1173 | 2 | 090F86 | 09up86 homo sapien | 199 | 79.5 | 4.7 | 431 | 2 | 097G69 | 097g69 clostridium |
| 127 | 81.5 | 4.8 | 1312 | 2 | 092878 | 092878 homo sapien | 200 | 79.5 | 4.7 | 445 | 2 | 09XGG3 | 09xgg3 phalaenopsi |
| 128 | 81 | 4.8 | 477 | 2 | P94005 | P94005 lycopersico | 201 | 79.5 | 4.7 | 449 | 2 | 0754Y6 | 0754y6 aebhya goss |
| 129 | 81 | 4.8 | 485 | 1 | 1A12_LYCXS | 066h13 lycopersico | 202 | 79.5 | 4.7 | 459 | 2 | 086ME2 | 086me2 caenorhabdi |
| 130 | 81 | 4.8 | 485 | 2 | 06EH13 | 06eh13 lycopersico | 203 | 79.5 | 4.7 | 536 | 2 | 09J2L9 | 09j2l9 thesus monk |
| 131 | 81 | 4.8 | 485 | 2 | 066773 | 066773 equine rocta | 204 | 79.5 | 4.7 | 545 | 1 | SECY_SPIOL | 093690 spincia ol |
| 132 | 81 | 4.8 | 504 | 2 | 064R82 | 064r82 bacteroides | 205 | 79.5 | 4.7 | 618 | 2 | 07QIE8 | 07qie8 giardia lam |
| 133 | 81 | 4.8 | 635 | 2 | 06AHQ4 | 06ahq4 caenorhabdi | 206 | 79.5 | 4.7 | 661 | 2 | 06PEB0 | 06peb0 mus musculu |
| 134 | 81 | 4.8 | 723 | 2 | 06GMT7 | 06gmt7 homo sapien | 207 | 79.5 | 4.7 | 714 | 2 | 06B005 | 06b005 enterococcu |
| 135 | 81 | 4.8 | 774 | 2 | 08S3P4 | 08s3p4 oryza sativ | 208 | 79.5 | 4.7 | 790 | 2 | 06CLM7 | 06clm7 yarrowia li |
| 136 | 81 | 4.8 | 848 | 2 | 09PE39 | 09pe39 xyella fas | 209 | 79.5 | 4.7 | 846 | 2 | 084FU0 | 084fu0 chlamydia t |
| 137 | 81 | 4.8 | 1032 | 2 | 097P86 | 097p86 streptococc | 210 | 79.5 | 4.7 | 846 | 2 | 084FU1 | 084fu1 chlamydia t |
| 138 | 81 | 4.8 | 1032 | 2 | 08DP39 | 08dp39 streptococc | 211 | 79.5 | 4.7 | 846 | 2 | 084FU3 | 084fu3 chlamydia t |
| 139 | 81 | 4.8 | 1609 | 1 | LMGI_HUMAN | 06p1047 homo sapien | 212 | 79.5 | 4.7 | 846 | 2 | 084FU5 | 084fu5 chlamydia t |
| 140 | 81 | 4.8 | 2798 | 1 | NPBL_MOUSE | 06kcds mus musculu | 213 | 79.5 | 4.7 | 891 | 2 | 08GHR8 | 08ghr8 pseudomonas |
| 141 | 80.5 | 4.8 | 282 | 1 | NADA_APLKU | 027312 aplysia kur | 214 | 79.5 | 4.7 | 1072 | 2 | 080Y84 | 080y84 mus musculu |
| 142 | 80.5 | 4.8 | 426 | 2 | 08BWX1 | 08bwx1 mus musculu | 215 | 79.5 | 4.7 | 1122 | 1 | TIE2_MOUSE | 002858 mus musculu |
| 143 | 80.5 | 4.8 | 453 | 2 | 064767 | 064767 avian adeno | 216 | 79.5 | 4.7 | 1124 | 1 | PHYA_PEA | 015001 pisum sativ |
| 144 | 80.5 | 4.8 | 459 | 1 | FA9_MOUSE | 062294 mus musculu | 217 | 79.5 | 4.7 | 1357 | 1 | MYP_STRPU | 019615 strongyloce |
| 145 | 80.5 | 4.8 | 471 | 2 | 06VPL7 | 06vpl7 salmoneilla | 218 | 79.5 | 4.7 | 1578 | 2 | 09AV25 | 09av25 oryza sativ |
| 146 | 80.5 | 4.8 | 471 | 2 | 09EXV9 | 09exv9 salmoneilla | 219 | 79.5 | 4.7 | 1726 | 2 | 08UVK2 | 08uvk2 brachydanio |
| 147 | 80.5 | 4.8 | 475 | 1 | ATXX_MOUSE | 028658 mus musculu | 220 | 79.5 | 4.7 | 1726 | 2 | 06PAU2 | 06pau2 brachydanio |
| 148 | 80.5 | 4.8 | 563 | 2 | 07RX55 | 07rx55 neurospora | 221 | 79.5 | 4.7 | 4880 | 2 | 06FIU8 | 06fiu8 candida gla |
| 149 | 80.5 | 4.8 | 608 | 2 | 06MT71 | 06mt71 mycoplasma | 222 | 78.5 | 4.6 | 193 | 2 | 09KCS7 | 09kcs7 bacillus ha |
| 150 | 80.5 | 4.8 | 661 | 2 | 023611 | 023611 arabidopsis | 223 | 78.5 | 4.6 | 341 | 2 | 06D035 | 06d035 erwina car |
| 151 | 80.5 | 4.8 | 720 | 2 | 019718 | 019718 caenorhabdi | 224 | 78.5 | 4.6 | 377 | 2 | 008R06 | 008r06 mus musculu |
| 152 | 80.5 | 4.8 | 904 | 2 | 08A1K1 | 08a1k1 bacteroides | 225 | 78.5 | 4.6 | 377 | 2 | 080Y29 | 080y29 mus musculu |
| 153 | 80.5 | 4.8 | 956 | 2 | 099K64 | 099k64 mus musculu | 226 | 78.5 | 4.6 | 453 | 2 | 06S1J7 | 06s1j7 escherichia |
| 154 | 80.5 | 4.8 | 1430 | 2 | 09VMA7 | 09vma7 drosophila | 227 | 78.5 | 4.6 | 453 | 2 | 09WTG1 | 09wtg1 plasmod r10 |
| 155 | 80.5 | 4.8 | 2042 | 2 | 06TXG6 | 06txg6 rattus norv | 228 | 78.5 | 4.6 | 460 | 2 | 06PAJ7 | 06paj7 xenopus tro |
| 156 | 80.5 | 4.8 | 2342 | 2 | 065980 | 065980 cherry viru | 229 | 78.5 | 4.6 | 479 | 2 | 06DC80 | 06dc80 brachydanio |
| 157 | 80.5 | 4.8 | 2386 | 1 | EFLA_HUMAN | 077rm0 homo sapien | 230 | 78.5 | 4.6 | 521 | 1 | FAEB_ASPNG | 06wz18 aspergillus |
| 158 | 80 | 4.7 | 119 | 1 | MOTI_PIG | 061307 sus scrofa | 231 | 78.5 | 4.6 | 553 | 2 | 08ZUJ4 | 08zuj4 salmoneilla |
| 159 | 80 | 4.7 | 168 | 2 | 095UH3 | 095uh3 trichosurus | 232 | 78.5 | 4.6 | 668 | 2 | 09XX27 | 09xx27 caenorhabdi |
| 160 | 80 | 4.7 | 286 | 2 | 08BPAV4 | 08bpa4 xanthomonas | 233 | 78.5 | 4.6 | 705 | 2 | 066INO | 066ino xenopus lae |
| 161 | 80 | 4.7 | 455 | 2 | 06C960 | 06c960 yarrowia li | 234 | 78.5 | 4.6 | 1436 | 2 | 09LFF6 | 09lff6 arabidopsis |
| 162 | 80 | 4.7 | 486 | 2 | 041178 | 041178 porcine rot | 235 | 78.5 | 4.6 | 1449 | 2 | 08YWC0 | 08ywc0 anabena sp |
| 163 | 80 | 4.7 | 486 | 2 | P87724 | 087724 rotavirus a | 236 | 78.5 | 4.6 | 1984 | 2 | 09QBH5 | 09qbh5 viral hemor |
| 164 | 80 | 4.7 | 491 | 1 | VNS3_ROTBR | 073u45 anopheles g | 237 | 78.5 | 4.6 | 277 | 2 | 08FI02 | 08fi02 escherichia |
| 165 | 80 | 4.7 | 575 | 2 | 09VWP2 | 09vwp2 drosophila | 238 | 78.5 | 4.6 | 1124 | 2 | 08MQJ8 | 08mqj8 dengue viru |
| 166 | 80 | 4.7 | 614 | 2 | 09K5S1 | 09k5s1 bacillus ha | 239 | 78.5 | 4.6 | 1127 | 2 | P89531 | 089531 leishmania |
| 167 | 80 | 4.7 | 1224 | 2 | 06PCT5 | 06pct5 xenopus lae | 240 | 78.5 | 4.6 | 1436 | 2 | 09LFF6 | 09lff6 arabidopsis |
| 168 | 80 | 4.7 | 1580 | 2 | 0754A4 | 0754a4 aebhya goss | 241 | 78.5 | 4.6 | 1449 | 2 | 08YWC0 | 08ywc0 anabena sp |
| 169 | 80 | 4.7 | 2042 | 2 | 0703U4 | 073u45 anopheles g | 242 | 78.5 | 4.6 | 1984 | 2 | 09QBH5 | 09qbh5 viral hemor |
| 170 | 80 | 4.7 | 4207 | 2 | 07R3Y5 | 07r3y5 giardia lam | 243 | 78.5 | 4.6 | 277 | 2 | 08FI02 | 08fi02 escherichia |
| 171 | 79.5 | 4.7 | 335 | 2 | 07OD23 | 07od23 anopheles g | 244 | 78.5 | 4.6 | 327 | 2 | 09NDY9 | 09ndy9 leishmania |
| 172 | 79.5 | 4.7 | 395 | 2 | 09DC34 | 09dc34 mus musculu | 245 | 78.5 | 4.6 | 348 | 2 | 07QSH5 | 07qsh5 anopheles g |
| 173 | 79.5 | 4.7 | 406 | 2 | 068E09 | 068e09 xenopus tro | 246 | 78.5 | 4.6 | 366 | 2 | 08FGQ4 | 08fgq4 escherichia |
| 174 | 79.5 | 4.7 | 435 | 2 | 0765H8 | 0765h8 flaveria tr | 247 | 78.5 | 4.6 | 370 | 2 | 09LH03 | 09lh03 arabidopsis |
| 175 | 79.5 | 4.7 | 469 | 1 | T8G2_ORYSA | 049068 oryza sativ | 248 | 78.5 | 4.6 | 458 | 2 | 081PB8 | 081pb8 bacillus an |
| 176 | 79.5 | 4.7 | 486 | 2 | 082013 | 082013 human rotav | 249 | 78.5 | 4.6 | 468 | 2 | 063AV0 | 063av0 bacillus ce |
| 177 | 79.5 | 4.7 | 579 | 2 | 076JQ2 | 076jq2 rattus norv | 250 | 78.5 | 4.6 | 538 | 2 | 06BC96 | 06bc96 mumps virus |

| | | | | | | | | | | | | | |
|-----|------|-----|------|---|------------|----------------------|-----|------|-----|------|---|------------|----------------------|
| 251 | 78 | 4.6 | 564 | 1 | YUES CAERL | P90859 caenorhabdi | 324 | 77 | 4.5 | 481 | 2 | 0831B5 | 0831b5 enterococcu |
| 252 | 78 | 4.6 | 601 | 2 | 08B131 | 08b131 shewanella | 325 | 77 | 4.5 | 491 | 2 | 08J213 | 08j213 bovine rota |
| 253 | 78 | 4.6 | 624 | 2 | 094487 | 094487 schizosacch | 326 | 77 | 4.5 | 597 | 2 | 08L4C7 | 08l4c7 arabidopsis |
| 254 | 78 | 4.6 | 645 | 2 | 091Q73 | 091q73 influenza c | 327 | 77 | 4.5 | 599 | 2 | 07N219 | 07n219 photorhabdu |
| 255 | 78 | 4.6 | 655 | 2 | 0617C1 | 0617c1 influenza c | 328 | 77 | 4.5 | 640 | 2 | 084MH1 | 084mh1 oryza sativ |
| 256 | 78 | 4.6 | 700 | 2 | 08WS94 | 08ws94 caenorhabdi | 329 | 77 | 4.5 | 645 | 2 | 091Q74 | 091q74 influenza c |
| 257 | 78 | 4.6 | 828 | 2 | 06FL29 | 06fl29 candida gla | 330 | 77 | 4.5 | 647 | 2 | 08MLX3 | 08mlx3 caenorhabdi |
| 258 | 78 | 4.6 | 846 | 2 | 083TT8 | 083tt8 chlamydia t | 331 | 77 | 4.5 | 647 | 2 | 08MM25 | 08mm25 caenorhabdi |
| 259 | 78 | 4.6 | 846 | 2 | 084FU2 | 084fu2 chlamydia t | 332 | 77 | 4.5 | 647 | 2 | 08MV49 | 08mv49 caenorhabdi |
| 260 | 78 | 4.6 | 846 | 2 | 084FU4 | 084fu4 chlamydia t | 333 | 77 | 4.5 | 647 | 2 | 08MV50 | 08mv50 caenorhabdi |
| 261 | 78 | 4.6 | 927 | 2 | 0823X9 | 0823x9 chlamydophi | 334 | 77 | 4.5 | 647 | 2 | 08MV51 | 08mv51 caenorhabdi |
| 262 | 78 | 4.6 | 1114 | 2 | 08S6D2 | 08s6d2 oryza sativ | 335 | 77 | 4.5 | 647 | 2 | 08MV52 | 08mv52 caenorhabdi |
| 263 | 78 | 4.6 | 1189 | 2 | 08RKM7 | 08rkm7 providencia | 336 | 77 | 4.5 | 647 | 2 | 08MV53 | 08mv53 caenorhabdi |
| 264 | 78 | 4.6 | 3898 | 2 | 06S535 | 06s535 classica s | 337 | 77 | 4.5 | 647 | 2 | 08NV54 | 08nv54 caenorhabdi |
| 265 | 78 | 4.6 | 166 | 2 | 08YPM1 | 08ypm1 anabaena sp | 338 | 77 | 4.5 | 661 | 2 | 09TVY6 | 09tvy6 caenorhabdi |
| 266 | 77.5 | 4.6 | 287 | 2 | 09UT16 | 09ut16 schizosacch | 339 | 77 | 4.5 | 714 | 2 | 060149 | 060149 streptococc |
| 267 | 77.5 | 4.6 | 324 | 1 | FB22 RAT | P97578 rattus norv | 340 | 77 | 4.5 | 719 | 1 | PRH1_SCHPO | 003319 schizosacch |
| 268 | 77.5 | 4.6 | 348 | 2 | 076LH9 | 076lh9 rattus norv | 341 | 77 | 4.5 | 846 | 2 | 083U50 | 083u50 chlamydia t |
| 269 | 77.5 | 4.6 | 375 | 2 | 076LH9 | 076lh9 rattus norv | 342 | 77 | 4.5 | 846 | 2 | 084FT9 | 084ft9 chlamydia t |
| 270 | 77.5 | 4.6 | 414 | 2 | 09UM44 | 09um44 homo sapien | 343 | 77 | 4.5 | 858 | 1 | H105_HUMAN | 092598 homo sapien |
| 271 | 77.5 | 4.6 | 417 | 2 | 06PRG7 | 06prg7 mus musculu | 344 | 77 | 4.5 | 878 | 1 | PMPI_CHLTR | 064882 chlamydia t |
| 272 | 77.5 | 4.6 | 425 | 1 | PLA2_MOUSE | 096f57 mus musculu | 345 | 77 | 4.5 | 1037 | 2 | 06K8D6 | 06k8d6 oryza sativ |
| 273 | 77.5 | 4.6 | 462 | 1 | SCB1_MOUSE | 096r85 mus musculu | 346 | 77 | 4.5 | 1083 | 2 | 09QW24 | 09qw24 rattus sp. |
| 274 | 77.5 | 4.6 | 463 | 1 | SCB1_MOUSE | P31644 homo sapien | 347 | 77 | 4.5 | 1085 | 1 | 6124_HUMAN | 09up95 homo sapien |
| 275 | 77.5 | 4.6 | 463 | 2 | 08BH57 | 08bh57 m mus muscu | 348 | 77 | 4.5 | 1578 | 2 | 09Y2H3 | 09y2h3 homo sapien |
| 276 | 77.5 | 4.6 | 464 | 1 | GA45 RAT | 08bhj7 m mus muscu | 349 | 77 | 4.5 | 2255 | 2 | 07YV63 | 07yyv63 cryptospori |
| 277 | 77.5 | 4.6 | 464 | 2 | Q9D4Z5 | P19969 rattus norv | 350 | 77 | 4.5 | 4010 | 1 | FRS1_MOUSE | 06f120 mus musculu |
| 278 | 77.5 | 4.6 | 503 | 1 | NQRB_CHLCV | 09d4z5 mus musculu | 351 | 77 | 4.5 | 193 | 2 | 06LFZ0 | 06lfz0 photobacter |
| 279 | 77.5 | 4.6 | 530 | 1 | VC04_SWPK | 0823p2 chlamydophi | 352 | 77 | 4.5 | 254 | 2 | 09CLD2 | 09cl22 pasteurella |
| 280 | 77.5 | 4.6 | 530 | 2 | Q8V3S6 | P33228 swinepox vi | 353 | 77 | 4.5 | 352 | 2 | 086FF1 | 086ff1 schistosoma |
| 281 | 77.5 | 4.6 | 545 | 1 | TM26_PIG | 08v3s6 swinepox vi | 354 | 77 | 4.5 | 363 | 2 | 08DRC8 | 08dr8c streptococc |
| 282 | 77.5 | 4.6 | 597 | 1 | NUCD_BUCBP | 077666 sus scrofa | 355 | 76.5 | 4.5 | 375 | 2 | 094K53 | 094k53 arabidopsis |
| 283 | 77.5 | 4.6 | 632 | 2 | 069T22 | 089844 buchnera ap | 356 | 76.5 | 4.5 | 449 | 2 | 004496 | 004496 arabidopsis |
| 284 | 77.5 | 4.6 | 639 | 2 | 09FLA9 | 069c22 oryza sativ | 357 | 76.5 | 4.5 | 458 | 2 | 06HNR2 | 06hn22 bacillus th |
| 285 | 77.5 | 4.6 | 641 | 2 | Q8M0M0 | 09fla9 arabidopsis | 358 | 76.5 | 4.5 | 465 | 2 | 08KX83 | 08kx83 chlorobium |
| 286 | 77.5 | 4.6 | 646 | 2 | Q23521 | 08mqm0 drosophila | 359 | 76.5 | 4.5 | 471 | 2 | 090577 | 090577 gallus galli |
| 287 | 77.5 | 4.6 | 657 | 1 | CSPI CORGL | 001377 corynebacte | 360 | 76.5 | 4.5 | 501 | 2 | 06DUV7 | 06duv7 brachydiano |
| 288 | 77.5 | 4.6 | 665 | 2 | 038925 | 038925 arabidopsis | 361 | 76.5 | 4.5 | 531 | 2 | 06DJ55 | 06dj55 xenopus tro |
| 289 | 77.5 | 4.6 | 665 | 2 | 09FFZ9 | 09ffz9 arabidopsis | 362 | 76.5 | 4.5 | 556 | 2 | 08H023 | 08h023 oryza sativ |
| 290 | 77.5 | 4.6 | 669 | 2 | Q9S2D5 | 09s2d5 arabidopsis | 363 | 76.5 | 4.5 | 564 | 2 | 0883V6 | 0883v6 pseudomonas |
| 291 | 77.5 | 4.6 | 696 | 2 | Q8S793 | 08s793 arabidopsis | 364 | 76.5 | 4.5 | 569 | 2 | 098QW0 | 098qmw0 mycoplasma |
| 292 | 77.5 | 4.6 | 701 | 2 | 08CN81 | 08cn81 strephyllococ | 365 | 76.5 | 4.5 | 570 | 2 | 096M46 | 096m46 homo sapien |
| 293 | 77.5 | 4.6 | 753 | 2 | 090275 | 090275 dromaius no | 366 | 76.5 | 4.5 | 597 | 2 | 07FX914 | 07fx914 oryza sativ |
| 294 | 77.5 | 4.6 | 753 | 2 | Q90276 | 090276 dromaius no | 367 | 76.5 | 4.5 | 607 | 2 | 07FA04 | 07fa04 oryza sativ |
| 295 | 77.5 | 4.6 | 760 | 2 | Q920P3 | 0920p3 m bmp/retin | 368 | 76.5 | 4.5 | 657 | 2 | 06FU72 | 06fu72 candida gla |
| 296 | 77.5 | 4.6 | 760 | 2 | Q925T8 | 0925t8 rattus norv | 369 | 76.5 | 4.5 | 657 | 2 | 0832P3 | 0832p3 corynebacte |
| 297 | 77.5 | 4.6 | 760 | 2 | Q8C1C9 | 08c1c9 mus musculu | 370 | 76.5 | 4.5 | 717 | 2 | 095JW2 | 095jw2 macaca fasc |
| 298 | 77.5 | 4.6 | 761 | 2 | 090X10 | 090x10 mus musculu | 371 | 76.5 | 4.5 | 745 | 2 | 067PP5 | 067pp5 symbiobacte |
| 299 | 77.5 | 4.6 | 761 | 2 | 07ZZR3 | 07zzr3 gallus galli | 372 | 76.5 | 4.5 | 809 | 2 | 07OSH7 | 07osh7 anopheles g |
| 300 | 77.5 | 4.6 | 800 | 2 | Q9KPY4 | 09kpy4 bacillus ha | 373 | 76.5 | 4.5 | 810 | 2 | 08C435 | 08c435 mus musculu |
| 301 | 77.5 | 4.6 | 810 | 2 | Q6GUA3 | 06gua3 mus musculu | 374 | 76.5 | 4.5 | 956 | 1 | MTN2_MOUSE | 086746 mus musculu |
| 302 | 77.5 | 4.6 | 853 | 2 | Q9Y1Y4 | 09y1y4 ephydactia f | 375 | 76.5 | 4.5 | 979 | 2 | Q7SX56 | 07sx56 mus musculu |
| 303 | 77.5 | 4.6 | 890 | 1 | GLND_SALTY | 08z9a7 salmoneella | 376 | 76.5 | 4.5 | 1191 | 2 | Q9VUX8 | 09vux8 brachydiano |
| 304 | 77.5 | 4.6 | 890 | 1 | GLND_SALTY | P21679 salmoneella | 377 | 76.5 | 4.5 | 1191 | 2 | Q9VUX8 | 09vux8 drosophila |
| 305 | 77.5 | 4.6 | 892 | 2 | Q25243 | 025243 lucilia cup | 378 | 76.5 | 4.5 | 1331 | 2 | 090W93 | 090w93 poecilia re |
| 306 | 77.5 | 4.6 | 892 | 2 | Q6PUN3 | 06pun3 ambystoma m | 379 | 76.5 | 4.5 | 1666 | 2 | 08MXG2 | 08mxg2 caenorhabdi |
| 307 | 77.5 | 4.6 | 1078 | 2 | Q6VSS9 | 06vss9 drosophila | 380 | 76.5 | 4.5 | 1949 | 2 | 08MXG3 | 08mxg3 caenorhabdi |
| 308 | 77.5 | 4.6 | 1099 | 2 | Q69K21 | 069k21 oryza sativ | 381 | 76.5 | 4.5 | 1960 | 2 | 081Z83 | 081z83 mus musculu |
| 309 | 77.5 | 4.6 | 1259 | 1 | CAML RAT | 005695 rattus norv | 382 | 76.5 | 4.5 | 2009 | 2 | Q9VXM0 | 09vxm0 drosophila |
| 310 | 77.5 | 4.6 | 1654 | 2 | 07SEMG | 07sem6 abhyva goos | 383 | 76.5 | 4.5 | 2895 | 2 | HYD DROME | P51592 drosophila |
| 311 | 77.5 | 4.6 | 1684 | 2 | 090JY4 | 090jy4 viral hemor | 384 | 76.5 | 4.5 | 152 | 2 | 08ZMR9 | 08zmr9 salmoneella |
| 312 | 77.5 | 4.6 | 2653 | 2 | Q25253 | 025253 lucilia cup | 385 | 76.5 | 4.5 | 160 | 2 | 08C254 | 08c254 mus musculu |
| 313 | 77.5 | 4.6 | 286 | 2 | Q6FJ13 | 06fj13 candida gla | 386 | 76.5 | 4.5 | 160 | 2 | Q8C254 | 08c254 mus musculu |
| 314 | 77.5 | 4.6 | 286 | 2 | Q8AXC0 | 08axc0 xenopus lae | 387 | 76.5 | 4.5 | 243 | 1 | TLPI_CASSA | 08fmh2 catatana ba |
| 315 | 77.5 | 4.6 | 288 | 2 | Q9DG22 | 09dg22 gallus galli | 388 | 76.5 | 4.5 | 247 | 2 | 081FT8 | 081ft8 bacillus ce |
| 316 | 77.5 | 4.6 | 330 | 2 | Q9KP40 | 09kp40 vibrio chol | 389 | 76.5 | 4.5 | 265 | 2 | 08S5X7 | 08s5x7 oryza sativ |
| 317 | 77.5 | 4.6 | 364 | 2 | Q9T099 | 09t099 arabidopsis | 390 | 76.5 | 4.5 | 277 | 1 | HEMK_ECOLI | P37186 escherichia |
| 318 | 77.5 | 4.6 | 374 | 2 | Q6CQ14 | 06cq14 kluyveromyc | 391 | 76.5 | 4.5 | 293 | 2 | 08NV67 | 08nv67 strephyllococ |
| 319 | 77.5 | 4.6 | 375 | 2 | Q7OT29 | 07ot29 bixa orella | 392 | 76.5 | 4.5 | 375 | 2 | 08Y572 | 08y572 listeria mo |
| 320 | 77.5 | 4.6 | 392 | 2 | Q6VTN6 | 06vtn6 choriostomeu | 393 | 76.5 | 4.5 | 381 | 2 | Q6BLV2 | 06blv2 debaryomyce |
| 321 | 77.5 | 4.6 | 398 | 2 | Q6CS23 | 06cs23 kluyveromyc | 394 | 76.5 | 4.5 | 390 | 1 | Y109_NPYOP | 010348 oryza psen |
| 322 | 77.5 | 4.6 | 472 | 2 | 08TRU6 | 08tru6 drosophila | 395 | 76.5 | 4.5 | 450 | 2 | Q9VH28 | 09vh28 drosophila |
| 323 | 77.5 | 4.6 | 475 | 1 | ARCD_LACCK | 050392 lactobacilli | 396 | 76.5 | 4.5 | 464 | 1 | YMG8_YEAST | 004638 saccharomyc |

| | | | | | | | | | | | | | |
|-----|------|-----|------|---|------------|----------------------|-----|------|-----|------|---|-------------|---------------------|
| 397 | 76 | 4.5 | 485 | 2 | Q9PWC0 | Q9PWC0 gallus gall | 470 | 75 | 4.4 | 221 | 2 | Q8AXC1 | Q8AXC1 xenopus lae |
| 398 | 76 | 4.5 | 486 | 2 | Q82043 | Q82043 human rotav | 471 | 75 | 4.4 | 263 | 2 | Q8F7C7 | Q8F7C7 leptospira |
| 399 | 76 | 4.5 | 486 | 2 | Q82045 | Q82045 human rotav | 472 | 75 | 4.4 | 277 | 2 | Q8XDR2 | Q8XDR2 escherichia |
| 400 | 76 | 4.5 | 491 | 2 | Q8E194 | Q8E194 human rotav | 473 | 75 | 4.4 | 293 | 2 | Q99RUS | Q99RUS staphylococ |
| 401 | 76 | 4.5 | 551 | 2 | Q9D1C6 | Q9D1C6 lettuce nec | 474 | 75 | 4.4 | 293 | 2 | Q7A3Z5 | Q7A3Z5 staphylococ |
| 402 | 76 | 4.5 | 572 | 2 | Q19594 | Q19594 caenorhabdi | 475 | 75 | 4.4 | 293 | 2 | Q6GEA6 | Q6GEA6 staphylococ |
| 403 | 76 | 4.5 | 598 | 2 | Q6D799 | Q6D799 erwina car | 476 | 75 | 4.4 | 321 | 2 | Q6NJ01 | Q6NJ01 corynebacte |
| 404 | 76 | 4.5 | 609 | 2 | Q82674 | Q82674 influenza c | 477 | 75 | 4.4 | 346 | 2 | Q9VYCO | Q9VYCO drosophila |
| 405 | 76 | 4.5 | 648 | 1 | HEMA_INCB | P87691 influenza c | 478 | 75 | 4.4 | 357 | 2 | Q8YUJ4 | Q8YUJ4 anabaena sp |
| 406 | 76 | 4.5 | 652 | 2 | Q81MX7 | Q81MX7 drosophila | 479 | 75 | 4.4 | 357 | 2 | Q9DG33 | Q9DG33 gallus gall |
| 407 | 76 | 4.5 | 663 | 2 | Q8BURA | Q6DJ14 dedaromyce | 480 | 75 | 4.4 | 358 | 2 | Q6FG19 | Q6FG19 actinobact |
| 408 | 76 | 4.5 | 673 | 2 | Q81MX6 | Q81MX6 drosophila | 481 | 75 | 4.4 | 384 | 2 | Q7ON64 | Q7ON64 amopheles g |
| 409 | 76 | 4.5 | 700 | 2 | Q62299 | Q62299 caenorhabdi | 482 | 75 | 4.4 | 402 | 1 | GUNI_HUMIN | P56680 humicola in |
| 410 | 76 | 4.5 | 745 | 2 | Q8EH07 | Q8EH07 shewanella | 483 | 75 | 4.4 | 435 | 1 | GUNI_HUMGT | P102622 humicola gr |
| 411 | 76 | 4.5 | 830 | 2 | Q17995 | Q17995 caenorhabdi | 484 | 75 | 4.4 | 461 | 2 | Q9CIC9 | Q9CIC9 lactococcus |
| 412 | 76 | 4.5 | 869 | 2 | Q8TL14 | Q8TL14 methanosarc | 485 | 75 | 4.4 | 468 | 2 | Q8K1R8 | Q8K1R8 mus musculu |
| 413 | 76 | 4.5 | 942 | 2 | Q9JUT01 | Q9JUT01 mus musculu | 486 | 75 | 4.4 | 472 | 2 | Q9VAC8 | Q9VAC8 drosophila |
| 414 | 76 | 4.5 | 1299 | 2 | Q9YTV1 | Q9YTV1 ateline her | 487 | 75 | 4.4 | 483 | 2 | Q938Q6 | Q938Q6 lactobacilli |
| 415 | 76 | 4.5 | 1471 | 1 | MY51_SCHPO | Q74805 schizosacch | 488 | 75 | 4.4 | 486 | 1 | VN53_ROTTHI | P30212 human rotav |
| 416 | 76 | 4.5 | 1509 | 2 | Q75AF6 | Q75AF6 ashbya gos | 489 | 75 | 4.4 | 507 | 2 | Q84150 | Q84150 chlamydia t |
| 417 | 76 | 4.5 | 1687 | 2 | Q61204 | Q61204 mus musculu | 490 | 75 | 4.4 | 536 | 2 | Q96M34 | Q96M34 homo sapien |
| 418 | 76 | 4.5 | 1828 | 1 | MY5A_RAT | Q9GYF3 rattus norv | 491 | 75 | 4.4 | 536 | 2 | Q96M34 | Q96M34 macaca mula |
| 419 | 76 | 4.5 | 1855 | 1 | MY5A_HUMAN | Q9Y411 homo sapien | 492 | 75 | 4.4 | 538 | 2 | Q807P1 | Q807P1 mumps virus |
| 420 | 76 | 4.5 | 1911 | 2 | Q8H7V4 | Q8H7V4 oryza sativ | 493 | 75 | 4.4 | 631 | 1 | Q6NTN9 | Q6NTN9 xenopus lae |
| 421 | 76 | 4.5 | 1911 | 2 | Q8H7V4 | Q991N2 little cher | 494 | 75 | 4.4 | 637 | 1 | SEPD1_RAT | Q62991 rattus norv |
| 422 | 76 | 4.5 | 2025 | 2 | Q99P2 | Q99P2 mus musculu | 495 | 75 | 4.4 | 639 | 1 | SEPD1_MOUSE | Q8BRF7 mus musculu |
| 423 | 76 | 4.5 | 2581 | 2 | Q82S63 | Q82S63 anabaena sp | 496 | 75 | 4.4 | 641 | 2 | Q8B077 | Q8B077 influenza c |
| 424 | 76 | 4.5 | 4699 | 2 | Q9Y383 | Q9Y383 drosophila | 497 | 75 | 4.4 | 642 | 1 | SEPD1_HUMAN | Q8WYH8 homo sapien |
| 425 | 75.5 | 4.5 | 213 | 2 | Q9PE57 | Q9PE57 campylobact | 498 | 75 | 4.4 | 648 | 2 | Q91Q69 | Q91Q69 influenza c |
| 426 | 75.5 | 4.5 | 233 | 2 | Q7MJG7 | Q7MJG7 vibrio vuln | 499 | 75 | 4.4 | 648 | 2 | Q91Q66 | Q91Q66 influenza c |
| 427 | 75.5 | 4.5 | 237 | 2 | Q83909 | Q83909 ovine adeno | 500 | 75 | 4.4 | 695 | 2 | Q8W2R3 | Q8W2R3 oryza sativ |
| 428 | 75.5 | 4.5 | 247 | 2 | Q81SN8 | Q81SN8 bacillus an | 501 | 75 | 4.4 | 695 | 2 | Q7XGR2 | Q7XGR2 oryza sativ |
| 429 | 75.5 | 4.5 | 264 | 2 | Q8BWM1 | Q8BWM1 m. mus muscu | 502 | 75 | 4.4 | 775 | 2 | Q13971 | Q13971 schizosacch |
| 430 | 75.5 | 4.5 | 282 | 2 | Q7SX78 | Q7SX78 brachydantio | 503 | 75 | 4.4 | 970 | 2 | Q9CA47 | Q9CA47 arabidopsis |
| 431 | 75.5 | 4.5 | 304 | 1 | PLA2_HUMAN | Q9HD19 homo sapien | 504 | 75 | 4.4 | 994 | 2 | Q9ALU6 | Q9ALU6 pseudomonas |
| 432 | 75.5 | 4.5 | 330 | 2 | Q8P9W4 | Q8P9W4 xanthomonas | 505 | 75 | 4.4 | 1036 | 1 | YG35_YEAST | P53273 saccharomyc |
| 433 | 75.5 | 4.5 | 363 | 2 | Q97ST2 | Q97ST2 streptococc | 506 | 75 | 4.4 | 1085 | 1 | SI24_RABIT | Q28677 oryctolagus |
| 434 | 75.5 | 4.5 | 406 | 2 | Q61NE8 | Q61NE8 xenopus lae | 507 | 75 | 4.4 | 1158 | 2 | Q6C2G1 | Q6C2G1 yarrowia li |
| 435 | 75.5 | 4.5 | 410 | 2 | Q80919 | Q80919 arabidopsis | 508 | 75 | 4.4 | 1207 | 2 | Q9CPK1 | Q9CPK1 arabidopsis |
| 436 | 75.5 | 4.5 | 414 | 2 | Q9ZVM6 | Q9ZVM6 arabidopsis | 509 | 75 | 4.4 | 1216 | 1 | P1B1_BOVIN | P10894 bos taurus |
| 437 | 75.5 | 4.5 | 430 | 2 | Q8BHX9 | Q8BHX9 mus musculu | 510 | 75 | 4.4 | 1276 | 2 | Q9S6F7 | Q9S6F7 arabidopsis |
| 438 | 75.5 | 4.5 | 447 | 2 | Q8ZPB1 | Q8ZPB1 salmoneilla | 511 | 75 | 4.4 | 1334 | 2 | Q9CTV1 | Q9CTV1 arabidopsis |
| 439 | 75.5 | 4.5 | 454 | 2 | Q82905 | Q82905 escherichia | 512 | 75 | 4.4 | 1334 | 2 | Q9FHZ9 | Q9FHZ9 arabidopsis |
| 440 | 75.5 | 4.5 | 463 | 2 | Q7QYAS | Q7QYAS giardia lam | 513 | 75 | 4.4 | 1496 | 2 | Q8ZAV4 | Q8ZAV4 yersinia pe |
| 441 | 75.5 | 4.5 | 474 | 2 | Q9FRU9 | Q9FRU9 nicotiana t | 514 | 75 | 4.4 | 1516 | 2 | Q8D1P6 | Q8D1P6 yersinia pe |
| 442 | 75.5 | 4.5 | 474 | 2 | Q9LEB3 | Q9LEB3 nicotiana t | 515 | 75 | 4.4 | 1827 | 2 | Q6RSH4 | Q6RSH4 strongyloce |
| 443 | 75.5 | 4.5 | 476 | 2 | Q6ERT1 | Q6ERT1 pfeiffia mos | 516 | 75 | 4.4 | 1875 | 2 | Q6NR36 | Q6NR36 xenopus lae |
| 444 | 75.5 | 4.5 | 497 | 2 | Q6GQAS | Q6GQAS xenopus lae | 517 | 75 | 4.4 | 3734 | 2 | Q9CIG0 | Q9CIG0 kallichroma |
| 445 | 75.5 | 4.5 | 513 | 2 | Q7TPS8 | Q7TPS8 mus musculu | 518 | 75 | 4.4 | 3898 | 2 | Q68R72 | Q68R72 classical s |
| 446 | 75.5 | 4.5 | 535 | 2 | Q9FEZ3 | Q9FEZ3 nicotiana t | 519 | 75 | 4.4 | 4306 | 2 | Q9JUT9 | Q9JUT9 rattus norv |
| 447 | 75.5 | 4.5 | 546 | 2 | Q8BTR8 | Q8BTR8 mus musculu | 520 | 74.5 | 4.4 | 179 | 2 | Q6SCS6 | Q6SCS6 bacillus li |
| 448 | 75.5 | 4.5 | 547 | 2 | P97531 | P97531 rattus norv | 521 | 74.5 | 4.4 | 205 | 2 | Q7MDZ4 | Q7MDZ4 vibrio vuln |
| 449 | 75.5 | 4.5 | 547 | 2 | Q99110 | Q99110 mus musculu | 522 | 74.5 | 4.4 | 205 | 2 | Q8D734 | Q8D734 vibrio vuln |
| 450 | 75.5 | 4.5 | 547 | 2 | Q6E744 | Q6E744 rattus norv | 523 | 74.5 | 4.4 | 304 | 2 | Q8SRU1 | Q8SRU1 encephalito |
| 451 | 75.5 | 4.5 | 561 | 2 | Q7V9F1 | Q7V9F1 prochloroco | 524 | 74.5 | 4.4 | 357 | 2 | Q17591 | Q17591 caenorhabdi |
| 452 | 75.5 | 4.5 | 591 | 2 | Q8W433 | Q8W433 gentiana lu | 525 | 74.5 | 4.4 | 406 | 2 | Q6NY99 | Q6NY99 brachydantio |
| 453 | 75.5 | 4.5 | 602 | 2 | Q8R433 | Q8R433 mus musculu | 526 | 74.5 | 4.4 | 415 | 2 | Q92PU9 | Q92PU9 rhizobium m |
| 454 | 75.5 | 4.5 | 603 | 2 | Q8CJ53 | Q8CJ53 mus musculu | 527 | 74.5 | 4.4 | 430 | 2 | Q264Z4 | Q264Z4 crassostrea |
| 455 | 75.5 | 4.5 | 628 | 2 | Q6AMC4 | Q6AMC4 desulfotocale | 528 | 74.5 | 4.4 | 433 | 1 | U21_HAV62 | Q6GJ45 human herpe |
| 456 | 75.5 | 4.5 | 698 | 2 | Q709D7 | Q709D7 fusarium ox | 529 | 74.5 | 4.4 | 437 | 1 | ATLY_CLOAB | Q97KES clostridium |
| 457 | 75.5 | 4.5 | 749 | 2 | Q9LHT9 | Q9LHT9 oryza sativ | 530 | 74.5 | 4.4 | 453 | 2 | Q758K5 | Q758K5 ashbya gos |
| 458 | 75.5 | 4.5 | 754 | 1 | UBP9_YEAST | P39967 saccharomyc | 531 | 74.5 | 4.4 | 453 | 2 | Q6EMF4 | Q6EMF4 escherichia |
| 459 | 75.5 | 4.5 | 907 | 2 | Q6MIL5 | Q6MIL5 bdellovibri | 532 | 74.5 | 4.4 | 469 | 2 | Q9M4Z1 | Q9M4Z1 hordeum vul |
| 460 | 75.5 | 4.5 | 988 | 2 | Q9XIF2 | Q9XIF2 arabidopsis | 533 | 74.5 | 4.4 | 470 | 1 | TRG_ASHO | Q75A43 ashbya gos |
| 461 | 75.5 | 4.5 | 1092 | 2 | Q6ZJ20 | Q6ZJ20 oryza sativ | 534 | 74.5 | 4.4 | 475 | 1 | ATYX_RAT | Q9ER24 rattus norv |
| 462 | 75.5 | 4.5 | 1201 | 2 | Q8DAL0 | Q8DAL0 vibrio vuln | 535 | 74.5 | 4.4 | 476 | 1 | VTDB_MOUSE | P21614 mus musculu |
| 463 | 75.5 | 4.5 | 1284 | 2 | Q74842 | Q74842 schizosacch | 536 | 74.5 | 4.4 | 478 | 2 | Q7V9R3 | Q7V9R3 prochloroco |
| 464 | 75.5 | 4.5 | 1515 | 2 | Q6AV56 | Q6AV56 oryza sativ | 537 | 74.5 | 4.4 | 482 | 2 | Q962F6 | Q962F6 leishmania |
| 465 | 75.5 | 4.5 | 1630 | 2 | Q8BTF5 | Q8BTF5 methanosarc | 538 | 74.5 | 4.4 | 500 | 2 | Q9WT43 | Q9WT43 human herpe |
| 466 | 75.5 | 4.5 | 1659 | 2 | Q7RQ12 | Q7RQ12 plasmodium | 539 | 74.5 | 4.4 | 505 | 1 | V1L1_HPUM | P27964 human papil |
| 467 | 75.5 | 4.5 | 1837 | 2 | Q91U53 | Q91U53 arabidopsis | 540 | 74.5 | 4.4 | 525 | 1 | CO2A_HUMAN | Q92828 homo sapien |
| 468 | 75.5 | 4.5 | 2472 | 2 | Q811P3 | Q811P3 plasmodium | 541 | 74.5 | 4.4 | 539 | 1 | TM26_HUMAN | Q12899 homo sapien |
| 469 | 75 | 4.4 | 213 | 2 | Q93HW9 | Q93HW9 magnetospir | 542 | 74.5 | 4.4 | 539 | 1 | TM26_PANTR | Q7YR34 pan troglod |

| | | | | | | | | | | | | | |
|-----|------|-----|------|---|-------------|---------------------|-----|----|-----|------|---|--------|--------------------|
| 543 | 74.5 | 4.4 | 542 | 2 | 061WL4 | 061w14 brachydanio | 616 | 74 | 4.4 | 756 | 2 | 06FY8 | 06fjy8 candida gla |
| 544 | 74.5 | 4.4 | 542 | 2 | 07SXX1 | 07sxx1 brachydanio | 617 | 74 | 4.4 | 776 | 2 | 06IR70 | 06ir70 xenopus lae |
| 545 | 74.5 | 4.4 | 590 | 2 | 08BGV1 | 08bgy1 macaca fasc | 618 | 74 | 4.4 | 805 | 2 | 06LM47 | 06lm47 photobacter |
| 546 | 74.5 | 4.4 | 596 | 2 | 08RTW0 | 08rtw0 homo sapien | 619 | 74 | 4.4 | 818 | 2 | 09KBB8 | 09kbb8 bacillus ha |
| 547 | 74.5 | 4.4 | 603 | 2 | 07WAN3 | 07wan3 bordetella | 620 | 74 | 4.4 | 830 | 2 | 087E49 | 087e49 xyella fas |
| 548 | 74.5 | 4.4 | 605 | 2 | 07WJTE | 07wjte bordetella | 621 | 74 | 4.4 | 846 | 2 | 084FT7 | 084ft7 chlamydia t |
| 549 | 74.5 | 4.4 | 620 | 2 | 07WVR3 | 07wvr3 bordetella | 622 | 74 | 4.4 | 846 | 2 | 084FT8 | 084ft8 chlamydia t |
| 550 | 74.5 | 4.4 | 623 | 2 | 09ZMY7 | 09zmy7 helicobacte | 623 | 74 | 4.4 | 893 | 2 | 001596 | 001596 caenorhabdi |
| 551 | 74.5 | 4.4 | 691 | 2 | 06ESV5 | 06esv5 oryza sativ | 624 | 74 | 4.4 | 902 | 2 | 08S191 | 08s191 oryza sativ |
| 552 | 74.5 | 4.4 | 696 | 2 | 09BWX3 | 09bwx3 homo sapien | 625 | 74 | 4.4 | 907 | 2 | 004631 | 004631 arabidopsis |
| 553 | 74.5 | 4.4 | 699 | 2 | 07JQH0 | 07jqh0 treponema d | 626 | 74 | 4.4 | 927 | 2 | 08BJL5 | 08bjl5 mus musculu |
| 554 | 74.5 | 4.4 | 716 | 2 | 093875 | 093875 caenorhabdi | 627 | 74 | 4.4 | 961 | 2 | 06ZQ92 | 06zq92 mus musculu |
| 555 | 74.5 | 4.4 | 717 | 2 | 08NA44 | 08na44 homo sapien | 628 | 74 | 4.4 | 962 | 2 | 089443 | 089443 african swi |
| 556 | 74.5 | 4.4 | 719 | 2 | 08NC57 | 08nc57 homo sapien | 629 | 74 | 4.4 | 984 | 2 | 09GQNI | 09gqni callitricis |
| 557 | 74.5 | 4.4 | 733 | 1 | 06CP47 | 06cp47 medicago tr | 630 | 74 | 4.4 | 984 | 2 | 09GQNI | 09gqni callitricis |
| 558 | 74.5 | 4.4 | 761 | 2 | 060477 | 060477 homo sapien | 631 | 74 | 4.4 | 993 | 2 | 06S144 | 06s144 uncultured |
| 559 | 74.5 | 4.4 | 761 | 2 | 06B1A0 | 06b1a0 homo sapien | 632 | 74 | 4.4 | 1073 | 2 | 083C50 | 083c50 coxiella bu |
| 560 | 74.5 | 4.4 | 833 | 2 | 08RTB0 | 08rtb0 homo sapien | 633 | 74 | 4.4 | 1113 | 2 | 07Q416 | 07q416 anophelis g |
| 561 | 74.5 | 4.4 | 906 | 2 | 09M2B1 | 09m2b1 arabidopsis | 634 | 74 | 4.4 | 1130 | 2 | 09XTI9 | 09xti9 caenorhabdi |
| 562 | 74.5 | 4.4 | 1007 | 2 | 09M285 | 09m285 arabidopsis | 635 | 74 | 4.4 | 1141 | 1 | 08E272 | 08e272 mus musculu |
| 563 | 74.5 | 4.4 | 1009 | 1 | 09M285 | 09m285 homo sapien | 636 | 74 | 4.4 | 1193 | 2 | 086VJ6 | 086vj6 homo sapien |
| 564 | 74.5 | 4.4 | 1009 | 2 | 06EMF2 | 06emf2 homo sapien | 637 | 74 | 4.4 | 1216 | 1 | 086VJ6 | 086vj6 homo sapien |
| 565 | 74.5 | 4.4 | 1009 | 2 | 06EMF2 | 06emf2 homo sapien | 638 | 74 | 4.4 | 1216 | 1 | 086VJ6 | 086vj6 homo sapien |
| 566 | 74.5 | 4.4 | 1019 | 2 | 06BVM3 | 06bvm3 debaryomyce | 639 | 74 | 4.4 | 1216 | 1 | 06PDH1 | 06pdh1 mus musculu |
| 567 | 74.5 | 4.4 | 1125 | 2 | 091L16 | 091l16 turkey aster | 640 | 74 | 4.4 | 1487 | 1 | 06PDH1 | 06pdh1 mus musculu |
| 568 | 74.5 | 4.4 | 1139 | 1 | 091L16 | 091l16 turkey aster | 641 | 74 | 4.4 | 1487 | 1 | 06PDH1 | 06pdh1 mus musculu |
| 569 | 74.5 | 4.4 | 1139 | 1 | 091L16 | 091l16 turkey aster | 642 | 74 | 4.4 | 1487 | 1 | 06PDH1 | 06pdh1 mus musculu |
| 570 | 74.5 | 4.4 | 1160 | 2 | 091L16 | 091l16 turkey aster | 643 | 74 | 4.4 | 1487 | 1 | 06PDH1 | 06pdh1 mus musculu |
| 571 | 74.5 | 4.4 | 1342 | 1 | 091L16 | 091l16 turkey aster | 644 | 74 | 4.4 | 1487 | 1 | 06PDH1 | 06pdh1 mus musculu |
| 572 | 74.5 | 4.4 | 1513 | 2 | 091L16 | 091l16 turkey aster | 645 | 74 | 4.4 | 1487 | 1 | 06PDH1 | 06pdh1 mus musculu |
| 573 | 74.5 | 4.4 | 1600 | 2 | 091L16 | 091l16 turkey aster | 646 | 74 | 4.4 | 1487 | 1 | 06PDH1 | 06pdh1 mus musculu |
| 574 | 74.5 | 4.4 | 3210 | 1 | 091L16 | 091l16 turkey aster | 647 | 74 | 4.4 | 1487 | 1 | 06PDH1 | 06pdh1 mus musculu |
| 575 | 74.5 | 4.4 | 3343 | 2 | 091L16 | 091l16 turkey aster | 648 | 74 | 4.4 | 1487 | 1 | 06PDH1 | 06pdh1 mus musculu |
| 576 | 74.5 | 4.4 | 3343 | 2 | 091L16 | 091l16 turkey aster | 649 | 74 | 4.4 | 1487 | 1 | 06PDH1 | 06pdh1 mus musculu |
| 577 | 74.5 | 4.4 | 1430 | 2 | 06ERN0 | 06ern0 oryza sativ | 650 | 74 | 4.4 | 1487 | 1 | 06PDH1 | 06pdh1 mus musculu |
| 578 | 74.5 | 4.4 | 160 | 2 | 062N44 | 062n44 oryza sativ | 651 | 74 | 4.4 | 1487 | 1 | 06PDH1 | 06pdh1 mus musculu |
| 579 | 74.5 | 4.4 | 243 | 2 | 08Y796 | 08y796 listeria mo | 652 | 74 | 4.4 | 1487 | 1 | 06PDH1 | 06pdh1 mus musculu |
| 580 | 74.5 | 4.4 | 247 | 2 | 06AXUS | 06axus rattus norv | 653 | 74 | 4.4 | 1487 | 1 | 06PDH1 | 06pdh1 mus musculu |
| 581 | 74.5 | 4.4 | 326 | 2 | 08K6Z6 | 08k6z6 streptococc | 654 | 74 | 4.4 | 1487 | 1 | 06PDH1 | 06pdh1 mus musculu |
| 582 | 74.5 | 4.4 | 326 | 2 | 04Z086 | 04z086 human rolev | 655 | 74 | 4.4 | 1487 | 1 | 06PDH1 | 06pdh1 mus musculu |
| 583 | 74.5 | 4.4 | 326 | 2 | 083441 | 083441 murine rolev | 656 | 74 | 4.4 | 1487 | 1 | 06PDH1 | 06pdh1 mus musculu |
| 584 | 74.5 | 4.4 | 354 | 2 | 09NDU0 | 09ndu0 dirosophila | 657 | 74 | 4.4 | 1487 | 1 | 06PDH1 | 06pdh1 mus musculu |
| 585 | 74.5 | 4.4 | 354 | 2 | 09SRV2 | 09srv2 arabidopsis | 658 | 74 | 4.4 | 1487 | 1 | 06PDH1 | 06pdh1 mus musculu |
| 586 | 74.5 | 4.4 | 410 | 2 | 08DV08 | 08dv08 streptococc | 659 | 74 | 4.4 | 1487 | 1 | 06PDH1 | 06pdh1 mus musculu |
| 587 | 74.5 | 4.4 | 474 | 2 | 07P577 | 07p577 fusobacteri | 660 | 74 | 4.4 | 1487 | 1 | 06PDH1 | 06pdh1 mus musculu |
| 588 | 74.5 | 4.4 | 476 | 2 | 08BUT5 | 08but5 mus musculu | 661 | 74 | 4.4 | 1487 | 1 | 06PDH1 | 06pdh1 mus musculu |
| 589 | 74.5 | 4.4 | 489 | 2 | 08XZV1 | 08xzv1 ralsctonia s | 662 | 74 | 4.4 | 1487 | 1 | 06PDH1 | 06pdh1 mus musculu |
| 590 | 74.5 | 4.4 | 504 | 2 | 064H84 | 064h84 pelteobagru | 663 | 74 | 4.4 | 1487 | 1 | 06PDH1 | 06pdh1 mus musculu |
| 591 | 74.5 | 4.4 | 511 | 1 | 07S6A5 | 07s6a5 boe taurus | 664 | 74 | 4.4 | 1487 | 1 | 06PDH1 | 06pdh1 mus musculu |
| 592 | 74.5 | 4.4 | 520 | 2 | 07S6A5 | 07s6a5 boe taurus | 665 | 74 | 4.4 | 1487 | 1 | 06PDH1 | 06pdh1 mus musculu |
| 593 | 74.5 | 4.4 | 531 | 1 | 06MT1 MYCMB | 06mt1 mycoplasma | 666 | 74 | 4.4 | 1487 | 1 | 06PDH1 | 06pdh1 mus musculu |
| 594 | 74.5 | 4.4 | 531 | 1 | 06MT1 MYCMB | 06mt1 mycoplasma | 667 | 74 | 4.4 | 1487 | 1 | 06PDH1 | 06pdh1 mus musculu |
| 595 | 74.5 | 4.4 | 531 | 1 | 06MT1 MYCMB | 06mt1 mycoplasma | 668 | 74 | 4.4 | 1487 | 1 | 06PDH1 | 06pdh1 mus musculu |
| 596 | 74.5 | 4.4 | 531 | 1 | 06MT1 MYCMB | 06mt1 mycoplasma | 669 | 74 | 4.4 | 1487 | 1 | 06PDH1 | 06pdh1 mus musculu |
| 597 | 74.5 | 4.4 | 531 | 1 | 06MT1 MYCMB | 06mt1 mycoplasma | 670 | 74 | 4.4 | 1487 | 1 | 06PDH1 | 06pdh1 mus musculu |
| 598 | 74.5 | 4.4 | 531 | 1 | 06MT1 MYCMB | 06mt1 mycoplasma | 671 | 74 | 4.4 | 1487 | 1 | 06PDH1 | 06pdh1 mus musculu |
| 599 | 74.5 | 4.4 | 531 | 1 | 06MT1 MYCMB | 06mt1 mycoplasma | 672 | 74 | 4.4 | 1487 | 1 | 06PDH1 | 06pdh1 mus musculu |
| 600 | 74.5 | 4.4 | 531 | 1 | 06MT1 MYCMB | 06mt1 mycoplasma | 673 | 74 | 4.4 | 1487 | 1 | 06PDH1 | 06pdh1 mus musculu |
| 601 | 74.5 | 4.4 | 531 | 1 | 06MT1 MYCMB | 06mt1 mycoplasma | 674 | 74 | 4.4 | 1487 | 1 | 06PDH1 | 06pdh1 mus musculu |
| 602 | 74.5 | 4.4 | 531 | 1 | 06MT1 MYCMB | 06mt1 mycoplasma | 675 | 74 | 4.4 | 1487 | 1 | 06PDH1 | 06pdh1 mus musculu |
| 603 | 74.5 | 4.4 | 531 | 1 | 06MT1 MYCMB | 06mt1 mycoplasma | 676 | 74 | 4.4 | 1487 | 1 | 06PDH1 | 06pdh1 mus musculu |
| 604 | 74.5 | 4.4 | 531 | 1 | 06MT1 MYCMB | 06mt1 mycoplasma | 677 | 74 | 4.4 | 1487 | 1 | 06PDH1 | 06pdh1 mus musculu |
| 605 | 74.5 | 4.4 | 531 | 1 | 06MT1 MYCMB | 06mt1 mycoplasma | 678 | 74 | 4.4 | 1487 | 1 | 06PDH1 | 06pdh1 mus musculu |
| 606 | 74.5 | 4.4 | 531 | 1 | 06MT1 MYCMB | 06mt1 mycoplasma | 679 | 74 | 4.4 | 1487 | 1 | 06PDH1 | 06pdh1 mus musculu |
| 607 | 74.5 | 4.4 | 531 | 1 | 06MT1 MYCMB | 06mt1 mycoplasma | 680 | 74 | 4.4 | 1487 | 1 | 06PDH1 | 06pdh1 mus musculu |
| 608 | 74.5 | 4.4 | 531 | 1 | 06MT1 MYCMB | 06mt1 mycoplasma | 681 | 74 | 4.4 | 1487 | 1 | 06PDH1 | 06pdh1 mus musculu |
| 609 | 74.5 | 4.4 | 531 | 1 | 06MT1 MYCMB | 06mt1 mycoplasma | 682 | 74 | 4.4 | 1487 | 1 | 06PDH1 | 06pdh1 mus musculu |
| 610 | 74.5 | 4.4 | 531 | 1 | 06MT1 MYCMB | 06mt1 mycoplasma | 683 | 74 | 4.4 | 1487 | 1 | 06PDH1 | 06pdh1 mus musculu |
| 611 | 74.5 | 4.4 | 531 | 1 | 06MT1 MYCMB | 06mt1 mycoplasma | 684 | 74 | 4.4 | 1487 | 1 | 06PDH1 | 06pdh1 mus musculu |
| 612 | 74.5 | 4.4 | 531 | 1 | 06MT1 MYCMB | 06mt1 mycoplasma | 685 | 74 | 4.4 | 1487 | 1 | 06PDH1 | 06pdh1 mus musculu |
| 613 | 74.5 | 4.4 | 531 | 1 | 06MT1 MYCMB | 06mt1 mycoplasma | 686 | 74 | 4.4 | 1487 | 1 | 06PDH1 | 06pdh1 mus musculu |
| 614 | 74.5 | 4.4 | 531 | 1 | 06MT1 MYCMB | 06mt1 mycoplasma | 687 | 74 | 4.4 | 1487 | 1 | 06PDH1 | 06pdh1 mus musculu |
| 615 | 74.5 | 4.4 | 531 | 1 | 06MT1 MYCMB | 06mt1 mycoplasma | 688 | 74 | 4.4 | 1487 | 1 | 06PDH1 | 06pdh1 mus musculu |

| | | | | | | | | | | | | | |
|-----|------|-----|------|---|-------------|---------------------|-----|------|-----|------|---|------------|---------------------|
| 689 | 73.5 | 4.3 | 2204 | 2 | Q913F4 | Q913f4 newcastle d | 762 | 72.5 | 4.3 | 326 | 2 | Q7VJ10 | Q7vj10 helicobacte |
| 690 | 73.5 | 4.3 | 2294 | 2 | Q7OU56 | Q7ou56 giardia lam | 763 | 72.5 | 4.3 | 330 | 2 | Q88CR3 | Q88cr3 pseudomonas |
| 691 | 73.5 | 4.3 | 2397 | 1 | MOKB_SCHPO | Q09854 schizosacch | 764 | 72.5 | 4.3 | 338 | 2 | Q03BE19 | Q03be19 coxiella bu |
| 692 | 73.5 | 4.3 | 2845 | 1 | APC_MOUSE | Q6115 mus musculu | 765 | 72.5 | 4.3 | 338 | 2 | Q7MPC7 | Q7mpc7 vibrio vuln |
| 693 | 73.5 | 4.3 | 3153 | 1 | Q6C6F9 | Q6c6f9 yarrowia li | 766 | 72.5 | 4.3 | 342 | 2 | Q83Z52 | Q83z52 uncultured |
| 694 | 73 | 4.3 | 144 | 2 | Q6RC41 | Q6rc41 dirosophila | 767 | 72.5 | 4.3 | 344 | 2 | Q8BMK7 | Q8bmK7 mus musculu |
| 695 | 73 | 4.3 | 238 | 2 | Q85093 | Q85093 pseudomonas | 768 | 72.5 | 4.3 | 359 | 1 | WECF_ECOLI | WECF eccherichia |
| 696 | 73 | 4.3 | 276 | 1 | NCT2_HUMAN | Q95444 homo sapien | 769 | 72.5 | 4.3 | 359 | 1 | WECF_SH1FL | WECF shigella fl |
| 697 | 73 | 4.3 | 295 | 2 | Q6FJ11 | Q6fj11 candida gla | 770 | 72.5 | 4.3 | 366 | 2 | Q6FT57 | Q6ft57 candida gla |
| 698 | 73 | 4.3 | 298 | 2 | Q8U710 | Q8u710 agrobacteri | 771 | 72.5 | 4.3 | 371 | 2 | Q7M8X9 | Q7m8x9 wolfinella s |
| 699 | 73 | 4.3 | 366 | 1 | TORY_ECOLI | P52005 escherichia | 772 | 72.5 | 4.3 | 377 | 2 | Q92T54 | Q92t54 rhizobium m |
| 700 | 73 | 4.3 | 375 | 2 | Q9U1L4 | Q9u1l4 dirosophila | 773 | 72.5 | 4.3 | 390 | 2 | Q66KX2 | Q66kx2 xenopus lae |
| 701 | 73 | 4.3 | 388 | 2 | Q8R464 | Q8r464 mus musculu | 774 | 72.5 | 4.3 | 452 | 2 | Q65OR4 | Q65or4 bacteroides |
| 702 | 73 | 4.3 | 390 | 2 | Q7ULP9 | Q7ulp9 choristoneu | 775 | 72.5 | 4.3 | 456 | 2 | Q6BJH0 | Q6bjh0 bacteroides |
| 703 | 73 | 4.3 | 416 | 2 | Q7MNV1 | Q7mrv1 porphyromon | 776 | 72.5 | 4.3 | 464 | 2 | Q8K2P4 | Q8k2p4 klebsiella |
| 704 | 73 | 4.3 | 451 | 2 | Q6ST57 | Q6st57 human rhino | 777 | 72.5 | 4.3 | 484 | 2 | Q48972 | Q48972 hordeum vul |
| 705 | 73 | 4.3 | 458 | 2 | Q736K9 | Q736k9 bacillus ce | 778 | 72.5 | 4.3 | 485 | 1 | GLGA_BACST | GLGA bacillus st |
| 706 | 73 | 4.3 | 468 | 1 | DNAB_MYCGE | P47340 mycoplasma | 779 | 72.5 | 4.3 | 485 | 2 | Q7V0R0 | Q7v0r0 prochloroco |
| 707 | 73 | 4.3 | 472 | 2 | TBG_ANEPH | Q9W859 porcine ade | 780 | 72.5 | 4.3 | 504 | 2 | Q8U178 | Q8u178 agrobacteri |
| 708 | 73 | 4.3 | 474 | 2 | Q9W859 | Q9w859 porcine ade | 781 | 72.5 | 4.3 | 552 | 2 | Q86SV6 | Q86sv6 homo sapien |
| 709 | 73 | 4.3 | 485 | 2 | Q57916 | Q57916 pyrococcus | 782 | 72.5 | 4.3 | 552 | 2 | CM39_MOUSE | CM39 mus musculu |
| 710 | 73 | 4.3 | 485 | 2 | Q25870 | Q25870 helicobacte | 783 | 72.5 | 4.3 | 582 | 2 | Q636Z8 | Q636z8 |
| 711 | 73 | 4.3 | 486 | 2 | Q91M71 | Q91m71 human rotav | 784 | 72.5 | 4.3 | 599 | 2 | Q8SV72 | Q8sv72 |
| 712 | 73 | 4.3 | 491 | 2 | Q76VW3 | Q76vw3 rotavirus s | 785 | 72.5 | 4.3 | 603 | 2 | Q975V6 | Q975v6 sulfolobus |
| 713 | 73 | 4.3 | 491 | 2 | Q89895 | Q89895 bovine rota | 786 | 72.5 | 4.3 | 619 | 2 | Q91L56 | Q91l56 oryza sativ |
| 714 | 73 | 4.3 | 491 | 2 | Q9WAA8 | Q9waa8 human rotav | 787 | 72.5 | 4.3 | 631 | 2 | Q650A7 | Q650a7 manheimia |
| 715 | 73 | 4.3 | 494 | 2 | Q02641 | Q02641 caenorhabdi | 788 | 72.5 | 4.3 | 631 | 2 | Q90ZAI | Q90za1 xenopus lae |
| 716 | 73 | 4.3 | 500 | 2 | Q7XN10 | Q7xn10 oryza sativ | 789 | 72.5 | 4.3 | 640 | 2 | Q6BNT1 | Q6bnt1 debaryomyce |
| 717 | 73 | 4.3 | 544 | 2 | Q6N827 | Q6n827 rhodospseudo | 790 | 72.5 | 4.3 | 645 | 1 | VP74_NPVCF | VP74 neurospora |
| 718 | 73 | 4.3 | 546 | 2 | Q9ADU0 | Q9adu0 salmomella | 791 | 72.5 | 4.3 | 660 | 2 | Q7S125 | Q7s125 neurospora |
| 719 | 73 | 4.3 | 617 | 1 | BFSI_RAT | Q02435 rattus norv | 792 | 72.5 | 4.3 | 669 | 2 | Q04914 | Q04914 pellicium nu |
| 720 | 73 | 4.3 | 635 | 2 | Q9VUK7 | Q9vuk7 dirosophila | 793 | 72.5 | 4.3 | 711 | 2 | Q656W9 | Q656w9 oryza sativ |
| 721 | 73 | 4.3 | 644 | 1 | NAH9_MOUSE | Q8b200 mus musculu | 794 | 72.5 | 4.3 | 721 | 2 | Q66H87 | Q66h87 rattus norv |
| 722 | 73 | 4.3 | 663 | 2 | Q6WE37 | Q6we37 paramylumd | 795 | 72.5 | 4.3 | 736 | 2 | Q7RRP2 | Q7rrp2 plasmodium |
| 723 | 73 | 4.3 | 668 | 1 | BAY_FIVC6 | P21443 feline leuk | 796 | 72.5 | 4.3 | 750 | 1 | GSN1_STRA3 | GSN1 streptococc |
| 724 | 73 | 4.3 | 671 | 1 | CHEA_BACSU | P29072 bacillus su | 797 | 72.5 | 4.3 | 750 | 1 | GSN1_STRAS | GSN1 streptococc |
| 725 | 73 | 4.3 | 688 | 2 | Q9TY27 | Q9ty27 caenorhabdi | 798 | 72.5 | 4.3 | 769 | 2 | Q9PLI5 | Q9pli5 chlamydia m |
| 726 | 73 | 4.3 | 692 | 2 | Q9VI90 | Q9vi90 dirosophila | 799 | 72.5 | 4.3 | 794 | 2 | Q7XKVI | Q7xkvi oryza sativ |
| 727 | 73 | 4.3 | 715 | 2 | Q84GX2 | Q84gx2 photorhabdu | 800 | 72.5 | 4.3 | 836 | 1 | YGL1_SCHPO | YGL1 schizosacch |
| 728 | 73 | 4.3 | 730 | 2 | Q614A9 | Q614a9 solanum dem | 801 | 72.5 | 4.3 | 843 | 2 | Q47802 | Q47802 enterococcu |
| 729 | 73 | 4.3 | 742 | 2 | Q7QC58 | Q7qc58 anopheles g | 802 | 72.5 | 4.3 | 911 | 2 | Q8GD70 | Q8gd70 neurospora |
| 730 | 73 | 4.3 | 813 | 2 | Q7Q1I6 | Q7q1i6 anopheles g | 803 | 72.5 | 4.3 | 931 | 2 | Q7SE30 | Q7se30 neurospora |
| 731 | 73 | 4.3 | 814 | 2 | Q9KPY1 | Q9kpy1 vibrio chol | 804 | 72.5 | 4.3 | 946 | 2 | Q07153 | Q07153 torpedo cal |
| 732 | 73 | 4.3 | 844 | 2 | Q6DD03 | Q6dd03 xenopus lae | 805 | 72.5 | 4.3 | 1036 | 2 | Q64819 | Q64819 arabidopsis |
| 733 | 73 | 4.3 | 971 | 1 | CSEI1_PAGMA | Q9ptc3 pagrus majo | 806 | 72.5 | 4.3 | 1075 | 1 | MTR3_MOUSE | MTR3 mus musculu |
| 734 | 73 | 4.3 | 996 | 2 | Q9ENP6 | Q9enp6 arabidopsis | 807 | 72.5 | 4.3 | 1079 | 2 | Q85ZG2 | Q85zg2 |
| 735 | 73 | 4.3 | 1014 | 1 | CINI_YEAST | P49987 saccharomyc | 808 | 72.5 | 4.3 | 1114 | 2 | Q8GT16 | Q8gt16 |
| 736 | 73 | 4.3 | 1022 | 2 | Q7Q9D9 | Q7q9d9 anopheles g | 809 | 72.5 | 4.3 | 1125 | 2 | Q6K3D1 | Q6k3d1 oryza sativ |
| 737 | 73 | 4.3 | 1039 | 1 | SYI_METUA | Q58357 mechanococc | 810 | 72.5 | 4.3 | 1159 | 2 | Q66145 | Q66145 mus musculu |
| 738 | 73 | 4.3 | 1189 | 2 | Q8KQJ7 | Q8kqu7 vibrio chol | 811 | 72.5 | 4.3 | 1188 | 2 | Q9USG8 | Q9usg8 schizosacch |
| 739 | 73 | 4.3 | 1216 | 1 | P1B1_HUMAN | Q9ng66 homo sapien | 812 | 72.5 | 4.3 | 1451 | 1 | YGL2_CVCAI | YGL2 cvcai |
| 740 | 73 | 4.3 | 1221 | 2 | Q9N5Z3 | Q9n5z3 caenorhabdi | 813 | 72.5 | 4.3 | 1466 | 2 | Q6YU44 | Q6yu44 |
| 741 | 73 | 4.3 | 1259 | 2 | Q614D7 | Q614d7 oryza sativ | 814 | 72.5 | 4.3 | 1508 | 1 | CEM5_HUMAN | CEM5 human |
| 742 | 73 | 4.3 | 1259 | 2 | Q65XG9 | Q65xg9 oryza sativ | 815 | 72.5 | 4.3 | 1602 | 2 | Q6BF00 | Q6bf00 |
| 743 | 73 | 4.3 | 1336 | 2 | Q6L3Q0 | Q6l3q0 solanum dem | 816 | 72.5 | 4.3 | 1858 | 2 | Q7RXM6 | Q7rxm6 neurospora |
| 744 | 73 | 4.3 | 1502 | 2 | Q6C0U5 | Q6c0u5 yarrowia li | 817 | 72.5 | 4.3 | 2225 | 2 | Q6RCQ4 | Q6rcq4 legionella |
| 745 | 73 | 4.3 | 1679 | 1 | PUR2_DROME | P30432 dirosophila | 818 | 72.5 | 4.3 | 2226 | 1 | POLG_HPAV2 | POLG hpav2 |
| 746 | 73 | 4.3 | 1726 | 1 | SUGH_HUMAN | Q7kz85 homo sapien | 819 | 72.5 | 4.3 | 2264 | 2 | Q6RK72 | Q6rk72 |
| 747 | 73 | 4.3 | 1726 | 1 | SUGH_MOUSE | Q63383 mus musculu | 820 | 72.5 | 4.3 | 2402 | 2 | Q9AER7 | Q9aer7 staphylococ |
| 748 | 73 | 4.3 | 1877 | 1 | PCK5_MOUSE | Q04592 mus musculu | 821 | 72.5 | 4.3 | 2667 | 2 | Q7RWZ8 | Q7rwz8 neurospora |
| 749 | 73 | 4.3 | 2548 | 2 | Q81E95 | Q81e95 plasmodium | 822 | 72.5 | 4.3 | 2735 | 2 | Q8WZK6 | Q8wzk6 neurospora |
| 750 | 73 | 4.3 | 3025 | 2 | Q962J9 | Q962j9 plasmodium | 823 | 72.5 | 4.3 | 2964 | 2 | Q817W7 | Q817w7 dictyostel |
| 751 | 73 | 4.3 | 5327 | 1 | MACP_MOUSE | Q9gx20 mus musculu | 824 | 72.5 | 4.3 | 3085 | 2 | Q6XW15 | Q6xw15 beet mosaic |
| 752 | 72.5 | 4.3 | 177 | 1 | CUP2_SCHPO | Q94588 schizosacch | 825 | 72.5 | 4.3 | 4969 | 2 | Q8CP91 | Q8cp91 mus musculu |
| 753 | 72.5 | 4.3 | 180 | 2 | Q7XI71 | Q7xi71 oryza sativ | 826 | 72.5 | 4.3 | 5054 | 2 | Q7RPE1 | Q7rpe1 plasmodium |
| 754 | 72.5 | 4.3 | 242 | 2 | Q13919 | Q13919 caenorhabdi | 827 | 72.5 | 4.3 | 5165 | 2 | Q8CP92 | Q8cp92 mus musculu |
| 755 | 72.5 | 4.3 | 248 | 2 | Q93MFO | Q93mfo amycolatops | 828 | 72 | 4.3 | 143 | 2 | Q6RC97 | Q6rc97 dirosophila |
| 756 | 72.5 | 4.3 | 295 | 2 | Q83VCG | Q8c7c3 mus musculu | 829 | 72 | 4.3 | 143 | 2 | Q6RC93 | Q6rc93 dirosophila |
| 757 | 72.5 | 4.3 | 295 | 2 | Q83VGI | Q83v91 lactococcus | 830 | 72 | 4.3 | 143 | 2 | Q6RC94 | Q6rc94 dirosophila |
| 758 | 72.5 | 4.3 | 295 | 2 | Q7YV99 | Q7yv99 cryptospori | 831 | 72 | 4.3 | 143 | 2 | Q6RC95 | Q6rc95 dirosophila |
| 759 | 72.5 | 4.3 | 303 | 2 | Q93SA1 | Q93sa3 rhizobium m | 832 | 72 | 4.3 | 202 | 2 | Q9GRC4 | Q9grc4 megabalanus |
| 760 | 72.5 | 4.3 | 311 | 2 | Q6O9A1 | Q6o941 uncultured | 833 | 72 | 4.3 | 217 | 2 | Q7TIC3 | Q7tic3 ambystoma b |
| 761 | 72.5 | 4.3 | 322 | 2 | Q82TH2 | Q82th2 nitrosomona | 834 | 72 | 4.3 | 222 | 2 | Q91214 | Q91214 mus musculu |

| | | | | | | | | | | | | | |
|-----|----|-----|-----|---|------------|----------------------|-----|----|-----|------|---|------------|------------------------|
| 835 | 72 | 4.3 | 234 | 1 | A29B_DROSI | 09u968 drosophila | 908 | 72 | 4.3 | 641 | 2 | 08B071 | 08B071 influenza c |
| 836 | 72 | 4.3 | 245 | 2 | 07T0U7 | 07U0u7 xenopus lae | 909 | 72 | 4.3 | 641 | 2 | 08B072 | 08B072 influenza c |
| 837 | 72 | 4.3 | 251 | 2 | 07QWJ2 | 07QWj2 giardia lam | 910 | 72 | 4.3 | 641 | 2 | 08B076 | 08B076 influenza c |
| 838 | 72 | 4.3 | 263 | 2 | 072P38 | 072Pj8 leptospira | 911 | 72 | 4.3 | 641 | 2 | 08B082 | 08B082 influenza c |
| 839 | 72 | 4.3 | 276 | 2 | 085MA9 | 085Maj9 monoblephar | 912 | 72 | 4.3 | 641 | 2 | 091Q72 | 091Q72 influenza c |
| 840 | 72 | 4.3 | 278 | 2 | 08N7V2 | 08N7v2 homo sapien | 913 | 72 | 4.3 | 645 | 2 | 06CYA8 | 06CYA8 kluyveromyc |
| 841 | 72 | 4.3 | 279 | 2 | 0640X0 | 0640x0 xenopus lae | 914 | 72 | 4.3 | 645 | 2 | 08H241 | 08H241 goessypium h |
| 842 | 72 | 4.3 | 306 | 2 | 06F9I5 | 06F9i5 actinobact | 915 | 72 | 4.3 | 649 | 2 | 039661 | 039661 influenza c |
| 843 | 72 | 4.3 | 310 | 2 | 09M2Y9 | 09M2y9 arabidopsis | 916 | 72 | 4.3 | 649 | 2 | 067416 | 067416 influenza c |
| 844 | 72 | 4.3 | 311 | 2 | 08CQC9 | 08Cqc9 staphylococ | 917 | 72 | 4.3 | 652 | 2 | 0711P7 | 0711P7 leishmania |
| 845 | 72 | 4.3 | 312 | 2 | 09DPS7 | 09Dps7 meleagrid h | 918 | 72 | 4.3 | 654 | 1 | HEMA_INCCA | HEMA_INCCA influenza c |
| 846 | 72 | 4.3 | 312 | 2 | 09ELI3 | 09ELi3 meleagrid h | 919 | 72 | 4.3 | 655 | 1 | HEMA_INCUH | P07975 influenza c |
| 847 | 72 | 4.3 | 316 | 2 | 08PLU9 | 08Plu9 xanthomonas | 920 | 72 | 4.3 | 655 | 1 | NA10_HUMAN | 08Ew26 homo sapien |
| 848 | 72 | 4.3 | 320 | 2 | 09BRJ5 | 09BRj5 mycoplasma | 921 | 72 | 4.3 | 658 | 2 | 08BE51 | 08BE51 shewanella |
| 849 | 72 | 4.3 | 328 | 2 | 083GG6 | 083gg6 tropheryma | 922 | 72 | 4.3 | 697 | 2 | 06PAA6 | 06Paa6 actinobact |
| 850 | 72 | 4.3 | 330 | 2 | 09KAA4 | 09Kaa4 bacillus ha | 923 | 72 | 4.3 | 712 | 2 | 08CIS1 | 08Cis1 lactococcus |
| 851 | 72 | 4.3 | 342 | 2 | 096BE4 | 096be4 homo sapien | 924 | 72 | 4.3 | 737 | 1 | 09DW97 | 09DW97 rat cytoleg |
| 852 | 72 | 4.3 | 346 | 2 | P91677 | P91677 drosophila | 925 | 72 | 4.3 | 751 | 1 | UAS3_DROME | 09vce9 drosophila |
| 853 | 72 | 4.3 | 350 | 2 | 06A0B4 | 06A0b4 mus musculu | 926 | 72 | 4.3 | 760 | 2 | 06ZCS7 | 06Zcs7 oryza sativ |
| 854 | 72 | 4.3 | 352 | 1 | COBT_CLOAB | 097jb4 clostridium | 927 | 72 | 4.3 | 768 | 2 | 09ZS81 | 09Zs81 lycopersico |
| 855 | 72 | 4.3 | 353 | 2 | 076LNO | 076lno homo sapien | 928 | 72 | 4.3 | 781 | 2 | 041269 | 041269 spodoptera |
| 856 | 72 | 4.3 | 353 | 2 | 06ARE1 | 06Are1 desulfofatale | 929 | 72 | 4.3 | 790 | 2 | 06CSV0 | 06CSV0 kluyveromyc |
| 857 | 72 | 4.3 | 360 | 2 | 02S195 | 02S195 helicobacte | 930 | 72 | 4.3 | 812 | 2 | 06P3N7 | 06P3n7 xenopus tro |
| 858 | 72 | 4.3 | 370 | 1 | H181_BACCR | 081fq1 bacillus ce | 931 | 72 | 4.3 | 839 | 2 | 06P3N7 | 06P3n7 xenopus tro |
| 859 | 72 | 4.3 | 372 | 2 | 07YSL1 | 07Ysl1 cullex pipie | 932 | 72 | 4.3 | 860 | 2 | 09FHN0 | 09Fhn0 arabidopsis |
| 860 | 72 | 4.3 | 372 | 2 | 07Z0Z4 | P39048 anabaena sp | 933 | 72 | 4.3 | 882 | 1 | ALKS_PSBOL | P17051 pseudomonas |
| 861 | 72 | 4.3 | 379 | 1 | PATR_ANASP | 09pah1 xyella fas | 934 | 72 | 4.3 | 998 | 2 | 08ZXL7 | 08Zxl7 pyrobaculum |
| 862 | 72 | 4.3 | 387 | 1 | SUCC_XYLFA | 087a98 xyella fas | 935 | 72 | 4.3 | 1038 | 2 | 06MDY1 | 06MDy1 parachlamyd |
| 863 | 72 | 4.3 | 387 | 1 | SUCC_XYLFT | 06u9x9 bacterioph | 936 | 72 | 4.3 | 1048 | 1 | S24B_ARATH | 06fK38 candida gla |
| 864 | 72 | 4.3 | 396 | 2 | 06U9K9 | 07vps0 chlamydia p | 937 | 72 | 4.3 | 1069 | 1 | S24B_ARATH | 09m081 arabidopsis |
| 865 | 72 | 4.3 | 416 | 2 | 07VPS0 | 09jrz1 chlamydia p | 938 | 72 | 4.3 | 1081 | 2 | 094LJ2 | 094Lj2 oryza sativ |
| 866 | 72 | 4.3 | 430 | 2 | 09JZR1 | 0976u2 chlamydia p | 939 | 72 | 4.3 | 1114 | 2 | 0717V6 | 0717v6 stellaria l |
| 867 | 72 | 4.3 | 430 | 2 | 09Z6U2 | P22933 mus musculu | 940 | 72 | 4.3 | 1118 | 2 | 041335 | 041335 lycopersico |
| 868 | 72 | 4.3 | 449 | 1 | GAD_MOUSE | 08vdb6 mus musculu | 941 | 72 | 4.3 | 1125 | 2 | 0925C2 | 0925C2 mus musculu |
| 869 | 72 | 4.3 | 449 | 1 | Q8VBV6 | 08vdb6 mus musculu | 942 | 72 | 4.3 | 1158 | 2 | 0889H3 | 0889H3 pseudomonas |
| 870 | 72 | 4.3 | 450 | 2 | 09FIA0 | 09fiao arabidopsis | 943 | 72 | 4.3 | 1166 | 2 | 08RWT2 | 08Rwt2 arabidopsis |
| 871 | 72 | 4.3 | 450 | 2 | 0654Z5 | 0654z5 arabidopsis | 944 | 72 | 4.3 | 1166 | 2 | 09LHR9 | 09Lhr9 arabidopsis |
| 872 | 72 | 4.3 | 454 | 2 | 06SLNO | 06slno bacillus li | 945 | 72 | 4.3 | 1166 | 2 | 09SNF0 | 09Snf0 arabidopsis |
| 873 | 72 | 4.3 | 454 | 2 | FKB5_SAGOE | 09xei2 seguinus oe | 946 | 72 | 4.3 | 1177 | 2 | 06A086 | 06A086 mus musculu |
| 874 | 72 | 4.3 | 457 | 2 | Q8LWP9 | 08lwp9 ranodon sib | 947 | 72 | 4.3 | 1247 | 2 | 07P06 | 07P06 anopheles g |
| 875 | 72 | 4.3 | 462 | 2 | 09M97 | 09m97 mus musculu | 948 | 72 | 4.3 | 1351 | 2 | 07P223 | 07P223 anopheles g |
| 876 | 72 | 4.3 | 464 | 2 | 09F199 | 09f199 arabidopsis | 949 | 72 | 4.3 | 1411 | 2 | 06V3V8 | 06V3v8 drosophila |
| 877 | 72 | 4.3 | 470 | 1 | VAH2_CABEL | 022494 caenorhabdi | 950 | 72 | 4.3 | 1411 | 2 | 09S3J2 | 09S3j2 arabidopsis |
| 878 | 72 | 4.3 | 477 | 2 | 08YVB6 | 08Yyb6 anabaena ep | 951 | 72 | 4.3 | 1429 | 2 | 015764 | 015764 tetrahymena |
| 879 | 72 | 4.3 | 480 | 2 | Q7SC42 | 07sc42 neurospora | 952 | 72 | 4.3 | 1459 | 1 | LHN2_HUMAN | 095490 homo sapien |
| 880 | 72 | 4.3 | 490 | 2 | Q6BP12 | 06bp12 debaryomyce | 953 | 72 | 4.3 | 1524 | 2 | 06CBR1 | 06Cbr1 yarrowia li |
| 881 | 72 | 4.3 | 495 | 2 | Q6ESK6 | 06esk6 oryza sativ | 954 | 72 | 4.3 | 1583 | 2 | 08K4P8 | 08K4p8 mus musculu |
| 882 | 72 | 4.3 | 499 | 2 | Q9A9H8 | 09a9h8 caulobacter | 955 | 72 | 4.3 | 1589 | 2 | 09U0Q9 | 09U0q9 metarhizium |
| 883 | 72 | 4.3 | 512 | 2 | 056677 | 056677 coecal virus | 956 | 72 | 4.3 | 1618 | 2 | 07ZT77 | 07Zt77 xenopus lae |
| 884 | 72 | 4.3 | 538 | 2 | Q9JAE2 | 09jae2 mumps virus | 957 | 72 | 4.3 | 1664 | 2 | 06BNP3 | 06Bnp3 debaryomyce |
| 885 | 72 | 4.3 | 552 | 2 | Q7UM91 | 07um91 rhodopirelli | 958 | 72 | 4.3 | 1784 | 2 | 09CDB1 | 09Cdb1 mycobacteri |
| 886 | 72 | 4.3 | 554 | 2 | Q6GV72 | 06gv72 olkopleura | 959 | 72 | 4.3 | 1902 | 2 | 06FVQ9 | 06Fvq9 candida gla |
| 887 | 72 | 4.3 | 600 | 1 | NUCD_ECOLI | P33599 escherichia | 960 | 72 | 4.3 | 2006 | 2 | Q7RW52 | 07RW52 giardia lam |
| 888 | 72 | 4.3 | 611 | 1 | RBT3_MOUSE | 09ctna mus musculu | 961 | 72 | 4.3 | 2073 | 2 | 06M6M6 | 06M6m6 homo sapien |
| 889 | 72 | 4.3 | 641 | 2 | 08OZNF7 | 08Ozn7 influenza c | 962 | 72 | 4.3 | 2104 | 2 | 06FM73 | 06Fm73 candida gla |
| 890 | 72 | 4.3 | 641 | 2 | 08OZNF8 | 08Ozn8 influenza c | 963 | 72 | 4.3 | 2176 | 2 | 06Q883 | 06Q883 leptospheer |
| 891 | 72 | 4.3 | 641 | 2 | 08OZNF9 | 08Ozn9 influenza c | 964 | 72 | 4.3 | 2222 | 2 | Q7R4B1 | 07R4b1 giardia lam |
| 892 | 72 | 4.3 | 641 | 2 | 08OZNF0 | 08Ozn0 influenza c | 965 | 72 | 4.3 | 3011 | 1 | YOS1_SCHPO | P87319 schizosacch |
| 893 | 72 | 4.3 | 641 | 2 | 08OZNF1 | 08Ozn1 influenza c | 966 | 72 | 4.3 | 3088 | 1 | 09WID3 | 09Wid3 chilli vein |
| 894 | 72 | 4.3 | 641 | 2 | 08OZNF2 | 08Ozn2 influenza c | 967 | 72 | 4.3 | 4533 | 2 | 09BIX3 | 09Bix3 tetrahymena |
| 895 | 72 | 4.3 | 641 | 2 | 08OZNF3 | 08Ozn3 influenza c | 968 | 72 | 4.3 | 4533 | 2 | 0181S8 | 0181s8 caenorhabdi |
| 896 | 72 | 4.3 | 641 | 2 | 08OZNF4 | 08Ozn4 influenza c | 969 | 72 | 4.3 | 4533 | 2 | 09XUN4 | 09Xun4 caenorhabdi |
| 897 | 72 | 4.3 | 641 | 2 | 08OZNF5 | 08Ozn5 influenza c | 970 | 72 | 4.3 | 4533 | 2 | 09XUN4 | 09Xun4 caenorhabdi |
| 898 | 72 | 4.3 | 641 | 2 | 08OZNF6 | 08Ozn6 influenza c | 971 | 72 | 4.3 | 4533 | 2 | 09XUN4 | 09Xun4 caenorhabdi |
| 899 | 72 | 4.3 | 641 | 2 | 08OZNF7 | 08Ozn7 influenza c | 972 | 72 | 4.3 | 4533 | 2 | 09XUN4 | 09Xun4 caenorhabdi |
| 900 | 72 | 4.3 | 641 | 2 | 08OZNF8 | 08Ozn8 influenza c | 973 | 72 | 4.3 | 4533 | 2 | 09XUN4 | 09Xun4 caenorhabdi |
| 901 | 72 | 4.3 | 641 | 2 | 08OZNF9 | 08Ozn9 influenza c | 974 | 72 | 4.3 | 4533 | 2 | 09XUN4 | 09Xun4 caenorhabdi |
| 902 | 72 | 4.3 | 641 | 2 | 08OZNF0 | 08Ozn0 influenza c | 975 | 72 | 4.3 | 4533 | 2 | 09XUN4 | 09Xun4 caenorhabdi |
| 903 | 72 | 4.3 | 641 | 2 | 08OZNF1 | 08Ozn1 influenza c | 976 | 72 | 4.3 | 4533 | 2 | 09XUN4 | 09Xun4 caenorhabdi |
| 904 | 72 | 4.3 | 641 | 2 | 08OZNF2 | 08Ozn2 influenza c | 977 | 72 | 4.3 | 4533 | 2 | 09XUN4 | 09Xun4 caenorhabdi |
| 905 | 72 | 4.3 | 641 | 2 | 08OZNF3 | 08Ozn3 influenza c | 978 | 72 | 4.3 | 4533 | 2 | 09XUN4 | 09Xun4 caenorhabdi |
| 906 | 72 | 4.3 | 641 | 2 | 08OZNF4 | 08Ozn4 influenza c | 979 | 72 | 4.3 | 4533 | 2 | 09XUN4 | 09Xun4 caenorhabdi |
| 907 | 72 | 4.3 | 641 | 2 | 08OZNF5 | 08Ozn5 influenza c | 980 | 72 | 4.3 | 4533 | 2 | 09XUN4 | 09Xun4 caenorhabdi |

| | | | | | | | | | | | | | |
|------|------|-----|------|---|------------|---------------------|------|------|-----|------|---|-------------|---------------------|
| 981 | 71.5 | 4.2 | 326 | 2 | 08JHW3 | 08Jhw3 xenopus lae | 1054 | 71.5 | 4.2 | 1627 | 2 | 084ZL0 | 084z10 oryza sativ |
| 982 | 71.5 | 4.2 | 338 | 2 | 08JH92 | 08Jh92 xenopus lae | 1055 | 71.5 | 4.2 | 1712 | 2 | 08IY21 | 08Iy21 homo sapien |
| 983 | 71.5 | 4.2 | 338 | 2 | 08DRA7 | 08Dra7 xenopus lae | 1056 | 71.5 | 4.2 | 1744 | 2 | 08CHH1 | 08Chh1 mus musculu |
| 984 | 71.5 | 4.2 | 340 | 2 | 08IPY9 | 08Ipy9 bacillus an | 1057 | 71.5 | 4.2 | 1896 | 2 | 06FV91 | 06Fv91 candida gla |
| 985 | 71.5 | 4.2 | 340 | 2 | 06H167 | 06H167 bacillus th | 1058 | 71.5 | 4.2 | 1916 | 2 | 075AP0 | 075afo ashbya gos |
| 986 | 71.5 | 4.2 | 346 | 2 | 09ZFW7 | 09Zfw7 pseudomonas | 1059 | 71.5 | 4.2 | 2013 | 2 | 06PHU4 | 06Phu4 mus musculu |
| 987 | 71.5 | 4.2 | 353 | 2 | 06ZOV7 | 06Zov7 oryza sativ | 1060 | 71.5 | 4.2 | 2273 | 2 | 086AJ5 | 086aj5 dictyosteli |
| 988 | 71.5 | 4.2 | 357 | 2 | 08R112 | 08R112 mus musculu | 1061 | 71.5 | 4.2 | 2427 | 2 | 080SU7 | 080su7 mus musculu |
| 989 | 71.5 | 4.2 | 359 | 1 | MECF_ECOS7 | 08aag8 escherichia | 1062 | 71.5 | 4.2 | 2567 | 2 | 09U0J6 | 09u0j6 plasmodium |
| 990 | 71.5 | 4.2 | 359 | 1 | MECF_ECOL6 | 08Dbp2 escherichia | 1063 | 71.5 | 4.2 | 2715 | 1 | MLA_HUMAN | 09um6 homo sapien |
| 991 | 71.5 | 4.2 | 359 | 1 | 06FMP2 | 08fmp2 candida gla | 1064 | 71.5 | 4.2 | 2867 | 2 | 08YEPI | 08yep1 brucella me |
| 992 | 71.5 | 4.2 | 362 | 2 | 022486 | 022486 oryza sativ | 1065 | 71.5 | 4.2 | 3056 | 2 | 06YID8 | 06yid8 bean yellow |
| 993 | 71.5 | 4.2 | 378 | 2 | 06Z012 | 06Z012 caenorhabdi | 1066 | 71.5 | 4.2 | 3075 | 2 | 08AW10 | 08aw10 brachydantio |
| 994 | 71.5 | 4.2 | 379 | 2 | 09XNX6 | 09xnx6 akodon nigr | 1067 | 71.5 | 4.2 | 144 | 2 | 06RC42 | 06rc42 drosophila |
| 995 | 71.5 | 4.2 | 380 | 2 | 066SS6 | 066se6 geocalamus | 1068 | 71.5 | 4.2 | 198 | 2 | 08YZE9 | 08yze9 anabaena sp |
| 996 | 71.5 | 4.2 | 394 | 2 | 0745Y2 | 0745y2 thermus the | 1069 | 71.5 | 4.2 | 200 | 2 | 06DIY3 | 06diy3 xenopus tro |
| 997 | 71.5 | 4.2 | 400 | 2 | 09GZH7 | 09gzh7 caenorhabdi | 1070 | 71.5 | 4.2 | 220 | 2 | 020008 | 020008 caenorhabdi |
| 998 | 71.5 | 4.2 | 412 | 2 | 09P9X9 | 09p9x9 xytella fas | 1071 | 71.5 | 4.2 | 234 | 1 | LUXG_PHOLE | P29237 photobacter |
| 999 | 71.5 | 4.2 | 421 | 1 | 09PLI9 | 041874 zea mays (m | 1072 | 71.5 | 4.2 | 257 | 2 | NDDB_PIG | P01214 sus scrofa |
| 1000 | 71.5 | 4.2 | 424 | 2 | 09PLI9 | 09plh9 chlamydia m | 1073 | 71.5 | 4.2 | 262 | 2 | 09C9Q0 | 09c9q0 arabidopsis |
| 1001 | 71.5 | 4.2 | 428 | 1 | RP4_KULU | P09806 kluyveromyc | 1074 | 71.5 | 4.2 | 291 | 2 | 09JMF0 | 09jmf0 mus musculu |
| 1002 | 71.5 | 4.2 | 453 | 2 | 006671 | 006671 saccharomyc | 1075 | 71.5 | 4.2 | 307 | 2 | 07XYL6 | 07xyl6 chlorarachn |
| 1003 | 71.5 | 4.2 | 457 | 2 | 0644G9 | 0644g9 gyriophyllu | 1076 | 71.5 | 4.2 | 337 | 2 | 024344 | 024344 scorpium bic |
| 1004 | 71.5 | 4.2 | 493 | 2 | 073N78 | 073n78 treponema d | 1077 | 71.5 | 4.2 | 327 | 1 | SIN4_ARATH | Q9stn6 arabidopsis |
| 1005 | 71.5 | 4.2 | 519 | 2 | 08C249 | 08c249 m mus muscu | 1078 | 71.5 | 4.2 | 331 | 1 | RBSR_HABIN | P44329 haemophilus |
| 1006 | 71.5 | 4.2 | 520 | 2 | 08MNJ4 | 08mnj4 dictyosteli | 1079 | 71.5 | 4.2 | 336 | 2 | 06CUP5 | 06cup5 kluyveromyc |
| 1007 | 71.5 | 4.2 | 563 | 2 | 075IM3 | 075im3 ashbya gos | 1080 | 71.5 | 4.2 | 366 | 1 | TORY_ECOS7 | P58361 escherichia |
| 1008 | 71.5 | 4.2 | 567 | 2 | 08XIM6 | 08xim6 clostridium | 1081 | 71.5 | 4.2 | 375 | 2 | 08AXN2 | 08axn2 xenopus lae |
| 1009 | 71.5 | 4.2 | 569 | 2 | 09W250 | 09w250 dirosophila | 1082 | 71.5 | 4.2 | 388 | 2 | 08NEU7 | 08neu7 homo sapien |
| 1010 | 71.5 | 4.2 | 585 | 2 | 08UVV3 | 08uvv3 brachydantio | 1083 | 71.5 | 4.2 | 390 | 2 | 09FZK6 | 09fzk6 mycoplasma |
| 1011 | 71.5 | 4.2 | 590 | 2 | 09FNM8 | 09fnm8 arabidopsis | 1084 | 71.5 | 4.2 | 392 | 2 | Q7N247 | Q7n247 chromobacte |
| 1012 | 71.5 | 4.2 | 598 | 2 | 09LVS1 | 09lvs1 arabidopsis | 1085 | 71.5 | 4.2 | 399 | 2 | 086VH6 | 086vh6 homo sapien |
| 1013 | 71.5 | 4.2 | 601 | 2 | 06RCV3 | 06rcv3 brachydantio | 1086 | 71.5 | 4.2 | 410 | 1 | GNR58 | 09nr58 homo sapien |
| 1014 | 71.5 | 4.2 | 601 | 2 | 07ZML2 | 07zml2 xenopus lae | 1087 | 71.5 | 4.2 | 439 | 2 | GC5B_MOUSE | 092320 mus musculu |
| 1015 | 71.5 | 4.2 | 621 | 2 | 066708 | 066708 aquilex aeo | 1088 | 71.5 | 4.2 | 413 | 2 | 06CLA9 | 06cla9 kluyveromyc |
| 1016 | 71.5 | 4.2 | 632 | 2 | 08AUT3 | 08aut3 brachydantio | 1089 | 71.5 | 4.2 | 420 | 2 | 06ZAU8 | 06zau8 oryza sativ |
| 1017 | 71.5 | 4.2 | 658 | 1 | SYM_ARCFU | 028a13 archaeoglob | 1090 | 71.5 | 4.2 | 441 | 2 | 08D384 | 08d384 wigleswort |
| 1018 | 71.5 | 4.2 | 664 | 2 | 07OX73 | 07ox73 giardia lam | 1091 | 71.5 | 4.2 | 455 | 2 | Q43168 | Q43168 solanum tub |
| 1019 | 71.5 | 4.2 | 672 | 2 | 09RO93 | 09rox73 nicotiana t | 1092 | 71.5 | 4.2 | 464 | 2 | 07VLH5 | 07vlh5 haemophilus |
| 1020 | 71.5 | 4.2 | 679 | 2 | 06FF73 | 06ff73 candida gla | 1093 | 71.5 | 4.2 | 487 | 2 | 08ELI8 | 08eli8 oceanobacil |
| 1021 | 71.5 | 4.2 | 691 | 1 | VPJ3_YEAST | P20795 saccharomyc | 1094 | 71.5 | 4.2 | 491 | 2 | 06CIJ3 | 06cij3 kluyveromyc |
| 1022 | 71.5 | 4.2 | 725 | 2 | 098TA2 | 098ta2 brachydantio | 1095 | 71.5 | 4.2 | 491 | 2 | 08EHY2 | 08ehy2 shewanella |
| 1023 | 71.5 | 4.2 | 726 | 2 | 08AYH1 | 08ayh1 brachydantio | 1096 | 71.5 | 4.2 | 511 | 1 | HUTH_VIBCH | Q8hsg4 vibrio chol |
| 1024 | 71.5 | 4.2 | 735 | 2 | 09YK07 | 09ykc7 dirosophila | 1097 | 71.5 | 4.2 | 511 | 2 | 084AO2 | 084ao2 pseudomonas |
| 1025 | 71.5 | 4.2 | 737 | 2 | 08JZM4 | 08jzm4 mus musculu | 1098 | 71.5 | 4.2 | 538 | 1 | 06EAM3 | 06eam3 mumps virus |
| 1026 | 71.5 | 4.2 | 737 | 2 | 08R4T6 | 08r4t6 mus musculu | 1099 | 71.5 | 4.2 | 566 | 2 | SNPC_YEAST | P53628 saccharomyc |
| 1027 | 71.5 | 4.2 | 745 | 2 | 08VD97 | 08vd97 mus musculu | 1100 | 71.5 | 4.2 | 572 | 2 | 07S3D6 | 07s3d6 neurospora |
| 1028 | 71.5 | 4.2 | 751 | 2 | 09FX37 | 09fx37 arabidopsis | 1101 | 71.5 | 4.2 | 589 | 2 | 08LQG2 | 08lqg2 oryza sativ |
| 1029 | 71.5 | 4.2 | 751 | 2 | 001497 | 001497 caenorhabdi | 1102 | 71.5 | 4.2 | 592 | 2 | 09LWZ0 | 09lwz0 oryza sativ |
| 1030 | 71.5 | 4.2 | 773 | 2 | 09VOR1 | 09vgr1 caenorhabdi | 1103 | 71.5 | 4.2 | 600 | 2 | 08FFU7 | 08ffu7 escherichia |
| 1031 | 71.5 | 4.2 | 796 | 1 | PTPR_RAT | 003348 rattus norv | 1104 | 71.5 | 4.2 | 600 | 2 | 08XCM9 | 08xcw9 escherichia |
| 1032 | 71.5 | 4.2 | 815 | 2 | Q19107 | Q19107 caenorhabdi | 1105 | 71.5 | 4.2 | 600 | 2 | 083Q65 | 083q65 shigella fl |
| 1033 | 71.5 | 4.2 | 822 | 2 | 07QWB9 | 07qwb9 giardia lam | 1106 | 71.5 | 4.2 | 601 | 2 | 08A4F7 | 08a4f7 bacteroides |
| 1034 | 71.5 | 4.2 | 825 | 2 | 06FXE2 | 06fxe2 candida gla | 1107 | 71.5 | 4.2 | 608 | 2 | 0993G8 | 0993g8 callitrichi |
| 1035 | 71.5 | 4.2 | 861 | 2 | 09XWP9 | 09xwf9 caenorhabdi | 1108 | 71.5 | 4.2 | 626 | 2 | 0782R2 | 0782r2 gallid hept |
| 1036 | 71.5 | 4.2 | 874 | 2 | 07SIP9 | 07sip9 chimpanzee | 1109 | 71.5 | 4.2 | 626 | 2 | 09MSY1 | 09msy1 marek's dis |
| 1037 | 71.5 | 4.2 | 908 | 2 | 086T00 | 086t00 dictyosteli | 1110 | 71.5 | 4.2 | 634 | 2 | 07KX02 | 07kx02 caenorhabdi |
| 1038 | 71.5 | 4.2 | 975 | 2 | 08OM30 | 08om30 mus musculu | 1111 | 71.5 | 4.2 | 637 | 2 | 06LR72 | 06lir72 photobacter |
| 1039 | 71.5 | 4.2 | 985 | 2 | 08OW52 | 08ow52 mus musculu | 1112 | 71.5 | 4.2 | 640 | 2 | 08QZM6 | 08qzm6 influenza c |
| 1040 | 71.5 | 4.2 | 1004 | 1 | 06XJG7 | 06xjg7 arabidopsis | 1113 | 71.5 | 4.2 | 640 | 2 | 08QZM7 | 08qzm7 influenza c |
| 1041 | 71.5 | 4.2 | 1056 | 1 | RIC1_YEAST | P40395 saccharomyc | 1114 | 71.5 | 4.2 | 640 | 2 | 08QZM8 | 08qzm8 influenza c |
| 1042 | 71.5 | 4.2 | 1063 | 1 | PDRI_YEAST | P12348 saccharomyc | 1115 | 71.5 | 4.2 | 640 | 2 | 08QZM9 | 08qzm9 influenza c |
| 1043 | 71.5 | 4.2 | 1063 | 2 | 08SRZ7 | 08srz7 encephalito | 1116 | 71.5 | 4.2 | 640 | 2 | 08QZNO | 08qzno influenza c |
| 1044 | 71.5 | 4.2 | 1067 | 2 | 07SHQ9 | 07shq9 neurospora | 1117 | 71.5 | 4.2 | 640 | 2 | 08QZN3 | 08qzn3 influenza c |
| 1045 | 71.5 | 4.2 | 1079 | 2 | 09HH48 | 09he48 neurospora | 1118 | 71.5 | 4.2 | 640 | 2 | 08QZN4 | 08qzn4 influenza c |
| 1046 | 71.5 | 4.2 | 1086 | 2 | 09TYN3 | 09tyn3 caenorhabdi | 1119 | 71.5 | 4.2 | 640 | 2 | 08QZNS | 08qzn5 influenza c |
| 1047 | 71.5 | 4.2 | 1115 | 2 | 08CBC1 | 08cbc1 mus musculu | 1120 | 71.5 | 4.2 | 640 | 2 | 08QZNS | 08qzn5 influenza c |
| 1048 | 71.5 | 4.2 | 1142 | 2 | 0751X9 | 0751x9 ashbya gos | 1121 | 71.5 | 4.2 | 640 | 2 | 08QZNS | 08qzn5 influenza c |
| 1049 | 71.5 | 4.2 | 1256 | 2 | 06LUI92 | 06lui92 photobacter | 1122 | 71.5 | 4.2 | 640 | 2 | 068CF6 | 068cf6 influenza c |
| 1050 | 71.5 | 4.2 | 1315 | 2 | 08CB49 | 08cb49 mus musculu | 1123 | 71.5 | 4.2 | 641 | 1 | HEMA_INCHY | P17003 influenza c |
| 1051 | 71.5 | 4.2 | 1450 | 2 | 08A097 | 08a097 bacteroides | 1124 | 71.5 | 4.2 | 641 | 1 | HEMA_INCKY | P17004 influenza c |
| 1052 | 71.5 | 4.2 | 1508 | 2 | 08OWMO | 08owmo mus musculu | 1125 | 71.5 | 4.2 | 641 | 1 | HEMA_INCNCA | P17005 influenza c |
| 1053 | 71.5 | 4.2 | 1558 | 2 | 06PAI6 | 06pai6 mus musculu | 1126 | 71.5 | 4.2 | 641 | 1 | | |

| | | | | | | | | | | | | | |
|------|------|-----|------|---|-------------|---------------------|------|------|-----|------|---|------------|---------------------|
| 1127 | 71 | 4.2 | 641 | 2 | 08QZP1 | 08qzp1 influenza c | 1200 | 70.5 | 4.2 | 397 | 2 | 06L1N30 | 06l1n30 photobacter |
| 1128 | 71 | 4.2 | 641 | 2 | 08B073 | 08b073 influenza c | 1201 | 70.5 | 4.2 | 411 | 2 | 09A311 | 09a311 caulobacter |
| 1129 | 71 | 4.2 | 641 | 2 | 08B075 | 08b075 influenza c | 1202 | 70.5 | 4.2 | 429 | 1 | THRC_SERVA | P27735 serratia ma |
| 1130 | 71 | 4.2 | 645 | 2 | 091Q68 | 091q68 influenza c | 1203 | 70.5 | 4.2 | 438 | 2 | 090ZM7 | 090zm7 petromyzon |
| 1131 | 71 | 4.2 | 650 | 2 | 091L54 | 091l54 oryza sativ | 1204 | 70.5 | 4.2 | 431 | 2 | 08N6V2 | 08n6v2 homo sapien |
| 1132 | 71 | 4.2 | 662 | 1 | APTX_DRONE | 09mgs8 drosophila | 1205 | 70.5 | 4.2 | 451 | 2 | 09LKG8 | 09lkg8 arabidopsis |
| 1133 | 71 | 4.2 | 665 | 2 | 09N2V0 | 09n2v0 caenorhabdi | 1206 | 70.5 | 4.2 | 452 | 2 | 09YH6 | 09yh6 gallus gall |
| 1134 | 71 | 4.2 | 668 | 2 | 06NRG6 | 06nr96 xenopus lae | 1207 | 70.5 | 4.2 | 458 | 2 | 08H50 | 08h50 dictyosteli |
| 1135 | 71 | 4.2 | 669 | 1 | NAH6_HUMAN | 092581 homo sapien | 1208 | 70.5 | 4.2 | 460 | 2 | 094SE6 | 094ae6 maacacamel |
| 1136 | 71 | 4.2 | 669 | 2 | 093ZA2 | 093za2 arabidopsis | 1209 | 70.5 | 4.2 | 464 | 2 | 09W212 | 09w212 drosophila |
| 1137 | 71 | 4.2 | 683 | 2 | 07XKL3 | 07xkl3 oryza sativ | 1210 | 70.5 | 4.2 | 469 | 1 | THG2_MALZE | 041808 zea mays (m |
| 1138 | 71 | 4.2 | 701 | 2 | 086V50 | 086v50 homo sapien | 1211 | 70.5 | 4.2 | 472 | 1 | ET2B_XENLA | 092710 xenopus lae |
| 1139 | 71 | 4.2 | 715 | 2 | 07NOY6 | 07noy6 photorhabdu | 1212 | 70.5 | 4.2 | 472 | 1 | 08GZT0 | 08gzt0 lupinus alb |
| 1140 | 71 | 4.2 | 721 | 2 | 087M06 | 087m06 vibrio para | 1213 | 70.5 | 4.2 | 472 | 1 | 06DE76 | 06de76 xenopus lae |
| 1141 | 71 | 4.2 | 728 | 1 | ANCC2_CAEEL | P34514 caenorhabdi | 1214 | 70.5 | 4.2 | 474 | 1 | TBG2_ARATH | P38558 arabidopsis |
| 1142 | 71 | 4.2 | 731 | 2 | 07ZXU8 | 07zxu8 xenopus lae | 1215 | 70.5 | 4.2 | 475 | 2 | 07XJCL | 07xjcl haplontiriu |
| 1143 | 71 | 4.2 | 735 | 2 | 09VP12 | 09vp12 drosophila | 1216 | 70.5 | 4.2 | 479 | 2 | 08CTE4 | 08cte4 staphylococ |
| 1144 | 71 | 4.2 | 749 | 2 | 09NC88 | 09nc88 strongyloce | 1217 | 70.5 | 4.2 | 496 | 2 | 09Z790 | 09z790 chlamydia p |
| 1145 | 71 | 4.2 | 751 | 1 | PHYB_ANASP | 09f6x3 anabaena sp | 1218 | 70.5 | 4.2 | 517 | 2 | 09CFN1 | 09cfn1 lactococcus |
| 1146 | 71 | 4.2 | 765 | 1 | METE_LISMO | 08f6k3 listeria mo | 1219 | 70.5 | 4.2 | 540 | 2 | 07TIM6 | 07tim6 silurus mer |
| 1147 | 71 | 4.2 | 774 | 2 | 08RP17 | 08rp17 pseudomonas | 1220 | 70.5 | 4.2 | 547 | 2 | 09LIR9 | 09lir9 artemiaia a |
| 1148 | 71 | 4.2 | 776 | 2 | 09C8H3 | 09c8h3 arabidopsis | 1221 | 70.5 | 4.2 | 547 | 2 | 09ST45 | 09st45 artemiaia a |
| 1149 | 71 | 4.2 | 784 | 2 | 07U6Y4 | 07u6y4 synecococc | 1222 | 70.5 | 4.2 | 557 | 2 | 07R3Y2 | 07r3y2 giardia lam |
| 1150 | 71 | 4.2 | 794 | 2 | 09V5N6 | 09v5n6 drosophila | 1223 | 70.5 | 4.2 | 592 | 2 | 0834P9 | 0834p9 enterococcu |
| 1151 | 71 | 4.2 | 794 | 2 | 09FL59 | 09fl59 arabidopsis | 1224 | 70.5 | 4.2 | 601 | 2 | 068975 | 068975 yersinia en |
| 1152 | 71 | 4.2 | 826 | 2 | 06C381 | 06c381 yarrowia li | 1225 | 70.5 | 4.2 | 605 | 1 | ALS_HUMAN | P33858 homo sapien |
| 1153 | 71 | 4.2 | 836 | 1 | POSN_HUMAN | 015063 homo sapien | 1226 | 70.5 | 4.2 | 605 | 2 | 08TAY0 | 08tay0 homo sapien |
| 1154 | 71 | 4.2 | 849 | 2 | 043393 | 043393 brassica na | 1227 | 70.5 | 4.2 | 623 | 2 | 061S16 | 061s16 homo sapien |
| 1155 | 71 | 4.2 | 850 | 2 | 06MZW3 | 06mzw3 homo sapien | 1228 | 70.5 | 4.2 | 626 | 2 | 07PNH3 | 07pnh3 anopheles g |
| 1156 | 71 | 4.2 | 891 | 1 | LHN2_MOUSE | 08j2z7 mus musculu | 1229 | 70.5 | 4.2 | 628 | 2 | 06MHW0 | 06mhw0 bdeliovibri |
| 1157 | 71 | 4.2 | 943 | 2 | 07ABN8 | 07abn8 escherichia | 1230 | 70.5 | 4.2 | 630 | 2 | 095Y88 | 095y88 caenorhabdi |
| 1158 | 71 | 4.2 | 944 | 2 | 06DCL5 | 06dcl5 xenopus lae | 1231 | 70.5 | 4.2 | 634 | 2 | 074879 | 074879 schizosacch |
| 1159 | 71 | 4.2 | 951 | 2 | 09HTC4 | 09htc4 pseudomonas | 1232 | 70.5 | 4.2 | 662 | 2 | 08YML4 | 08ym14 anabaena sp |
| 1160 | 71 | 4.2 | 952 | 2 | 08XC73 | 08xc73 escherichia | 1233 | 70.5 | 4.2 | 665 | 1 | RNR2_LACIA | 002146 lactococcus |
| 1161 | 71 | 4.2 | 963 | 2 | 08V9U2 | 08v9u2 african swi | 1234 | 70.5 | 4.2 | 680 | 1 | KALM_HUMAN | P23352 homo sapien |
| 1162 | 71 | 4.2 | 967 | 2 | 06SYZ9 | 06syz9 streptococc | 1235 | 70.5 | 4.2 | 697 | 2 | 09LUI6 | 09lui6 arabidopsis |
| 1163 | 71 | 4.2 | 980 | 2 | 07QOV6 | 07qov6 giardia lam | 1236 | 70.5 | 4.2 | 708 | 2 | 06P913 | 06p913 xenopus lae |
| 1164 | 71 | 4.2 | 1024 | 2 | 08A2X6 | 08a2x6 bacteroides | 1237 | 70.5 | 4.2 | 712 | 2 | 06P4W3 | 06p4w3 xenopus tro |
| 1165 | 71 | 4.2 | 1093 | 2 | 06MF79 | 06mf79 paracitlamyd | 1238 | 70.5 | 4.2 | 717 | 2 | 0043Z5 | 088967 mus musculu |
| 1166 | 71 | 4.2 | 1180 | 2 | 0751H7 | 0751h7 ashyba goss | 1239 | 70.5 | 4.2 | 735 | 2 | 051543 | 051543 borrelia bu |
| 1167 | 71 | 4.2 | 1219 | 2 | 07G7H3 | 07g7h3 oryza sativ | 1240 | 70.5 | 4.2 | 770 | 2 | 072J77 | 072j77 thermus che |
| 1168 | 71 | 4.2 | 1219 | 2 | 09AY59 | 09ay59 oryza sativ | 1241 | 70.5 | 4.2 | 786 | 2 | 06CC33 | 06cc33 yarrowia li |
| 1169 | 71 | 4.2 | 1219 | 2 | 09T087 | 09t0b7 arabidopsis | 1242 | 70.5 | 4.2 | 801 | 2 | 07XKVO | 07xkv0 oryza sativ |
| 1170 | 71 | 4.2 | 1453 | 2 | 094KV0 | 094kv0 arabidopsis | 1244 | 70.5 | 4.2 | 816 | 2 | 06FV19 | 06fv19 candida gla |
| 1171 | 71 | 4.2 | 1453 | 2 | 09C6F9 | 09c6f9 arabidopsis | 1245 | 70.5 | 4.2 | 855 | 2 | 086Y56 | 086y56 homo sapien |
| 1172 | 71 | 4.2 | 1485 | 2 | 080TZ5 | 080tz5 mus musculu | 1246 | 70.5 | 4.2 | 877 | 2 | 08K297 | 08k297 oryza sativ |
| 1173 | 71 | 4.2 | 1504 | 2 | 09LKT4 | 09lkt4 arabidopsis | 1247 | 70.5 | 4.2 | 893 | 2 | 053121 | 053121 mycobacteri |
| 1174 | 71 | 4.2 | 1535 | 2 | 07RK11 | 07rk11 plasmodium | 1248 | 70.5 | 4.2 | 901 | 2 | 09LRA3 | 09lra3 arabidopsis |
| 1175 | 71 | 4.2 | 2109 | 2 | 08B0H0 | 08b0h0 vesicular s | 1249 | 70.5 | 4.2 | 905 | 2 | 08T655 | 08t655 dirofilaria |
| 1176 | 71 | 4.2 | 2169 | 2 | 07R3M1 | 07r3m1 giardia lam | 1250 | 70.5 | 4.2 | 911 | 2 | 068KP9 | 068kp9 xenopus lae |
| 1177 | 71 | 4.2 | 2842 | 1 | APC_RAT | P70478 rattus norv | 1251 | 70.5 | 4.2 | 914 | 2 | 06N3P3 | 06n3p3 rhodospheuo |
| 1178 | 71 | 4.2 | 3122 | 2 | 066237 | 066237 citrus tris | 1252 | 70.5 | 4.2 | 935 | 2 | 0750Y5 | 0750y5 ashyba goss |
| 1179 | 71 | 4.2 | 3124 | 2 | 066237 | 066237 citrus tris | 1253 | 70.5 | 4.2 | 937 | 2 | 08CDG6 | 08cdg6 mus musculu |
| 1180 | 71 | 4.2 | 3403 | 2 | 07T5A6 | 07t5a6 onion, yello | 1254 | 70.5 | 4.2 | 937 | 2 | 09D5Y1 | 09d5y1 mus musculu |
| 1181 | 71 | 4.2 | 4717 | 2 | 0942A8 | 0942a8 schizosacch | 1255 | 70.5 | 4.2 | 944 | 1 | VP35_YEAST | P34510 saccharomyc |
| 1182 | 71 | 4.2 | 4717 | 2 | 092AK5 | 092ars listeria in | 1256 | 70.5 | 4.2 | 991 | 2 | 0941FA | 0941fa arabidopsis |
| 1183 | 70.5 | 4.2 | 1552 | 2 | 092AK5 | 092ars listeria in | 1257 | 70.5 | 4.2 | 995 | 2 | 092VW2 | 092vw2 arabidopsis |
| 1184 | 70.5 | 4.2 | 186 | 2 | 06QRLH | 06qrh8 eurycea tyn | 1258 | 70.5 | 4.2 | 1009 | 2 | 09M295 | 09m295 arabidopsis |
| 1185 | 70.5 | 4.2 | 232 | 2 | 06QRLH | 06qrh8 eurycea tyn | 1259 | 70.5 | 4.2 | 1031 | 2 | 08OU53 | 08ou53 mus musculu |
| 1186 | 70.5 | 4.2 | 241 | 2 | 08SFK2 | 08sfk2 oryzaomya pa | 1260 | 70.5 | 4.2 | 1035 | 2 | 06Y7W7 | 06y7w7 homo sapien |
| 1187 | 70.5 | 4.2 | 242 | 2 | 09Y1P9 | 09y1p9 pseudopois | 1261 | 70.5 | 4.2 | 1061 | 2 | 07T1B4 | 07t1b4 xenopus lae |
| 1188 | 70.5 | 4.2 | 246 | 2 | 089ZC2 | 089zc2 bacteroides | 1262 | 70.5 | 4.2 | 1061 | 2 | 064018 | 064018 xenopus lae |
| 1189 | 70.5 | 4.2 | 251 | 2 | 064XB3 | 064xb3 bacteroides | 1263 | 70.5 | 4.2 | 1066 | 2 | 018887 | 018887 sus scrofa |
| 1190 | 70.5 | 4.2 | 276 | 2 | 081EN6 | 081en6 bacillus ce | 1264 | 70.5 | 4.2 | 1123 | 2 | 08ZMB4 | 08zmb4 salmoneila |
| 1191 | 70.5 | 4.2 | 284 | 2 | 090Y00 | 090y00 petromyzon | 1265 | 70.5 | 4.2 | 1132 | 2 | 08ZPFG | 08zpf5 arabidopsis |
| 1192 | 70.5 | 4.2 | 288 | 2 | 08EBL1 | 08eb11 shewanella | 1266 | 70.5 | 4.2 | 1136 | 1 | CABA_BACTI | P05519 bacillus th |
| 1193 | 70.5 | 4.2 | 308 | 2 | 06LS59 | 06ls59 photobacter | 1267 | 70.5 | 4.2 | 1142 | 1 | GIGI_CHICK | 002391 gallus galli |
| 1194 | 70.5 | 4.2 | 334 | 2 | 017053 | 017053 caenorhabdi | 1267 | 70.5 | 4.2 | 1147 | 2 | 07Q6T2 | 07q6t2 anopheles g |
| 1195 | 70.5 | 4.2 | 351 | 2 | 07SEB3 | 07seb3 neurospora | 1268 | 70.5 | 4.2 | 1180 | 2 | CAAA_BACTI | P16480 bacillus th |
| 1196 | 70.5 | 4.2 | 370 | 2 | 08EB52 | 08eb52 shewanella | 1269 | 70.5 | 4.2 | 1180 | 1 | 06PBA3 | 06pb43 mus musculu |
| 1197 | 70.5 | 4.2 | 391 | 2 | 09FNNO | 09fnno arabidopsis | 1270 | 70.5 | 4.2 | 1193 | 1 | SPA5_HUMAN | 099r06 homo sapien |
| 1198 | 70.5 | 4.2 | 392 | 2 | 09N2S1 | 09n2s1 caenorhabdi | 1271 | 70.5 | 4.2 | 1279 | 2 | 026046 | 026046 helicobacte |
| 1199 | 70.5 | 4.2 | 395 | 2 | P91419 | P91419 caenorhabdi | 1272 | 70.5 | 4.2 | | | | |

| | | | | | | | | | | | | | | | |
|------|------|-----|------|---|-------------|---------|--------------|------|----|-----|------|---|------------|------------|--------------|
| 1273 | 70.5 | 4.2 | 1356 | 2 | O9G090 | O9G090 | dirofilaria | 1346 | 70 | 4.1 | 538 | 2 | O9DOA2 | O9dga2 | mumps virus |
| 1274 | 70.5 | 4.2 | 1370 | 1 | Z2S1 MOUSE | O9Jtm4 | mus musculus | 1347 | 70 | 4.1 | 538 | 2 | O9JAB4 | O9jae4 | mumps virus |
| 1275 | 70.5 | 4.2 | 1529 | 2 | O6TVX5 | O6TVX5 | oryza sativ | 1348 | 70 | 4.1 | 532 | 2 | O9JAB4 | O9jae4 | mumps virus |
| 1276 | 70.5 | 4.2 | 1553 | 2 | O96452 | O96452 | nosema locu | 1349 | 70 | 4.1 | 557 | 2 | O8RZ75 | O8RZ75 | cutubid ye |
| 1277 | 70.5 | 4.2 | 1770 | 2 | O07791 | O07791 | saccharomyc | 1350 | 70 | 4.1 | 557 | 2 | O8RZ75 | O8RZ75 | cutubid ye |
| 1278 | 70.5 | 4.2 | 1805 | 1 | HMW2 MYCGR | P47460 | mycoplasma | 1351 | 70 | 4.1 | 569 | 2 | O21837 | O21837 | caenorhabdi |
| 1279 | 70.5 | 4.2 | 1878 | 2 | O9SVJ7 | O9SVJ7 | arabidopsis | 1352 | 70 | 4.1 | 575 | 2 | O9H6R5 | O9h6r5 | homo sapien |
| 1280 | 70.5 | 4.2 | 1942 | 2 | O23450 | O23450 | arabidopsis | 1353 | 70 | 4.1 | 575 | 2 | O67MU2 | O67mu2 | symbiobacte |
| 1281 | 70.5 | 4.2 | 2233 | 2 | O94711 | O94711 | paramecium | 1354 | 70 | 4.1 | 578 | 1 | CTDD SCHRO | O9tcl9 | xenopus lae |
| 1282 | 70.5 | 4.2 | 2238 | 1 | G0A4 MOUSE | O91WV5 | mus musculus | 1355 | 70 | 4.1 | 585 | 2 | O9M255 | O9tcl9 | schizosacch |
| 1283 | 70.5 | 4.2 | 2443 | 1 | O96J17 | O96J17 | homo sapien | 1356 | 70 | 4.1 | 608 | 2 | O9M256 | O9m256 | arabidopsis |
| 1284 | 70.5 | 4.2 | 2603 | 1 | O869W9 | O869W9 | dictyostell | 1357 | 70 | 4.1 | 609 | 2 | O82670 | O9m256 | arabidopsis |
| 1285 | 70.5 | 4.2 | 2843 | 1 | APC HUMAN | P25054 | homo sapien | 1358 | 70 | 4.1 | 609 | 2 | O82671 | O82671 | influenza c |
| 1286 | 70.5 | 4.2 | 3329 | 1 | BRC2 MOUSE | P97929 | mus musculus | 1359 | 70 | 4.1 | 609 | 2 | O82675 | O82675 | influenza c |
| 1287 | 70.5 | 4.2 | 3329 | 1 | O8VHDO | O8vhd0 | mus musculus | 1360 | 70 | 4.1 | 619 | 2 | O754R0 | O82675 | influenza c |
| 1288 | 70.5 | 4.2 | 3868 | 2 | O9W090 | O9w090 | dirosophila | 1361 | 70 | 4.1 | 625 | 2 | O75319 | O754R0 | goss |
| 1289 | 70.5 | 4.2 | 3966 | 2 | O7KVA7 | O7Kva7 | dirosophila | 1362 | 70 | 4.1 | 633 | 2 | O9V6C5 | O75319 | neurospora |
| 1290 | 70.5 | 4.2 | 5120 | 1 | PCLO CHICK | O9u367 | gallus gall | 1363 | 70 | 4.1 | 633 | 2 | O9CN49 | O9V6C5 | dirosophila |
| 1291 | 70.5 | 4.2 | 8407 | 2 | O7RTM4 | O7rtm4 | homo sapien | 1364 | 70 | 4.1 | 640 | 2 | O8QZN2 | O9CN49 | pasteurella |
| 1292 | 70 | 4.1 | 138 | 2 | O91DB3 | O91db3 | oryza sativ | 1365 | 70 | 4.1 | 640 | 2 | O9Q206 | O8QZN2 | influenza c |
| 1293 | 70 | 4.1 | 144 | 2 | O6RC43 | O6rc43 | dirosophila | 1366 | 70 | 4.1 | 642 | 1 | HEMA INCYA | O9Q206 | influenza c |
| 1294 | 70 | 4.1 | 191 | 2 | O6ECM3 | O6ecm3 | yersinia ps | 1367 | 70 | 4.1 | 656 | 2 | O7R3F3 | HEMA INCYA | influenza c |
| 1295 | 70 | 4.1 | 191 | 2 | O8ZGE7 | O8zge7 | yersinia pe | 1368 | 70 | 4.1 | 665 | 1 | Y176 METTH | O7R3F3 | glardia lam |
| 1296 | 70 | 4.1 | 200 | 2 | O81308 | O81308 | arabidopsis | 1369 | 70 | 4.1 | 718 | 2 | O9B107 | Y176 METTH | methanobact |
| 1297 | 70 | 4.1 | 243 | 2 | O9SNT0 | O9snt0 | vitlis vinif | 1370 | 70 | 4.1 | 727 | 2 | O9TOB4 | O9B107 | entamoeba h |
| 1298 | 70 | 4.1 | 244 | 2 | O9SM95 | O9sm95 | oryza sativ | 1371 | 70 | 4.1 | 737 | 2 | O7PNF5 | O9TOB4 | arabidopsis |
| 1299 | 70 | 4.1 | 247 | 2 | O9HT53 | O9ht53 | pseudomonas | 1372 | 70 | 4.1 | 739 | 2 | O88CU2 | O7PNF5 | anopheles g |
| 1300 | 70 | 4.1 | 254 | 2 | O9M6K4 | O9mek4 | oryza sativ | 1373 | 70 | 4.1 | 767 | 2 | O8Q824 | O88CU2 | pseudomonas |
| 1301 | 70 | 4.1 | 256 | 2 | O9PMW7 | O9pmw7 | campylobact | 1374 | 70 | 4.1 | 770 | 2 | O22968 | O8Q824 | ponginge her |
| 1302 | 70 | 4.1 | 260 | 2 | O8DVQ5 | O8dvq5 | streptococc | 1375 | 70 | 4.1 | 772 | 2 | O6T286 | O22968 | arabidopsis |
| 1303 | 70 | 4.1 | 265 | 1 | O9C2G8 | O9c2g8 | neutropora | 1376 | 70 | 4.1 | 835 | 1 | RP13 ARATH | O6T286 | populus alb |
| 1304 | 70 | 4.1 | 269 | 1 | YH74 YEAST | P18838 | saccharomyc | 1377 | 70 | 4.1 | 840 | 2 | O9VZF2 | RP13 ARATH | arabidopsis |
| 1305 | 70 | 4.1 | 271 | 2 | O9SUT9 | O9sut9 | arabidopsis | 1378 | 70 | 4.1 | 887 | 2 | O6FOF0 | O9VZF2 | dirosophila |
| 1306 | 70 | 4.1 | 271 | 2 | O7VYK5 | O7vyk5 | bordetella | 1379 | 70 | 4.1 | 888 | 1 | EBL1 ARATH | O6FOF0 | candida gla |
| 1307 | 70 | 4.1 | 271 | 2 | O7W110 | O7w110 | bordetella | 1380 | 70 | 4.1 | 909 | 2 | O8BK12 | EBL1 ARATH | arabidopsis |
| 1308 | 70 | 4.1 | 275 | 2 | O9KTC3 | O9krc3 | vibrio chol | 1381 | 70 | 4.1 | 938 | 2 | O9N4C5 | O8BK12 | mus musculu |
| 1309 | 70 | 4.1 | 279 | 2 | O7Z242 | O7z242 | brachydanio | 1382 | 70 | 4.1 | 962 | 1 | SURR DROME | O9N4C5 | caenorhabdi |
| 1310 | 70 | 4.1 | 280 | 2 | O9YCP1 | O9ycp1 | aeropyrum p | 1383 | 70 | 4.1 | 964 | 2 | O72DIF8 | SURR DROME | desulfovibr |
| 1311 | 70 | 4.1 | 293 | 2 | O6G6Z2 | O6g6z2 | staphylococc | 1384 | 70 | 4.1 | 971 | 2 | O6GMW9 | O72DIF8 | mus musculu |
| 1312 | 70 | 4.1 | 308 | 2 | O8CU92 | O8cu92 | staphylococc | 1385 | 70 | 4.1 | 978 | 2 | O6ZU14 | O6GMW9 | xenopus lae |
| 1313 | 70 | 4.1 | 309 | 2 | O7UMX8 | O7umx8 | rhodospirell | 1386 | 70 | 4.1 | 1012 | 2 | O6ZU21 | O6ZU14 | homo sapien |
| 1314 | 70 | 4.1 | 321 | 2 | O6UR64 | O6ur64 | yersinia fir | 1387 | 70 | 4.1 | 1017 | 2 | O8T391 | O6ZU21 | homo sapien |
| 1315 | 70 | 4.1 | 326 | 2 | O8V707 | O8v707 | bovine rola | 1388 | 70 | 4.1 | 1029 | 2 | O9C099 | O8T391 | dirosophila |
| 1316 | 70 | 4.1 | 326 | 2 | O9QTF9 | O9qtf9 | human rotav | 1389 | 70 | 4.1 | 1037 | 2 | O6GL13 | O9C099 | homo sapien |
| 1317 | 70 | 4.1 | 328 | 2 | O8VYU6 | O8vyu6 | thermococc | 1390 | 70 | 4.1 | 1081 | 2 | O7RFQ7 | O6GL13 | xenopus tro |
| 1318 | 70 | 4.1 | 328 | 2 | O9WYU0 | O9wyu0 | thermocoga | 1391 | 70 | 4.1 | 1083 | 2 | O68FNT1 | O7RFQ7 | plasmodium |
| 1319 | 70 | 4.1 | 335 | 2 | O6BK54 | O6bk54 | debaromyce | 1392 | 70 | 4.1 | 1085 | 1 | S124 RAT | O68FNT1 | mus musculu |
| 1320 | 70 | 4.1 | 352 | 1 | HRCA COREF | O6b3f4 | corynebacte | 1393 | 70 | 4.1 | 1143 | 2 | O6MF84 | S124 RAT | rattus norv |
| 1321 | 70 | 4.1 | 359 | 2 | O7J3U3 | O7j3u3 | bacillus ce | 1394 | 70 | 4.1 | 1178 | 2 | O55693 | O6MF84 | parachlamyd |
| 1322 | 70 | 4.1 | 366 | 2 | O7UAC2 | O7uac2 | shigella fl | 1395 | 70 | 4.1 | 1207 | 1 | GAP2 CAEBL | O55693 | synchocyst |
| 1323 | 70 | 4.1 | 367 | 2 | O6IX33 | O6ix33 | hypholoma f | 1396 | 70 | 4.1 | 1222 | 2 | O8K048 | GAP2 CAEBL | caenorhabdi |
| 1324 | 70 | 4.1 | 373 | 2 | O87DW8 | O87dw8 | xyella fas | 1397 | 70 | 4.1 | 1248 | 2 | O8CH96 | O8K048 | mus musculu |
| 1325 | 70 | 4.1 | 373 | 2 | O9PDR6 | O9pdr6 | xyella fas | 1398 | 70 | 4.1 | 1249 | 2 | O8BS54 | O8CH96 | mus musculu |
| 1326 | 70 | 4.1 | 383 | 2 | O6FX16 | O6fx16 | candida gla | 1399 | 70 | 4.1 | 1252 | 2 | O75WU7 | O8BS54 | mus musculu |
| 1327 | 70 | 4.1 | 389 | 2 | O6CK37 | O6ck37 | kluyveromyc | 1400 | 70 | 4.1 | 1322 | 1 | O81490 | O75WU7 | mus musculu |
| 1328 | 70 | 4.1 | 391 | 2 | O6BFP7 | O6bfp7 | paramecium | 1401 | 70 | 4.1 | 1358 | 1 | S1R4 YEAST | O81490 | arabidopsis |
| 1329 | 70 | 4.1 | 397 | 2 | O7URL9 | O7url9 | rhodospirell | 1402 | 70 | 4.1 | 1409 | 1 | COP1 DROME | S1R4 YEAST | caenorhabdi |
| 1330 | 70 | 4.1 | 401 | 2 | O7RBS52 | O7rbs52 | plasmodium | 1403 | 70 | 4.1 | 1409 | 2 | O084E1 | COP1 DROME | dirosophila |
| 1331 | 70 | 4.1 | 411 | 2 | O2J351 | O2j351 | caenorhabdi | 1404 | 70 | 4.1 | 1482 | 2 | O8GSC4 | O084E1 | schizosacch |
| 1332 | 70 | 4.1 | 425 | 2 | O8ILOAS | O8ilas | oryza sativ | 1405 | 70 | 4.1 | 1557 | 2 | O6P405 | O8GSC4 | nicotiana t |
| 1333 | 70 | 4.1 | 449 | 1 | GAD RAT | P18506 | rattus norv | 1406 | 70 | 4.1 | 1748 | 1 | YNR2 YEAST | O6P405 | brachydanio |
| 1334 | 70 | 4.1 | 462 | 1 | TBGI HUMPCR | P54403 | euploes cr | 1407 | 70 | 4.1 | 1963 | 2 | O20641 | YNR2 YEAST | saccharomyc |
| 1335 | 70 | 4.1 | 468 | 1 | COO6 EUPCR | O9Y229 | homo sapien | 1408 | 70 | 4.1 | 1966 | 2 | O9SZW8 | O20641 | caenorhabdi |
| 1336 | 70 | 4.1 | 468 | 1 | O7TULZ5 | O7tul5 | rhodospirell | 1409 | 70 | 4.1 | 2052 | 1 | MY10 BOVIN | O9SZW8 | arabidopsis |
| 1337 | 70 | 4.1 | 472 | 2 | O9BKU0 | O9bku0 | caenorhabdi | 1410 | 70 | 4.1 | 2052 | 1 | UBR2 SCHPO | MY10 BOVIN | homo sapien |
| 1338 | 70 | 4.1 | 478 | 2 | O7RFZ2 | O7rfz2 | plasmodium | 1411 | 70 | 4.1 | 2196 | 1 | MOR2 SCHPO | UBR2 SCHPO | schizosacch |
| 1339 | 70 | 4.1 | 485 | 2 | O8ETD4 | O8etd4 | homo sapien | 1412 | 70 | 4.1 | 2493 | 1 | YBA4 YEAST | MOR2 SCHPO | schizosacch |
| 1340 | 70 | 4.1 | 486 | 2 | O82044 | O82044 | human rotav | 1413 | 70 | 4.1 | 2531 | 1 | NTCI MOUSE | YBA4 YEAST | saccharomyc |
| 1341 | 70 | 4.1 | 486 | 2 | O84939 | O84939 | porcine rot | 1414 | 70 | 4.1 | 2829 | 2 | O6IVD6 | NTCI MOUSE | mus musculu |
| 1342 | 70 | 4.1 | 486 | 2 | O9GNM9 | O9gna9 | human rotav | 1415 | 70 | 4.1 | 4007 | 1 | FRS1 HUMAN | O6IVD6 | strongyloce |
| 1343 | 70 | 4.1 | 507 | 2 | O9N3F2 | O9n3f2 | caenorhabdi | 1416 | 70 | 4.1 | 121 | 2 | O9FMN5 | FRS1 HUMAN | homo sapien |
| 1344 | 70 | 4.1 | 521 | 2 | O6S257 | O6s257 | arabidopsis | 1417 | 70 | 4.1 | 152 | 2 | O8Y6E4 | O9FMN5 | oryza sativ |
| 1345 | 70 | 4.1 | 530 | 2 | O6E2D8 | O6e2d8 | solanum dem | 1418 | 70 | 4.1 | 152 | 2 | O7IYB5 | O8Y6E4 | listeria mo |

| | | | | | | |
|------|------|-----|-----|---|------------|---------------------|
| 1419 | 69.5 | 4.1 | 170 | 2 | Q7WXA4 | Q7WXA4 alcaligenes |
| 1420 | 69.5 | 4.1 | 181 | 2 | Q3APN6 | Q9apn6 pseudalter |
| 1421 | 69.5 | 4.1 | 186 | 2 | Q7OMA2 | Q7oma2 anopheles g |
| 1422 | 69.5 | 4.1 | 191 | 1 | WAP_MACEU | Q9u018 macropus eu |
| 1423 | 69.5 | 4.1 | 209 | 2 | Q64873 | Q64873 arabidopsis |
| 1424 | 69.5 | 4.1 | 232 | 2 | Q6GQ65 | Q6gq65 eurycea spe |
| 1425 | 69.5 | 4.1 | 232 | 2 | Q6GQ65 | Q6gq65 eurycea tyn |
| 1426 | 69.5 | 4.1 | 232 | 2 | Q6GQ65 | Q6gq65 eurycea tyn |
| 1427 | 69.5 | 4.1 | 232 | 2 | Q6GQ65 | Q6gq65 eurycea tyn |
| 1428 | 69.5 | 4.1 | 232 | 2 | Q6GQ65 | Q6gq65 eurycea tyn |
| 1429 | 69.5 | 4.1 | 232 | 2 | Q6GQ65 | Q6gq65 eurycea tyn |
| 1430 | 69.5 | 4.1 | 232 | 2 | Q6GQ65 | Q6gq65 eurycea tyn |
| 1431 | 69.5 | 4.1 | 232 | 2 | Q6GQ65 | Q6gq65 eurycea tyn |
| 1432 | 69.5 | 4.1 | 232 | 2 | Q6GQ65 | Q6gq65 eurycea tyn |
| 1433 | 69.5 | 4.1 | 232 | 2 | Q6GQ65 | Q6gq65 eurycea tyn |
| 1434 | 69.5 | 4.1 | 232 | 2 | Q6GQ65 | Q6gq65 eurycea tyn |
| 1435 | 69.5 | 4.1 | 250 | 2 | Q9W0D2 | Q9w0d2 drosophila |
| 1436 | 69.5 | 4.1 | 253 | 2 | Q9D8H2 | Q9d8h2 m mus muscu |
| 1437 | 69.5 | 4.1 | 257 | 2 | Q9D8H2 | Q9d8h2 m mus muscu |
| 1438 | 69.5 | 4.1 | 261 | 2 | Q9D7L8 | Q9d7l8 m mus muscu |
| 1439 | 69.5 | 4.1 | 272 | 2 | Q7Q5A5 | Q7q5a5 anopheles g |
| 1440 | 69.5 | 4.1 | 272 | 2 | Q9XEN6 | Q9xen6 triticeum ae |
| 1441 | 69.5 | 4.1 | 294 | 2 | Q98QW9 | Q98qw9 mycoplasma |
| 1442 | 69.5 | 4.1 | 301 | 2 | Q3G621 | Q3g621 salmoneilla |
| 1443 | 69.5 | 4.1 | 309 | 2 | Q49746 | Q49746 arabidopsis |
| 1444 | 69.5 | 4.1 | 309 | 2 | Q9SSR0 | Q9ssr0 arabidopsis |
| 1445 | 69.5 | 4.1 | 316 | 1 | D57_ARATH | Q9ar16 arabidopsis |
| 1446 | 69.5 | 4.1 | 326 | 2 | Q87S03 | Q87s03 vibrio para |
| 1447 | 69.5 | 4.1 | 353 | 2 | Q01562 | Q01562 caenorhabdi |
| 1448 | 69.5 | 4.1 | 356 | 2 | Q19267 | Q19267 caenorhabdi |
| 1449 | 69.5 | 4.1 | 357 | 2 | Q7P740 | Q7p740 fusobacteri |
| 1450 | 69.5 | 4.1 | 357 | 2 | Q8BUP3 | Q8bup3 mus musculi |
| 1451 | 69.5 | 4.1 | 358 | 1 | Y701_CHLPR | Q927k4 chlamydia p |
| 1452 | 69.5 | 4.1 | 359 | 2 | Q7V628 | Q7vg28 helicobacte |
| 1453 | 69.5 | 4.1 | 362 | 2 | Q9LTC3 | Q9lct3 arabidopsis |
| 1454 | 69.5 | 4.1 | 377 | 2 | Q8BMT0 | Q8bmt0 mus musculi |
| 1455 | 69.5 | 4.1 | 380 | 2 | Q35970 | Q35970 thomabony |
| 1456 | 69.5 | 4.1 | 380 | 2 | Q9XNW3 | Q9xnw3 rhipidomy |
| 1457 | 69.5 | 4.1 | 381 | 2 | Q8W7D5 | Q8w7d5 calomys cal |
| 1458 | 69.5 | 4.1 | 399 | 2 | Q8B6V2 | Q8b6v2 mus musculi |
| 1459 | 69.5 | 4.1 | 400 | 2 | Q9D5T8 | Q9d5t8 mus musculi |
| 1460 | 69.5 | 4.1 | 409 | 2 | Q7UHB8 | Q7uhb8 rhodospirell |
| 1461 | 69.5 | 4.1 | 419 | 2 | Q21563 | Q21563 caenorhabdi |
| 1462 | 69.5 | 4.1 | 419 | 2 | Q9NA38 | Q9na38 caenorhabdi |
| 1463 | 69.5 | 4.1 | 420 | 2 | Q9NA61 | Q9na61 caenorhabdi |
| 1464 | 69.5 | 4.1 | 432 | 2 | Q7N824 | Q7n824 photorhabdu |
| 1465 | 69.5 | 4.1 | 452 | 2 | Q8V5A8 | Q8v5a8 caephallia e |
| 1466 | 69.5 | 4.1 | 456 | 2 | Q7RSB7 | Q7rsb7 plasmodium |
| 1467 | 69.5 | 4.1 | 456 | 2 | Q8R0R0 | Q8r0r0 mus musculi |
| 1468 | 69.5 | 4.1 | 460 | 2 | Q9B9U6 | Q9b9u6 aulopus jap |
| 1469 | 69.5 | 4.1 | 461 | 2 | Q9EXY2 | Q9exy2 escherichia |
| 1470 | 69.5 | 4.1 | 472 | 2 | Q95WM2 | Q95wm2 papilio can |
| 1471 | 69.5 | 4.1 | 473 | 2 | Q8NKT4 | Q8nkt4 acidianus s |
| 1472 | 69.5 | 4.1 | 476 | 2 | Q8XT06 | Q8xt06 ralsionia s |
| 1473 | 69.5 | 4.1 | 484 | 2 | Q7V4J9 | Q7v4j9 prochloroco |
| 1474 | 69.5 | 4.1 | 490 | 2 | Q61PW5 | Q61pw5 homo sapien |
| 1475 | 69.5 | 4.1 | 494 | 2 | Q825S5 | Q825s5 salmoneilla |
| 1476 | 69.5 | 4.1 | 500 | 2 | Q95WX2 | Q95wx2 papilio gla |
| 1477 | 69.5 | 4.1 | 502 | 2 | Q81915 | Q81915 arabidopsis |
| 1478 | 69.5 | 4.1 | 512 | 2 | Q6PEZ8 | Q6pez8 homo sapien |
| 1479 | 69.5 | 4.1 | 513 | 2 | Q8HV47 | Q8hv47 kaempferia |
| 1480 | 69.5 | 4.1 | 515 | 1 | GMT1_METAC | Q8mt6 methanosarc |
| 1481 | 69.5 | 4.1 | 515 | 1 | Q8HV16 | Q8hv16 stahlianthu |
| 1482 | 69.5 | 4.1 | 521 | 2 | Q8XYV0 | Q8xyv0 ralsionia s |
| 1483 | 69.5 | 4.1 | 537 | 2 | Q6FWK7 | Q6fwk7 pneumonia v |
| 1484 | 69.5 | 4.1 | 560 | 2 | Q8CEC2 | Q8cec2 mus musculi |
| 1485 | 69.5 | 4.1 | 607 | 1 | BLM3_MOUSE | Q8bzy7 mus musculi |
| 1486 | 69.5 | 4.1 | 608 | 2 | Q9GMB0 | Q9gmb0 sus scrofa |
| 1487 | 69.5 | 4.1 | 615 | 2 | Q9WY1 | Q9wy1 oryza sativ |
| 1488 | 69.5 | 4.1 | 621 | 2 | Q65451 | Q65451 arabidopsis |
| 1489 | 69.5 | 4.1 | 656 | 2 | Q6CNL5 | Q6cnl5 kluyveriomy |
| 1490 | 69.5 | 4.1 | 673 | 2 | Q9DBR3 | Q9db3 mus musculi |
| 1491 | 69.5 | 4.1 | 678 | 2 | Q6ZWC1 | Q6zwc1 homo sapien |

| | | | | | | |
|------|------|-----|-----|---|--------|---------------------|
| 1492 | 69.5 | 4.1 | 694 | 2 | Q9FH01 | Q9fh01 arabidopsis |
| 1493 | 69.5 | 4.1 | 700 | 2 | Q9FSB6 | Q9fsb6 raphanus sa |
| 1494 | 69.5 | 4.1 | 713 | 2 | Q6CN18 | Q6cn18 xenopus lae |
| 1495 | 69.5 | 4.1 | 719 | 2 | Q9U019 | Q9u019 giardia lam |
| 1496 | 69.5 | 4.1 | 719 | 2 | Q9U021 | Q9u021 giardia lam |
| 1497 | 69.5 | 4.1 | 720 | 2 | Q6PDE4 | Q6pde4 mus musculi |
| 1498 | 69.5 | 4.1 | 728 | 2 | Q94439 | Q94439 schizosacch |
| 1499 | 69.5 | 4.1 | 743 | 2 | Q8NFI3 | Q8nfi3 homo sapien |
| 1500 | 69.5 | 4.1 | 743 | 2 | Q7MAN9 | Q7man9 wolinnella s |

ALIGNMENTS

RESULT 1
CA08_HUMAN STANDARD; PRT; 323 AA.
AC Q9BXS4; Q75393;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 25-JAN-2005 (Rel. 46, Last annotation update)
DE Protein Clorf8 precursor (liver membrane-bound protein) (HSPC001)
UNQ169/PRO195).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Carnivora; Homiidae; Homo.
OX NCBI_TaxID=9606;
[1]
SEQUENCE FROM N.A.
RC TISSUE=Fetal liver;
OU X. Zhang C., Zhai Y., Wu S., Yu Y., Wei H., Xing G., Lu C.,
Zhou G., Dong C., He F.,
"Homo sapiens liver membrane-bound protein mRNA."
Submitted (JUL-2000) to the EMBL/Genbank/DBJ databases.
[2]
SEQUENCE FROM N.A.
RC TISSUE=umbilical cord blood;
Zhang Q.-H., Ye M., Wu X.-Y., Ren S.-X., Zhao M., Zhao C.-J., Fu G.,
Shen Y., Fan H.-Y., Lu G., Zhong M., Xu X.-R., Han Z.-G., Zhang J.-W.,
Tao J., Huang Q.-H., Zhou J., Hu G.-X., Gu J., Chen S.-J., Chen Z.;
"Cloning and functional analysis of cDNAs with open reading frames for
300 previously undefined genes expressed in CD34+ hematopoietic
stem/progenitor cells."
Genome Res. 10:1546-1560 (2000).
[3]
SEQUENCE FROM N.A.
MEDLINE=22887296; PubMed=12975309; DOI=10.1101/gr.1293003;
Clark H.F., Gurney A.L., Abaya E., Baker K., Baldwin D., Brush J.,
Chen J., Chow B., Chui C., Crowley C., Currell B., Devel B., Dowd P.,
Bacon D., Foster J., Grimaldi C., Gu Q., Haas P.E., Heldens S.,
Huang A., Kim H.S., Klimowski L., Jin Y., Johnson S., Lee J.,
Lewin L., Liao D., Mark M., Robble E., Sanchez C., Schoenfeld J.,
Seehagiri S., Simons C., Wicand D., Smith J., Stinson J., Vagstad A.,
Vandlen R., Watanabe C., Wicand D., Woods K., Xie M.-H., Yamaura D.,
Yi S., Yu G., Yuan J., Zhang M., Zhang Z., Goddard A., Wood W.I.,
Godowski P., Gray A.;
"The secreted protein discovery initiative (SPDI), a large-scale
effort to identify novel human secreted and transmembrane proteins: a
bioinformatics assessment."
Genome Res. 13:2265-2270 (2003).
[4]
SEQUENCE FROM N.A.
RC TISSUE=Brain;
MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
Struhsberg R.L., Feingold E.A., Gronow L.H., Derge J.G.,
Klausner R.D., Collins P.S., Wagner L., Shemmen C.M., Schuler G.D.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Hopkins R.F., Jordan H., Moore T., Wax S.I., Wang J., Hsieh F.,
Diatchenko L., Marubini K., Farmer A.A., Rubin G.M., Hong L.,
Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.B.,
Brownstein M.J., Udels T.B., Toshitsuki S., Carninci P., Prange C.,

RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smallus D.E.,
RA Scherch A., Schein J.E., Jones S.J.M., Maira M.A.,
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
CC -1- SUBCELLULAR LOCATION: Type I membrane protein (Potential).
CC -1- SIMILARITY: Belongs to the BSMAP family.
CC -1- CAUTION: Ref.2 sequence differs from that shown due to a
CC frameshift in position 6.

CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC EMBL; AF290615; AAK28026.1; -;
DR EMBL; AF047439; AAC39890.1; ALT_INIT.
DR EMBL; AY359029; AAC089388.1; -;
DR EMBL; BC003106; AAH03106.1; ALT_INIT.
DR Genew; HGNC:1239; Clorf8.
DR H-invdb; HIX000609; -;
DR Signal; Transmembrane.
FT SIGNAL 1 35 Potential.
FT CHAIN 36 323 Protein Clorf8.
FT DOMAIN 36 239 Extracellular (Potential).
FT TRANSMEM 240 262 Transmembrane (Potential).
FT DOMAIN 263 323 Cytoplasmic (Potential).
FT CAROHPD 90 90 N-linked (GlcNAc...) (Potential).
SQ SEQUENCE 323 AA; 36223 MW; 0926AB7D12D1B902 CRC64;

Query Match 100.0%; Score 1694; DB 1; Length 323;
Best Local Similarity 100.0%; Pred. No. 7.2e-144;
Matches 323; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAAPKGSIMVWRTQGLPPLILLTMALAGSGSTASAEAFDSVLTGDTASCHRACOLTYPLHT 60
DB 1 MAAPKGSIMVWRTQGLPPLILLTMALAGSGSTASAEAFDSVLTGDTASCHRACOLTYPLHT 60
QY 61 YPKKEELVACQRCGLFSICQFVDDGIDLNRTKLECSAECTEAYSQSDQYACHIGCONQ 120
DB 61 YPKKEELVACQRCGLFSICQFVDDGIDLNRTKLECSAECTEAYSQSDQYACHIGCONQ 120
QY 121 LPFAELROEQLSMIPKXHLPLPLTLVRSFWSMDMDSAQSFITTSWTFYTLQADDKIYIF 180
DB 121 LPFAELROEQLSMIPKXHLPLPLTLVRSFWSMDMDSAQSFITTSWTFYTLQADDKIYIF 180
QY 181 QSKPEIQYAPHLBOEPNLRSSLSKMSYLOKNSQAHNRFLEDSGDFLRCLSLNSG 240
DB 181 QSKPEIQYAPHLBOEPNLRSSLSKMSYLOKNSQAHNRFLEDSGDFLRCLSLNSG 240
QY 241 ILTTTLVLSVMVLLMTCATVATAVAYQYVPSSEKLSIYGDLEFPMNBQKLNRYPASSLVVYR 300
DB 241 ILTTTLVLSVMVLLMTCATVATAVAYQYVPSSEKLSIYGDLEFPMNBQKLNRYPASSLVVYR 300
QY 301 SKTEDEHBEAGPLPTKYNLAHSEI 323
DB 301 SKTEDEHBEAGPLPTKYNLAHSEI 323

RESULT 2
Q96KX7 PRELIMINARY; PRT; 324 AA.

AC Q96KX7;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Thymic dendritic cell-derived factor 1.
GN Name=Clorf8;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_Taxid=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Lung;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins P.S., Wagner L.H., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Uadiri T.B., Toshlyuk S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smallus D.E., Scherch A., Schein J.E.,
RA Jones S.J., Maira M.A.,
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Lung;
RA Strausberg R.;
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC016374; AAH16374.1; -;
SQ SEQUENCE 324 AA; 36262 MW; 59B10B582305275B CRC64;

Query Match 98.8%; Score 1674.5; DB 2; Length 324;
Best Local Similarity 99.4%; Pred. No. 4.1e-142;
Matches 322; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

QY 1 MAAPKGSIMVWRTQGLPPLILLTMALAGSGSTASAEAFDSVLTGDTASCHRACOLTYPLHT 60
DB 1 MAAPKGSIMVWRTQGLPPLILLTMALAGSGSTASAEAFDSVLTGDTASCHRACOLTYPLHT 60
QY 61 YPKKEELVACQRCGLFSICQFVDDGIDLNRTKLECSAECTEAYSQSDQYACHIGCONQ 120
DB 61 YPKKEELVACQRCGLFSICQFVDDGIDLNRTKLECSAECTEAYSQSDQYACHIGCONQ 120
QY 121 LPFAELROEQLSMIPKXHLPLPLTLVRSFWSMDMDSAQSFITTSWTFYTLQADDKIYIF 180
DB 121 LPFAELROEQLSMIPKXHLPLPLTLVRSFWSMDMDSAQSFITTSWTFYTLQADDKIYIF 180
QY 181 QSKPEIQYAPHLBOEPNLRSSLSKMSYLOKNSQAHNRFLEDSGDFLRCLSLNSG 240
DB 181 QSKPEIQYAPHLBOEPNLRSSLSKMSYLOKNSQAHNRFLEDSGDFLRCLSLNSG 240
QY 240 WILTTTLVLSVMVLLMTCATVATAVAYQYVPSSEKLSIYGDLEFPMNBQKLNRYPASSLVVY 299
DB 241 WILTTTLVLSVMVLLMTCATVATAVAYQYVPSSEKLSIYGDLEFPMNBQKLNRYPASSLVVY 300
QY 300 RSKTEDEHBEAGPLPTKYNLAHSEI 323
DB 301 RSKTEDEHBEAGPLPTKYNLAHSEI 324

RESULT 3
CA08_MOUSE

ID CA08 MOUSE STANDARD; PRT; 323 AA.
 AC Q9QY73; Q99LY8; Q9DLP9;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Protein Clorf8 homolog precursor (Thymic dendritic cell-derived factor 1).
 GN Name:Clorf8; Synonyms:ORF18, Tdcfl;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OC NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BALB/c; TISSUE=Thymus;
 RA Jin C.G., Chen W.F.;
 RT "Isolation and molecular cloning of gene encoding a novel dendritic cell-derived factor."
 RL Submitted (DEC-1998) to the EMBL/Genbank/DBJ databases.
 [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Embryo, and liver;
 MEDLINE=22354683; PubMed=12466851; DOI=10.1038/nature01266;
 RA Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S., Nikiado I., Oeato N., Saito R., Suzuki H., Yamana I., Kiyosawa H., Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojobori T., Balderelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J., Schriml L.M., Kanapin A., Mateuda H., Batalov S., Beisel K.W., Blake J.A., Brad D., Bruscia V., Choctia C., Corbani L.E., Cousins S., Dalia J.A., Dregani T.A., Fletcher C.F., Forrest A., Frazier K.S., Gaasterland T., Gariboldi M., Gissi C., Godzik A., Gough J., Grimmond S., Gustincich S., Hirokawa N., Jackson I.J., Jarvis E.D., Kanai A., Kawaji H., Kawasawa Y., Kedzierski R.M., King B.L., Konagaya A., Kurochkin I.V., Lee Y., Lennard B., Lyons P.A., Maglott D.R., Maltais L., Marchionni L., McKenzie L., Miki H., Nagashima T., Numa K., Okido T., Pavan W.J., Pereira G., Pesole G., Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramachandran S., Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M., Sandelin A., Schneider C., Sempile C.A., Setou M., Shimada K., Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M., Verardo R., Wagner L., Wahlestedt C., Wang Y., Watanabe Y., Wells C., Wilming L.G., Wyshaw-Boris A., Yanagisawa M., Yang L., Yuan Z., Zavolan M., Zhu Y., Zimmer A., Carninci P., Hayatsu N., Hirozane-Kishikawa T., Kono H., Nakamura M., Sakazume N., Sato K., Shiraki T., Waki K., Kawai J., Aizawa K., Aikawa T., Fukuda S., Hara A., Hashizume W., Imotani K., Ishii Y., Itoh M., Kagawa I., Miyazaki A., Sakai K., Sasaki D., Shibata K., Shinagawa A., Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J., Birney E., Hayashizaki Y.;
 RA "Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs."
 RL Nature 420:563-573 (2002).
 [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J, and FVB/N;
 TISSUE=Colon, Eye, Kidney, and Mammary gland;
 MEDLINE=22388577; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D., Altschul S.F., Zeeberg B., Buetow K.H., Scheffer C.F., Bhat N.K., Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh P., Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Stjepanec M., Soares M.B., Bonaldi M.P., Casavant T.L., Schetz T.E., Brownstein M.J., Ueda T.B., Toshiyuki S., Carninci P., Prange C., Rana S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J., Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., Richards S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulik S.W., Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A., Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,

RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences."
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein (Potential).
 CC -1- SIMILARITY: Belongs to the BSMAP family.
 CC -----
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 CC -----
 DR EMBL, AF116911; AAF20283.1; -
 DR EMBL, AK003252; BAB22668.2; -
 DR EMBL, AK050162; BAC34103.1; -
 DR EMBL, BC002164; AAH02164.1; -
 DR EMBL, BC014732; AAH14732.1; -
 DR EMBL, BC018379; AAH18379.1; -
 DR EMBL, BC045145; AAH45145.1; -
 DR EMBL, BC058273; AAH58273.1; -
 DR MGD; MGI:1929278; ORF18.
 KW Signal; Transmembrane.
 FT SIGNAL 1 34
 FT CHAIN 35 323 Potential.
 FT TRANSMEM 240 262 Protein Clorf8 homolog.
 FT CAROHYD 90 90 Potential.
 FT CONFLICT 48 48 N-linked (GlcNAc...) (Potential).
 FT CONFLICT 103 103 C -> V (in Ref. 1).
 FT CONFLICT 121 121 A -> T (in Ref. 1).
 FT CONFLICT 139 139 L -> W (in Ref. 1).
 FT CONFLICT 221 222 YL -> Q (in Ref. 1).
 FT CONFLICT 221 222 YL -> DR (in Ref. 1).
 FT CONFLICT 248 248 L -> F (in Ref. 3; AAH45145).
 FT CONFLICT 264 264 YGDLEFMEQKSRYPASLVVR -> IGHFQINQNL
 FT CONFLICT 277 300 YDLEFMEQKSRYPASLVVR (in Ref. 1).
 FT SEQUENCE 323 AA; 36313 MW; 0EB9FB6D7C7D96 CRC64; TYPE=PROTEIN
 Query Match 95.1%; Score 1611; DB 1; Length 323;
 Best Local Similarity 94.1%; Pred. No. 2.1e-136;
 Matches 304; Conservative 11; Mismatches 8; Indels 0; Gaps 0;
 QY 1 MAAPGKSMVPTQLGLPULLLITMALAGSGTASAEADSVLGDPTASCHRAQCLTYPLHT 60
 DB 1 MAAPGKSMVPTQLGLPULLLITMALAGSGTASAEADSVLGDPTASCHRAQCLTYPLHT 60
 QY 61 YPKBELVACORGRCLFSICQFVDDGIDLNRTKLECSACTEAYASQDEQYACHLGCQNO 120
 DB 61 YPKBELVACORGRCLFSICQFVDDGIDLNRTKLECSACTEAYASQDEQYACHLGCQNO 120
 QY 121 LPAELRQEQQLMSLMPKXHLFPPLTVLVSFMSDWDMSAQSFITSSWTFYLAQDDGKIYIF 180
 DB 121 LPAELRQEQQLMSLMPKXHLFPPLTVLVSFMSDWDMSAQSFITSSWTFYLAQDDGKIYIF 180
 QY 181 QSKPEIQYAPHLQEPPTLARSLSKMSYLVQNRNSQARNTLEDGESCGLFRLCLSLNSGW 240
 DB 181 QSKPEIQYAPHLQEPPTLARSLSKMSYLVQNRNSQARNTLEDGESCGLFRLCLSLNSGW 240
 QY 241 ILTTVLVSVMVLMICCATVATVQVVPSEKSIYGDLEFMEQKSRYPASLVYVR 300
 DB 241 ILTTVLVSVMVLMICCATVATVQVVPSEKSIYGDLEFMEQKSRYPASLVYVR 300
 QY 301 SKTDEHEAGPLPTKVNLAHSEI 323
 DB 301 SKTDEHEAGPLPTKVNLAHSEI 323
 RESULT 4
 Q6P5R1 PRELIMINARY; PRT; 239 AA.
 AC Q6P5R1;

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DT 05-JUL-2004 (TReMBLrel. 27, Created)
DT 05-JUL-2004 (TReMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TReMBLrel. 27, Last annotation update)
DE Clorf8 protein (Fragment).
GN Name=Clorf8;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Klausner R.D., Collins F.S., Wagner L., Shemmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Scheffer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.W., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Ueda T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Buterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Scherch A., Schein J.E.,
RA Jones S.J., Maiz M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RA Strausberg R.;
RL Submitted (NOV-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC062738; AAH62738.1; -.
FT NON TER
SQ SEQUENCE 239 AA; 27100 MW; F37D2FF1F83BD8F CRC64;

Query Match 72.8%; Score 1234; DB 2; Length 239;
Best Local Similarity 99.6%; Pred. No. 1.2e-102;
Matches 237; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 86 GIDNRTLCEESACTEAYSSDSBOYACHLGCQNLPPAEILROBOLMSIMPMLPLT 145
DB 2 GIDNRTLCEESACTEAYSSDSBOYACHLGCQNLPPAEILROBOLMSIMPMLPLT 61
QY 146 LVRSFMSDMDSAOSEFITSSWTFYQADDGKIVIQSKPEIQAYPHLEOEPTNLRESLS 205
DB 62 LVRSFMSDMDSAOSEFITSSWTFYQADDGKIVIQSKPEIQAYPHLEOEPTNLRESLS 121
QY 206 KMSYIQMNSQAHNRFLEDGESDGLRCLSLNSGMIITTTVLVSVMLIMTICATVATAV 265
DB 122 KMSYIQMNSQAHNRFLEDGESDGLRCLSLNSGMIITTTVLVSVMLIMTICATVATAV 181
QY 266 BOYVSEKLSYIGDLEFNNBOKLNRYPASSLVVVSXKTEDEHEAGPLPTKYNLAHSEI 323
DB 182 BOYVSEKLSYIGDLEFNNBOKLNRYPASSLVVVSXKTEDEHEAGPLPTKYNLAHSEI 239

RESULT 5
O6GNB1 PRELIMINARY; PRT; 324 AA.
AC O6GNB1;
DT 05-JUL-2004 (TReMBLrel. 27, Created)
DT 05-JUL-2004 (TReMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TReMBLrel. 27, Last annotation update)
DE MG82908 protein.
GN Name=MG82908;
OS Xenopus laevis (African clawed frog).
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OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidae; Pipidae;
OC Xenopodine; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Spleen;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Klausner R.D., Collins F.S., Wagner L., Shemmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Scheffer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.W., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Ueda T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Buterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Scherch A., Schein J.E.,
RA Jones S.J., Maiz M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Spleen;
RX MEDLINE=22341132; PubMed=12454917; DOI=10.1002/dvdy.10174;
RA Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,
RA Richardson P.;
RT "Genetic and genomic tools for Xenopus research: The NIH Xenopus
RT initiative.";
RL Dev. Dyn. 225:384-391(2002).
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE=Spleen;
RA Klein S., Gerhard D.S.;
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC073604; AAH73604.1; -.
SQ SEQUENCE 324 AA; 36080 MW; 786631B1D53DF8B0 CRC64;

Query Match 58.6%; Score 993.5; DB 2; Length 324;
Best Local Similarity 60.1%; Pred. No. 7.6e-81;
Matches 191; Conservative 39; Mismatches 75; Indels 13; Gaps 2;

QY 19 LLLTLMLAGSGGTAASAEAFDSVAGDPAAGHACOLTYPLHTYKBEELVACORGLFS 78
DB 7 LLLTLMLAGSARAEPAVNDVSLEDSCHGVCDGTYPLHTYKBEELVACORGLFS 66
QY 79 ICQVVDGIDINRTKYLCEESACTEAYSSDSBOYACHLGCQNLPPAEILROBOLMSIMP 138
DB 67 ICQVVDGIDINRTKYLCEESACTEAYSSDSBOYACHLGCQNLPPAEILROBOLMSIMP 126
QY 139 HILFPLTVLPSFMSDMDSAOSEFITSSWTFYQADDGKIVIQSKPEIQAYPHLEOEPT 196
DB 127 HILFPLTVLPSFMSDMDSAOSEFITSSWTFYQADDGKIVIQSKPEIQAYPHLEOEPT 186
QY 197 TNLRESLSIKMS-----YLQMRNSQAHNRFLEDGESDGLRCLSLNSGMIITTT 245
DB 187 TQPAESFLDKRISLDLMPGPGTQYGERMTDQGRSDSLNLBEGDNFLKCFNSANWSLISVT 246
QY 246 LVLSVMTLMTCCATVATAYEQVYPSKLSYIGDLEFNNBOKLNRYPASSLVVVSXKTEDE 305
DB 247 LVLSVMTLMTCCATVATAYEQVYPSKLSYIGDLEFNNBOKLNRYPATLVVHGPRBE 306
QY 306 HEAGPLPTKYNLAHSEI 323
DB 307 SEDAGPLTKVDLTQSAL 324
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RESULT 6
ID Q08P53 PRELIMINARY; PRT; 318 AA.
AC Q08P53
DT 01-JUN-2002 (TREMBlrel. 21, Created)
DT 01-JUN-2002 (TREMBlrel. 21, Last sequence update)
DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
DE H01CJC protein.
GN Name=H01CJC;
OS Tetradodon nigroviridis (Green puffer).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
OC Tetraodontidae; Tetraodontidae; Tetraodon.
OX NCBI_TaxID=99883;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=2263676; PubMed=12751327;
RA Bouneau L., Lardier G., Fischer C., Ronsin M., Weissenbach J.,
RA Bernot A.;
RT "Analysis of 148 kb of genomic DNA of Tetraodon nigroviridis covering
RT an amylase gene family."
RL DNA Seq. 14:1-13(2003).
DR EMBL; AJ427223; CAD20261.1; -.
SQ SEQUENCE 318 AA; 36409 MW; 42P2952DC770005A CRC64;

Query Match 56.5%; Score 957.5; DB 2; Length 318;
Best Local Similarity 59.6%; Pred. No. 1.3e-77;
Matches 186; Conservative 42; Mismatches 63; Indels 21; Gaps 4;

QY 16 LPLLLMALAGSGTASAPFSDVLDGTASCHACOLTYPLHTYPRKEBELYACORGR 75
DB 11 LGPVLPAFYA-----SASPVPFDSVLGNTASCSKSCMTYTLHTYPRGEGELYACORGR 64
QY 76 LFSICQFVDDGIDINRTYLCESACTEAYSGSDQYACHLCCONQLPRAELROEQLMSLM 135
DB 65 LFSICQFVDDGIDINRTYLCESACTEAYSGSDQYACHLCCONQLPRAELROEQLMSLM 124
QY 136 PKMHLPLTLVRSFWSMDMSAQSFTTSSWTFYLOADGKIVFQSPREIQAAPHLEOE 195
DB 125 PRHLYPLTLVRGFWEDVMNQASHLITSSWTFYLOADGKIVFQSPREIQAAPHLEOE 184
QY 196 PTNLRSSLSKMSYLOMNSQAHRNPLEDGSDDG-----FLACLSTN---SGMI 241
DB 185 KDGEEAQRSPGSPNPVFKDYHRTLIQERDRDGAERSYDDNYLFSCLSNPWLPGMI 244
QY 242 LTTTLVSVWVLMICATVATAVEQYVSEKLSIYGDLFEMNEOKLRYPASSILVVR 301
DB 245 LTTTLVSVWVLMICATVATAVADQYPAKLSIYGDKETWNEOKLRYPASSILVAT 304
QY 302 KTEDEEAGPLP 313
DB 305 KA-PVEEAEPPLP 315

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RESULT 7
ID Q08U8 PRELIMINARY; PRT; 309 AA.
AC Q08U8
DT 01-MAR-2002 (TREMBlrel. 20, Created)
DT 01-MAR-2002 (TREMBlrel. 20, Last sequence update)
DT 01-MAR-2002 (TREMBlrel. 20, Last annotation update)
DE AF290615-like protein.
GN Name=AF290615-like;
OS Tetradodon nigroviridis (Green puffer).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
OC Tetraodontidae; Tetraodontidae; Tetraodon.
OX NCBI_TaxID=99883;
RN [1]
RP SEQUENCE FROM N.A.

RESULT 8
ID Q712E2 PRELIMINARY; PRT; 339 AA.
AC Q712E2
DT 01-OCT-2003 (TREMBlrel. 25, Created)
DT 01-OCT-2003 (TREMBlrel. 25, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE Zgc:63977.
GN ORFNames=zgc:63977;
OS Brachydanio rerio (zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_TaxID=7955;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins P.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stropeton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein W.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Rana S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Wozny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettman M., Madan A.C., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzyzanski M.I., Skala U., Smailus D.E., Scherch A., Schein J.B.,
RA Jones S.J., Marra M.A.;

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"Generation and initial analysis of more than 15,000 full-length human RT and mouse cDNA sequences.";
 RT Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Kidney;
 RA Struhsberg R.;
 RL Submitted (JUL-2003) to the EMBL/GenBank/DBJ databases.
 DR EMBL: BC054584; AAH54584.1; -;
 ZFIN: ZDB-GENE-040426-2651; zgc:63977
 SQ SEQUENCE 339 AA; 37263 MW; 1E356BE07627DEDA CRC64;
 Query Match 35.2%; Score 595.5; DB 2; Length 339;
 Best Local Similarity 39.5%; Pred. No. 5-2e-45;
 Matches 134; Conservative 75; Mismatches 91; Indels 39; Gaps 11;
 QY 15 GLPPL-LITMALAGSGTAAAPDSVIGDTASCHRAQCLTYPLHTYKKEELVACORG 73
 DB 10 GPALVSLILVALA-----AASDLFDNOLGDTNYCKCKOQMSIKKNSPAKOSIMNACHRG 65
 QY 74 CRLFCICFVDGIDIDNRTKLECEACTEAYASQSDROYACHLGCNOLPFAELRQEOIMS 133
 DB 66 CRLVTCQFVNCNTGINTSKKECQACQEAISKLEDEACSTGCASQAPAEPIKRRKKA 125
 QY 134 LMPKMHLPPLTVLVSFMSDMSAOSFTTSWTFYLOADDKIYIPQSKPEIQYA-DHL 192
 DB 126 LTNRRKPSVMEAVSWCNDIVSNAQSFISSTWTFYLOADDKVVPFQSPREIELEBL 185
 QY 193 EOEPTNL-----RESSLSKMTYLOKRSQAHNPLEDESD-G 229
 DB 186 QAPRNVVDKPPQVNSHTQRPHTGRLRERNAKPG-VKQKNVSOH---AEDPAEHD 241
 QY 230 FLRCGLNSG---WITTTVLVSVMVLMICCATATAVEQVPESEKSIYDLEFENE- 285
 DB 242 FLGCSKRSGLPRWLLAACLFTISVWMLSCASVLAPEQHKTYQ-LSINGDEKFDMA 300
 QY 286 QKLNRYPPASISLVVR-SKTEDEHEAGPLPTKYNLAHSEI 323
 DB 301 QKVNPHYLPVIAVMTAQSSESKAEPPLPVKVDLKTSL 339
 RESULT 9
 BMAP HUMAN STANDARD; PRT; 342 AA.
 AC Q9UKZ8;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Brain specific membrane-anchored protein precursor.
 GN Name=BSMAP; Synonyms=C19orf4;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OK NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=99458621; PubMed=10527841; DOI=10.1006/bhrc.1999.1481;
 RA Elson G.C.A., Benoit de Coignac A., Aubry J.-P., Delneste Y.,
 RA Magistrelli G., Holzwarth U., Bonnefoy J.-Y., Gauchat J.-F.,
 RA "BSMAP", a novel protein expressed specifically in the brain whose gene
 RT is localized on chromosome 19p12.";
 RL Biochem. Biophys. Res. Commun. 264:55-62 (1999).
 RP SEQUENCE FROM N.A.
 RC TISSUE=Brain;
 RX MEDLINE=22388557; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schefer C.F., Bat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diachenko L., Marusina K., Farmer A.A., Rubin A.G., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Ussin T.B., Toshiyuki S., Carninci P., Prange C.,

RA Raha S.S., Loquellano N.A., Peters G.J., Adrmason R.D., Mullaly S.J.,
 RA Bosak S.A., McEwen P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Huliy S.W.,
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahy J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield V.S.N., Krzywinski M.I., Skalska U., Smallus D.E.,
 RA Schnerch A., Schein J.E., Jones S.J.M., Matra M.A.,
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
 CC -1- FUNCTION: May have a role in brain function.
 CC -1- SUBCELLULAR LOCATION: Could be associated with an intracellular
 CC -1- organelle or membrane (Potential).
 CC -1- TISSUE SPECIFICITY: Expressed preferentially at high level in the
 CC brain.
 CC -1- SIMILARITY: Belongs to the BSMAP family.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL Outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
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 CC or send an email to license@isb.ch).
 CC -----
 DR EMBL: AF186264; AAH00529.1; -;
 DR EMBL: BC010446; AAH10446.1; -;
 DR PIR: JC7110; JC7110.
 DR Genew: HGNC:13237; C19orf4.
 DR H-InVDB: HIX0014920; -;
 DR GO: GO:0016021; C:integral to membrane; TAS.
 DR GO: GO:0005624; C:membrane fraction; TAS.
 DR KEGG: K014920; -;
 FT SIGNAL 1 24 Potential.
 FT CHAIN 25 342 Brain specific membrane-anchored protein.
 FT TRANSMEM 268 292 Potential.
 FT SITE 340 342 Microbody targeting signal (Potential).
 FT CARBOHYD 97 97 N-linked (GlcNAc...) (Potential).
 SQ SEQUENCE 342 AA; 37619 MW; FB56BE37AF62569 CRC64;
 Query Match 25.0%; Score 423.5; DB 1; Length 342;
 Best Local Similarity 33.5%; Pred. No. 1.6e-29;
 Matches 107; Conservative 56; Mismatches 115; Indels 41; Gaps 8;
 QY 16 LPLLLITMALA---GGSGTASAPFSDVIGDTASCHRAQCLTYPLHTYKKEEL----- 67
 DB 7 MPPPLLLITLILASPAPASAPFAPQGLDTONCQLRCR-DRDLGPFQAGLEGASB 65
 QY 68 -----YACQGCRLFTICQFVDGIDLNRTKLECEACTEAYASQSDROYACHLGCQ 118
 DB 66 SPYRAVLISACERGRFSCRFVARSKKNATVTECAVAYVKEAQAQCSHCWC 125
 QY 119 NQLPFAELRQEOIMS LMPKMHLPPLTVLVSFMSDMSAOSFTTSWTFYLOADDKIY 178
 DB 126 SQAPPEPEQKRLVLEPSGLSL-LDLFTLCNDLVNSAGFTSSWTFYLOADDKIY 184
 QY 179 IFQSKPEIQ---YAPHLEQPTNLRS-----SLSKM---STYOMNSQAH 219
 DB 185 VFGQPIVIESIGFGGRLQREVETWGRSHPEALVHVDVPGLDKVRKAKIRVTSKAK 244
 QY 220 NPLDSESDGFLRCGLNSG---WITTTVLVSVMVLMICCATATAVEQVPESEKSI 276
 DB 245 VESSEPDNDPLSCMSRRSGLPRLWLLACCLFLSVLWMLMCSGLTVAPQGLKFPPLTL 304
 QY 277 YGDLEFNMNQKLNRYPPAS 295
 DB 305 EQHGPFMEPEPWPPIPPPS 323
 RESULT 10

07TN12
ID 07TN12 PRELIMINARY; PRT; 337 AA.
AC 07TN12;
DT 01-OCT-2003 (TREMBlrel. 25, Created)
DT 01-OCT-2003 (TREMBlrel. 25, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE RIKEN CDNA 5330410G16.
GN Name=5330410G16RLK;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6; TISSUE=Brain;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shennan C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Scheffer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Scheffer C.F., Bhat N.K.,
RA Datchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stopleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Uedlin T.B., Toshlyuk S., Carinci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Boeak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smalins D.E., Scherch A., Schein J.E.,
RA Jones S.J., Maira M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6; TISSUE=Brain;
RA Strausberg R.;
RL Submitted (Aug-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC056172; AAH56172.1; -
DR GO; GO:0005615; C:extracellular space; TAS.
SQ SEQUENCE 337 AA; 37661 MW; F58B93B07245E3A CRC64;

Query Match 24.5%; Score 415.5; DB 2; Length 337;
Best Local Similarity 34.3%; Pred. No. 8.1e-29;
Matches 107; Conservative 52; Mismatches 112; Indels 41; Gaps 9;

QY 18 PLULLTMAAGSGCTASAPDSVGDPAASCHRAQOLYPLHTYKERE----- 66
DB 7 PLULLLALV--TPPARDPFAVQGLDTPRCQQRQNRH--GSPAAQPEPESPPNNK 63
QY 67 ---LYACORGRGLFISICQFVDDGIDLNTKLECSACTEAYSQSDQYVACHLGCNOPLF 123
DB 64 AILISACRGRLRFTICRFVAKSRPNATETETCEALCTEAYVKAHQAACSGCGQIFR 123
QY 124 AELROEOL--MSLMPKMLLPPLTLVRSFMSDMDMSAQSFITSSWTFYIQLADGKIVIFQS 182
DB 124 PETOLEKQDLALDPGRGLSLRYLFMSCLDMSAQGFLSSSWTYSIQTDNRKVVVFOT 183
QY 183 KPEIQ-----YAPHLEQEPNTLR-----SLSKM--SYLQMRNSQAHRNTLE 223
DB 184 QPVANFNPFQSGHLQKRVETVWRSHPKALELHMDPVGPLDKVRKAKPRKTSKAVESD 243
QY 224 DGEISDGLRCLSLNSG--WILTTVLVSVWVLMICATVATAVEQVPSKLSYIDL 280
DB 244 QQESD-FISCKSRSGRLPRWVLFCLFLSILMLSLSCITLVTTGQHLKQPLAEGHK 302
QY 281 EFNNEQKLNRY 292
DB 303 GLLVESDWPVLP 314

RESULT 11
ID 081Y26 PRELIMINARY; PRT; 832 AA.
AC 081Y26;
DT 01-MAR-2003 (TREMBlrel. 23, Created)
DT 01-MAR-2003 (TREMBlrel. 23, Last sequence update)
DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
DE Hypothetical protein MGC33370.
GN Name=MGC33370;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Testis;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shennan C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Scheffer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Scheffer C.F., Bhat N.K.,
RA Datchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stopleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Uedlin T.B., Toshlyuk S., Carinci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Boeak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smalins D.E., Scherch A., Schein J.E.,
RA Jones S.J., Maira M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Testis;
RA Strausberg R.;
RL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC032859; AAH32859.1; -
KW Hypothetical protein.
SQ SEQUENCE 832 AA; 95559 MW; 54BDC52DCC4F0C03 CRC64;

Query Match 6.1%; Score 104; DB 2; Length 832;
Best Local Similarity 25.5%; Pred. No. 2.8;
Matches 50; Conservative 31; Mismatches 71; Indels 44; Gaps 10;

QY 137 KQHLFLPLTLVRSFMSDMDMSAQSFITSSWTFYIQA--DDGKIYFQSGRPIQ--YAPHLE 193
DB 529 KHLH-----WTNYTBAFLFSLTSGGTFLYALDDGVI-----QIDQVPLHLR 571
QY 194 QEPNLRSSLSKSYLQMRNSQA--RNFLEDS-----ESDGLRCLSLNSG 240
DB 572 AQ--SIATTTDKCPYMAFNHNVAVVFYLDKGEALVTWQIYVPENGLVYVYSSYSPK 629
QY 241 ILTTVLVSVWVLMICATVATAVEQVPSKLSYIDLRFNNEQKLNRYPASSLVYVR 300
DB 630 ILQSHNEISFPAAGQCYCKITLILTFYQNVYERISDY-----HTGLVLVQ 680
QY 301 SKTEDEHAEGLPTKV 316
DB 681 FRPSEYKACPIAQKV 696
RESULT 12
ID 081Y13 PRELIMINARY; PRT; 1250 AA.
AC 081Y13;
DT 01-MAR-2003 (TREMBlrel. 23, Created)

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DT 01-MAR-2003 (Tremblrel. 23, last sequence update)
DT 01-JUN-2003 (Tremblrel. 24, last annotation update)
DE Roller: helically twisted, animals roll when moving protein 3, isoform
DE b.
GN Name=rol-3; ORFNames=C16D9.2;
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RX MEDLINE=99069613; PubMed=9851916;
RG WormBase Consortium;
RT "Genome sequence of the nematode C. elegans: a platform for
RT investigating biology. The C. elegans Sequencing Consortium.";
RL Science 282:2012-2018 (1998).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RA Gattung S., Le T.T.;
RT "The sequence of C. elegans cosmid C16D9.";
RL Submitted (JUL-1996) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RA Waterston R.;
RL Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RA Wilson R.;
RL Submitted (AUG-2003) to the EMBL/GenBank/DBJ databases.
RN [5]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RG WormBase Consortium;
RL Submitted (SEP-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; U64858; AAN84865.1; -.
DR WormBase; WBGene0004395; rol-3.
DR WormPep; C16D9.2b; CE32799.
SQ SEQUENCE 1250 AA; 139843 MW; 268723A717DA6A05 CRC64;

Query Match
Best Local Similarity 21.7%; Pred. No. 7; Length 1250;
Matches 65; Conservative 38; Mismatches 97; Indels 100; Gaps 16;

QY 34 SAEAPDVLGDTASCHRAQ---LTYPLHT-----YKREELVACRGCRLLFSIC 80
DB 25 SATVSSSL---KTQSQCEERNLAVPLDSGEVHTGLAEVYSSRISCRHGC----- 76
QY 81 QFVDDGIDLNRTKLCESACTEAYSQSDQVACHGCONQ--PFAELRQEQMLMPPKH 139
DB 77 -----DVDERESKCDVACSEBGIVSN---ACKQGCRAVLVSFLAQAOALLIQVHVNNE 126
QY 140 IL-----PPLTVRS-----FMSDMMDASQFITSSWTFYLQADGKIVIFQ 181
DB 127 VLETSMKLKWEFFETLAEELKEIANADIFWFSQTKPLNGILGKRWI----- 172
QY 182 SKPEIQAYAPHLRQEPNTLRSSLSKN-----SYLQNRNSQAHNPLEDGESDGLRC 233
DB 173 SLFQ-----NSFRNSSLSSEVHPFEHGEHVEVRLALSYNQVLVSRTTYHLP 221
QY 234 LSLNSGMIITTTIVLSVMVL---LMIICATVATAEQVVPSEKLSIYGDLEFMNQKLN 289
DB 222 LS-KSG---TLLEVIQLOQLSDDRVAVCYRT-----NPTPKFKLITM---TLNDNTLN 268

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DT 01-MAR-2003 (Tremblrel. 23, last sequence update)
DT 01-MAR-2004 (Tremblrel. 26, last annotation update)
DE Roller: helically twisted, animals roll when moving protein 3, isoform
DE a.
GN Name=rol-3; ORFNames=C16D9.2;
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RX MEDLINE=99069613; PubMed=9851916;
RG WormBase Consortium;
RT "Genome sequence of the nematode C. elegans: a platform for
RT investigating biology. The C. elegans Sequencing Consortium.";
RL Science 282:2012-2018 (1998).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RA Gattung S., Le T.T.;
RT "The sequence of C. elegans cosmid C16D9.";
RL Submitted (JUL-1996) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RA Waterston R.;
RL Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RA Wilson R.;
RL Submitted (AUG-2003) to the EMBL/GenBank/DBJ databases.
RN [5]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RG WormBase Consortium;
RL Submitted (SEP-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; U64858; AAN84864.1; -.
DR HSSP; P08581; IRIW.
DR WormBase; WBGene0004395; rol-3.
DR WormPep; C16D9.2a; CE32798.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0004713; F:protein-tyrosine kinase activity; IEA.
DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR InterPro; IPR003961; FN.II.
DR InterPro; IPR01009; Kinase like.
DR InterPro; IPR000719; Prot_kinase.
DR InterPro; IPR001245; Tyr_kinase.
DR Pfam; PF00041; fn3; 3.
DR PRINTS; PR00109; TYRKINASE.
DR ProDom; PD000001; Prot_kinase; 1.
DR SMART; SM00060; FN3; 3.
DR SMART; SM00219; TYK; 1.
DR PROSITE; PS50853; FN3; 2.
DR PROSITE; PS50011; PROTEIN KINASE DOM; 1.
SQ SEQUENCE 2456 AA; 273833 MW; BBFA8BC75FF82B8 CRC64;

Query Match
Best Local Similarity 21.7%; Pred. No. 17; Length 2456;
Matches 65; Conservative 38; Mismatches 97; Indels 100; Gaps 16;

QY 34 SAEAPDVLGDTASCHRAQ---LTYPLHT-----YKREELVACRGCRLLFSIC 80
DB 25 SATVSSSL---KTQSQCEERNLAVPLDSGEVHTGLAEVYSSRISCRHGC----- 76
QY 81 QFVDDGIDLNRTKLCESACTEAYSQSDQVACHGCONQ--PFAELRQEQMLMPPKH 139
DB 77 -----DVDERESKCDVACSEBGIVSN---ACKQGCRAVLVSFLAQAOALLIQVHVNNE 126
QY 140 IL-----PPLTVRS-----FMSDMMDASQFITSSWTFYLQADGKIVIFQ 181
DB 127 VLETSMKLKWEFFETLAEELKEIANADIFWFSQTKPLNGILGKRWI----- 172

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QY 182 SKPEIQVAPHLQEPTNLRESLSKQ-----SYLQWRNSQAHNPLDESDGFLRC 233
DB 173 SLPO-----NSFRNSLSSEVAVPEFHGHVEVRLALSTRNOVLVSRITTTTHLP 221
QY 234 LLSNGSWLLTTTLVLSVWL-----LMICCATVATAVEQVPSSEKLSIYGDLEFPNNEOKLN 289
DB 222 LS-KSG---TLEVIQGLQLSDDRVAVCVRT-----NQPTPRFKLTIM---TLNDNTIN 268

RESULT 14

Q6ZOC8 PRELIMINARY; PRT; 808 AA.
AC 06ZOC8;
DT 05-JUN-2004 (TReMBLrel. 27, Created)
DT 05-JUN-2004 (TReMBLrel. 27, Last sequence update)
DT 05-JUN-2004 (TReMBLrel. 27, Last annotation update)
DE MK1AA0372 protein (Fragment).
GN Name=mk1AA0372;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX PubMed=14621295;
RA Okazaki N., Kikuno R., Ohara R., Inamoto S., Koseki H., Hirooka S.,
Saga Y., Nagase T., Ohara O., Koga H.;
RT "Prediction of the coding sequences of mouse homologues of KIAA gene:
RT I1. the complete nucleotide sequences of 500 mouse KIAA-homologous
RT cDNAs identified by screening of terminal sequences of cDNA clones
RT randomly sampled from size-fractionated libraries.";
RL DNA Res. 10:167-180(2003).
DR EMBL; AK129128; BAC97938.1; -
DR InterPro; IPR008940; Erenyl_trans.
DR InterPro; IPR011054; Rndmnt_hyb_motif.
DR InterPro; IPR001440; TPR.
DR InterPro; IPR008941; TPR-like.
DR Pfam; PF00515; TPR_1; 3.
DR SMART; SM00028; TPR; 5.
DR PROSITE; PS50005; TPR; 1.
DR PROSITE; PS50293; TPR_REGION; 1.
KW Repeat; TPR repeat.
FT NON TER
SQ SEQUENCE 808 AA; 89436 MW; 90055AA5183341C8 CRC64;

Query Match 5.9%; Score 100; DB 2; Length 808;
Best Local Similarity 23.1%; Pred. No. 6.1;
Matches 60; Conservative 36; Mismatches 94; Indels 70; Gaps 11;

QY 26 LAGSGGTA---SABAFDSV-----LGDITASCHRAQUTTPHATYKKEELX 68
DB 485 LAMGSSSTADKSNLKTIOKAFISPDPAVWAGIMAAACHADKALALINTQPKRVLDY 544
QY 69 ACORGC-----RLFSICQFVDDGIDINRTKLCESACTEAYSQSDQ 110
DB 545 LALSVAVALSKDKKILQNYNOSLEKWSFSQVVTGLITGKTS-EASICTOSLSKSNPDQ 603
QY 111 YACHLGCONLPFAELROEQLMPLKXHLFPLTLVBSFMSDMDSAQSFTTSWTFYL 170
DB 604 PAVIL-----LLRQVQCTSLLESQKL-PDAVLEBELQKTVMSNRS-VPAWQWLA 651
QY 171 QADDGKIVIFQSK-----PELOYAPHL-----EQEPTNLRESLSKMSYLOKRNQAH--- 218
DB 652 Q-----VYOSQGMGAEMCYKRSKLSQVASQOGNWSGKLSLKLALLALEVCANVSG 704
QY 219 ---RNFLDESDGFLRCIS 235
DB 705 DHMSLVQEAITSALKVCFPS 724

RESULT 15

097215

ID 097215 PRELIMINARY; PRT; 768 AA.
AC 097215;
DT 01-MAY-1999 (TReMBLrel. 10, Created)
DT 01-MAY-1999 (TReMBLrel. 10, Last sequence update)
DT 01-OCT-2003 (TReMBLrel. 25, Last annotation update)
DE Hypothetical protein I4830.11.
GN Name=I4830.11;
OS Leishmania major.
OC Eukaryota; Euklenozoa; Kinetoplastida; Trypanosomatidae; Leishmania.
OX NCBI_TaxID=5664;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Friedlin;
RX MEDLINE=98146435; PubMed=9477341;
RA Ivens A.C., Lewis S.M., Bagherzadeh A., Zhang L., Chan H.M.,
Smith D.F.;
RT "A physical map of the Leishmania major Friedlin genome.";
RT Genome Res. 8:135-145(1998).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=Friedlin;
RA Ivens A.C., Murphy L., Quail M., Harris D., Oliver K., Lawson D.,
Rajandream M.A., Barrell B.G.;
RL Submitted (Apr-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AL139794; CAC22617.1; -
KW Hypothetical protein.
SQ SEQUENCE 768 AA; 81914 MW; 3155EB10B176FE64 CRC64;

Query Match 5.7%; Score 96.5; DB 2; Length 768;
Best Local Similarity 20.2%; Pred. No. 12;
Matches 68; Conservative 37; Mismatches 125; Indels 107; Gaps 14;

QY 6 GSWRTQGLGPPILLITMALAGSGTASABAFDSVLDITAS-----CHRAQUTYP 57
DB 205 GDPMSRVVRGQPPCSRLT-----STSTASPOOQOQOQPTKGPVTMPVNLCFSTISCVOP 259
QY 58 LHTYKKEBELVACORGCRLFSICQFVDDGIDINRTKLCESACTEAYSQSDQVACHLGC 117
DB 260 VLTLP-----KMGALLAS-----EYFRALLCFHNAANYSLTQA---RIHGV 299
QY 118 QNQLPFAELROEQLM---SLMPKXHLF---PLTVRSF----- 150
DB 300 AQ--PPAPLRRALRCTVETLPKSHYTLVAAPLSEASTVALAVADYDPSGLORQLK 357
QY 151 WSDMDSHQ-----SPITSSTWTFYQADGKIVIFQSKPEIQVA----- 189
DB 358 WNSTFKTEQPIWVQPRFLRYVRPTWTIAKDQPDSESDSESPRSSTASRAVALYQLSI 417
QY 190 --PHLEGEPTNLRESLSKMSYLOKRNQAHNPLDESDGFLRCLSINSGMILTTTLV 247
DB 418 GLKMSVPLSLTDSKVLPSLTHRGAAVREVV---ASDGRVSVQLRK----- 465
QY 248 LSVWLLMICAATVATAVE-QVPSSEKLSIYGDLEFM 283
DB 466 -----CSTSTAEASRVPAVILMPGDTHLL 493

Search completed: March 28, 2005, 13:12:38
Job time : 107 secs

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GenCore version 5.1.6
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OM protein - protein search, using SW model

Run on: March 28, 2005, 13:08:45 ; Search time 24 Seconds
(without alignments)
1004.652 Million cell updates/sec

Title: US-09-978-299a-330

Perfect score: 1694

Sequence: 1 MAAKGSUMVQTGLPPL.....EDHEAGPLPKVLAHSEI 323

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 1500 summaries

Database :

Issued Patents AA:*

- 1: /cgn2_6/ptodata/1/1aa/5A.COMB.pep:*
- 2: /cgn2_6/ptodata/1/1aa/5B.COMB.pep:*
- 3: /cgn2_6/ptodata/1/1aa/6A.COMB.pep:*
- 4: /cgn2_6/ptodata/1/1aa/6B.COMB.pep:*
- 5: /cgn2_6/ptodata/1/1aa/6C.COMB.pep:*
- 6: /cgn2_6/ptodata/1/1aa/backfile1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
|------------|--------|-------------|--------|---------------------|---------------------|
| 1 | 1694 | 100.0 | 323 | US-09-976-594-818 | Sequence 818, App |
| 2 | 1262.5 | 74.5 | 273 | US-09-149-476-476 | Sequence 476, App |
| 3 | 707 | 41.7 | 132 | US-09-513-999C-4172 | Sequence 4172, App |
| 4 | 96 | 5.7 | 963 | US-09-949-016-11519 | Sequence 11519, App |
| 5 | 96 | 5.7 | 963 | US-09-949-016-11519 | Sequence 11519, App |
| 6 | 95.5 | 5.6 | 915 | US-09-907-794A-34 | Sequence 34, App1 |
| 7 | 95.5 | 5.6 | 915 | US-09-905-125A-34 | Sequence 34, App1 |
| 8 | 95.5 | 5.6 | 915 | US-09-902-775A-34 | Sequence 34, App1 |
| 9 | 95.5 | 5.6 | 915 | US-09-906-700-34 | Sequence 34, App1 |
| 10 | 95.5 | 5.6 | 915 | US-09-903-603A-34 | Sequence 34, App1 |
| 11 | 95.5 | 5.6 | 915 | US-09-904-920A-34 | Sequence 34, App1 |
| 12 | 95.5 | 5.6 | 915 | US-09-909-064-34 | Sequence 34, App1 |
| 13 | 95.5 | 5.6 | 915 | US-09-905-381A-34 | Sequence 34, App1 |
| 14 | 95.5 | 5.6 | 915 | US-09-906-618-34 | Sequence 34, App1 |
| 15 | 93.5 | 5.5 | 956 | US-09-949-016-6215 | Sequence 6215, App |
| 16 | 86 | 5.1 | 1106 | US-09-949-016-9626 | Sequence 9626, App |
| 17 | 85.5 | 5.0 | 2733 | US-09-949-016-11433 | Sequence 11433, App |
| 18 | 85.5 | 5.0 | 3259 | US-09-949-016-6507 | Sequence 6507, App |
| 19 | 84 | 5.0 | 1350 | US-08-319-866-9 | Sequence 9, App1 |
| 20 | 84 | 5.0 | 1350 | US-08-809-917-9 | Sequence 9, App1 |
| 21 | 83 | 4.9 | 503 | US-09-198-452A-263 | Sequence 263, App |
| 22 | 83 | 4.9 | 508 | US-09-438-185A-253 | Sequence 253, App |
| 23 | 82.5 | 4.9 | 698 | US-09-107-532A-5685 | Sequence 5685, App |
| 24 | 82 | 4.8 | 119 | US-09-046-479-4 | Sequence 4, App1 |
| 25 | 82 | 4.8 | 119 | US-08-822-897C-4 | Sequence 4, App1 |
| 26 | 82 | 4.8 | 119 | US-09-608-810A-5 | Sequence 5, App1 |
| 27 | 82 | 4.8 | 119 | US-09-404-417A-4 | Sequence 4, App1 |

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| 28 | 82 | 4.8 | 119 | US-09-794-987-4 | Sequence 4, App1 |
| 29 | 82 | 4.8 | 1564 | US-09-976-594-309 | Sequence 309, App |
| 30 | 82 | 4.8 | 1609 | US-09-562-702A-22 | Sequence 22, App1 |
| 31 | 82 | 4.8 | 1609 | US-09-561-818A-22 | Sequence 22, App1 |
| 32 | 82 | 4.8 | 1617 | US-09-562-702A-26 | Sequence 26, App1 |
| 33 | 82 | 4.8 | 2158 | US-10-144-198-34 | Sequence 34, App1 |
| 34 | 82 | 4.8 | 2265 | US-10-144-198-35 | Sequence 35, App1 |
| 35 | 82 | 4.8 | 2697 | US-10-144-198-12 | Sequence 12, App1 |
| 36 | 81.5 | 4.8 | 566 | US-07-955-905A-22 | Sequence 22, App1 |
| 37 | 81.5 | 4.8 | 566 | US-07-955-905A-22 | Sequence 22, App1 |
| 38 | 81.5 | 4.8 | 1312 | US-08-687-080-51 | Sequence 51, App1 |
| 39 | 81 | 4.8 | 485 | US-08-378-313-27 | Sequence 27, App1 |
| 40 | 81 | 4.8 | 485 | US-08-378-313-32 | Sequence 32, App1 |
| 41 | 81 | 4.8 | 959 | US-09-107-433-4334 | Sequence 4334, App |
| 42 | 81 | 4.8 | 1032 | US-09-583-110-3366 | Sequence 3366, App |
| 43 | 81 | 4.8 | 1609 | US-09-538-092-900 | Sequence 900, App |
| 44 | 80.5 | 4.8 | 453 | US-09-171-461-48 | Sequence 48, App1 |
| 45 | 80.5 | 4.8 | 453 | US-09-970-711-48 | Sequence 48, App1 |
| 46 | 80 | 4.7 | 305 | US-09-328-352-6445 | Sequence 6445, App |
| 47 | 80 | 4.7 | 1605 | US-09-562-702A-30 | Sequence 30, App1 |
| 48 | 80 | 4.7 | 1605 | US-09-561-818A-26 | Sequence 26, App1 |
| 49 | 79.5 | 4.7 | 485 | US-08-378-313-25 | Sequence 25, App1 |
| 50 | 79.5 | 4.7 | 701 | US-09-710-279-710 | Sequence 710, App |
| 51 | 79.5 | 4.7 | 703 | US-09-134-001C-3015 | Sequence 3015, App |
| 52 | 79.5 | 4.7 | 999 | US-09-747-371-2 | Sequence 2, App1 |
| 53 | 79 | 4.7 | 638 | US-08-897-443-1 | Sequence 1, App1 |
| 54 | 79 | 4.7 | 1118 | US-07-934-333B-2 | Sequence 2, App1 |
| 55 | 79 | 4.7 | 1118 | US-08-278-089A-2 | Sequence 2, App1 |
| 56 | 79 | 4.7 | 1118 | US-08-838-957A-2 | Sequence 2, App1 |
| 57 | 79 | 4.7 | 1122 | US-08-278-089A-6 | Sequence 6, App1 |
| 58 | 79 | 4.7 | 1122 | US-08-838-957A-6 | Sequence 6, App1 |
| 59 | 78.5 | 4.6 | 785 | US-09-902-540-16175 | Sequence 16175, App |
| 60 | 78.5 | 4.6 | 1312 | US-08-592-126-148 | Sequence 148, App |
| 61 | 78.5 | 4.6 | 1312 | US-09-168-595-148 | Sequence 148, App |
| 62 | 78 | 4.6 | 880 | US-09-556-877-175 | Sequence 175, App |
| 63 | 78 | 4.6 | 880 | US-09-620-412C-175 | Sequence 175, App |
| 64 | 78 | 4.6 | 880 | US-09-598-419-175 | Sequence 175, App |
| 65 | 77.5 | 4.6 | 447 | US-09-949-016-7884 | Sequence 7884, App |
| 66 | 77.5 | 4.6 | 462 | US-08-417-330A-16 | Sequence 16, App1 |
| 67 | 77.5 | 4.6 | 530 | US-08-307-439-29 | Sequence 29, App1 |
| 68 | 77.5 | 4.6 | 530 | US-09-299-268-29 | Sequence 29, App1 |
| 69 | 77.5 | 4.6 | 669 | US-09-345-473E-27 | Sequence 27, App1 |
| 70 | 77 | 4.5 | 489 | US-09-134-000C-5481 | Sequence 5481, App |
| 71 | 77 | 4.5 | 1101 | US-08-469-537A-96 | Sequence 96, App1 |
| 72 | 76.5 | 4.5 | 396 | US-09-488-029A-10242 | Sequence 10242, App |
| 73 | 76.5 | 4.5 | 657 | US-08-508-761B-2 | Sequence 2, App1 |
| 74 | 76.5 | 4.5 | 956 | US-08-897-443-3 | Sequence 3, App1 |
| 75 | 76 | 4.5 | 357 | US-09-535-909-8 | Sequence 8, App1 |
| 76 | 76 | 4.5 | 462 | US-09-134-001C-4300 | Sequence 4300, App |
| 77 | 76 | 4.5 | 464 | US-09-538-092-598 | Sequence 598, App |
| 78 | 76 | 4.5 | 467 | US-09-248-786A-16430 | Sequence 16430, App |
| 79 | 76 | 4.5 | 487 | US-09-535-909-4 | Sequence 4, App1 |
| 80 | 76 | 4.5 | 586 | US-09-270-767-45293 | Sequence 45293, App |
| 81 | 76 | 4.5 | 770 | US-09-784-316-5 | Sequence 5, App1 |
| 82 | 76 | 4.5 | 770 | US-10-229-124-5 | Sequence 5, App1 |
| 83 | 76 | 4.5 | 811 | US-08-426-627-2 | Sequence 2, App1 |
| 84 | 76 | 4.5 | 811 | US-08-426-627-22 | Sequence 22, App1 |
| 85 | 76 | 4.5 | 1542 | US-09-949-016-9215 | Sequence 9215, App |
| 86 | 75.5 | 4.5 | 323 | US-09-457-646-30 | Sequence 30, App1 |
| 87 | 75.5 | 4.5 | 323 | US-09-516-065-30 | Sequence 30, App1 |
| 88 | 75.5 | 4.5 | 376 | US-09-328-332-5970 | Sequence 5970, App |
| 89 | 75 | 4.4 | 402 | US-08-709-979A-3 | Sequence 3, App1 |
| 90 | 75 | 4.4 | 402 | US-08-709-974A-1 | Sequence 1, App1 |
| 91 | 75 | 4.4 | 402 | US-08-709-974A-5 | Sequence 5, App1 |
| 92 | 75 | 4.4 | 415 | US-08-709-974A-4 | Sequence 4, App1 |
| 93 | 75 | 4.4 | 415 | US-09-069-632-1 | Sequence 1, App1 |
| 94 | 75 | 4.4 | 435 | US-08-361-920-27 | Sequence 27, App1 |
| 95 | 75 | 4.4 | 435 | US-08-479-929-27 | Sequence 27, App1 |
| 96 | 75 | 4.4 | 435 | US-08-483-432-27 | Sequence 27, App1 |
| 97 | 75 | 4.4 | 435 | US-09-069-632-3 | Sequence 3, App1 |
| 98 | 75 | 4.4 | 866 | US-09-556-877-189 | Sequence 189, App |
| 99 | 75 | 4.4 | 866 | US-09-620-412C-189 | Sequence 189, App |
| 100 | 75 | 4.4 | 866 | US-09-598-419-189 | Sequence 189, App |

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| 101 | 74.5 | 4.4 | 142 | 4 | US-09-621-976-4664 | Sequence 4664, Ap | 174 | 70.5 | 4.2 | 680 | 4 | US-10-219-541-1 | Sequence 1, Appli |
| 102 | 74.5 | 4.4 | 539 | 4 | US-09-949-016-6363 | Sequence 6363, Ap | 175 | 70.5 | 4.2 | 771 | 1 | US-09-248-796A-20725 | Sequence 20725, A |
| 103 | 74.5 | 4.4 | 539 | 4 | US-09-949-016-9747 | Sequence 9747, Ap | 176 | 70.5 | 4.2 | 837 | 1 | US-08-426-677-23 | Sequence 23, Appli |
| 104 | 74.5 | 4.4 | 546 | 4 | US-09-949-016-8514 | Sequence 8514, Ap | 177 | 70.5 | 4.2 | 937 | 3 | US-09-005-180A-4 | Sequence 4, Appli |
| 105 | 74.5 | 4.4 | 627 | 4 | US-09-949-016-9447 | Sequence 9447, Ap | 178 | 70.5 | 4.2 | 944 | 4 | US-09-538-092-452 | Sequence 452, App |
| 106 | 74.5 | 4.4 | 761 | 4 | US-09-949-016-6880 | Sequence 6880, Ap | 179 | 70.5 | 4.2 | 2842 | 1 | US-07-741-940-7 | Sequence 7, Appli |
| 107 | 74.5 | 4.4 | 1125 | 4 | US-09-900-920-60 | Sequence 60, Appli | 180 | 70.5 | 4.2 | 2842 | 1 | US-08-289-548A-7 | Sequence 7, Appli |
| 108 | 74.5 | 4.4 | 1342 | 1 | US-07-978-895-4 | Sequence 4, Appli | 181 | 70.5 | 4.2 | 2842 | 1 | US-08-452-654-7 | Sequence 7, Appli |
| 109 | 74.5 | 4.4 | 1342 | 2 | US-08-473-119-4 | Sequence 4, Appli | 182 | 70.5 | 4.2 | 2842 | 1 | US-08-449-731-7 | Sequence 7, Appli |
| 110 | 74.5 | 4.4 | 1342 | 2 | US-08-475-352-4 | Sequence 4, Appli | 183 | 70.5 | 4.2 | 2843 | 1 | US-07-741-940-2 | Sequence 2, Appli |
| 111 | 74.5 | 4.4 | 1342 | 2 | US-08-170-699-4 | Sequence 4, Appli | 184 | 70.5 | 4.2 | 2843 | 1 | US-08-289-548A-7 | Sequence 2, Appli |
| 112 | 74.5 | 4.4 | 1343 | 6 | 5183884-4 | Sequence 6, Appli | 185 | 70.5 | 4.2 | 2843 | 1 | US-08-452-654-2 | Sequence 2, Appli |
| 113 | 74.5 | 4.4 | 1360 | 4 | US-09-949-016-8022 | Sequence 8022, Ap | 186 | 70.5 | 4.2 | 2843 | 1 | US-08-452-655B-2 | Sequence 2, Appli |
| 114 | 74.5 | 4.4 | 1439 | 4 | US-09-902-540-14072 | Sequence 14072, A | 187 | 70.5 | 4.2 | 2843 | 1 | US-08-370-235A-2 | Sequence 2, Appli |
| 115 | 74.5 | 4.4 | 2482 | 1 | US-08-328-254-6 | Sequence 6, Appli | 188 | 70.5 | 4.2 | 2843 | 3 | US-08-450-582-2 | Sequence 2, Appli |
| 116 | 74.5 | 4.4 | 3210 | 4 | US-09-538-092-1154 | Sequence 1154, Ap | 189 | 70.5 | 4.2 | 2843 | 3 | US-08-450-582-2 | Sequence 2, Appli |
| 117 | 74.5 | 4.4 | 3210 | 4 | US-08-353-700-1 | Sequence 1, Appli | 190 | 70.5 | 4.2 | 2843 | 3 | US-08-449-731-2 | Sequence 7, Appli |
| 118 | 74.5 | 4.4 | 3248 | 5 | PCT-US95-16216-1 | Sequence 1, Appli | 191 | 70.5 | 4.2 | 2843 | 4 | US-10-092-138A-30 | Sequence 30, Appli |
| 119 | 74.5 | 4.4 | 628 | 4 | US-09-360-545-4 | Sequence 4, Appli | 192 | 70.5 | 4.2 | 2843 | 4 | US-09-538-092-1007 | Sequence 1007, Ap |
| 120 | 74 | 4.4 | 628 | 4 | US-09-398-395A-20 | Sequence 20, Appli | 193 | 70.5 | 4.2 | 2973 | 2 | US-08-821-355A-7 | Sequence 7, Appli |
| 121 | 74 | 4.4 | 628 | 4 | US-09-887-586A-20 | Sequence 20, Appli | 194 | 70.5 | 4.2 | 2973 | 2 | US-09-003-687A-7 | Sequence 7, Appli |
| 122 | 74 | 4.4 | 628 | 4 | US-09-895-752-20 | Sequence 20, Appli | 195 | 70.5 | 4.2 | 2973 | 3 | US-09-136-605-7 | Sequence 7, Appli |
| 123 | 74 | 4.4 | 628 | 4 | US-09-903-012B-20 | Sequence 20, Appli | 196 | 70.5 | 4.2 | 2973 | 3 | US-08-709-979A-5 | Sequence 5, Appli |
| 124 | 74 | 4.4 | 629 | 3 | US-09-360-237-60 | Sequence 60, Appli | 197 | 70 | 4.1 | 200 | 2 | US-10-101-464A-959 | Sequence 959, App |
| 125 | 74 | 4.4 | 1049 | 3 | US-09-522-666-6 | Sequence 6, Appli | 198 | 70 | 4.1 | 264 | 4 | US-09-538-092-396 | Sequence 396, App |
| 126 | 74 | 4.4 | 1049 | 3 | US-08-131-365B-54 | Sequence 54, Appli | 199 | 70 | 4.1 | 264 | 4 | US-09-710-279-272 | Sequence 272, App |
| 127 | 74 | 4.4 | 1141 | 1 | US-08-668-123-54 | Sequence 54, Appli | 200 | 70 | 4.1 | 308 | 4 | US-09-134-001C-5171 | Sequence 5171, Ap |
| 128 | 74 | 4.4 | 3924 | 2 | US-09-538-092-1246 | Sequence 1246, Ap | 201 | 70 | 4.1 | 311 | 3 | US-09-252-991A-30298 | Sequence 30298, A |
| 129 | 74 | 4.4 | 304 | 4 | US-09-248-796A-20714 | Sequence 20714, A | 202 | 70 | 4.1 | 256 | 4 | US-09-371-056-8 | Sequence 8, Appli |
| 130 | 73.5 | 4.3 | 351 | 4 | US-09-270-767-43939 | Sequence 43939, A | 203 | 69.5 | 4.1 | 310 | 4 | US-09-371-056-8 | Sequence 2, Appli |
| 131 | 73.5 | 4.3 | 589 | 4 | US-09-543-681A-7643 | Sequence 7643, Ap | 204 | 69.5 | 4.1 | 344 | 4 | US-09-489-039A-848 | Sequence 848, Ap |
| 132 | 73 | 4.3 | 679 | 4 | US-09-252-991A-18681 | Sequence 18681, A | 205 | 69.5 | 4.1 | 358 | 4 | US-09-438-185A-703 | Sequence 703, App |
| 133 | 73 | 4.3 | 946 | 5 | PCT-US95-08493-13 | Sequence 13, Appli | 206 | 69.5 | 4.1 | 469 | 4 | US-09-489-039A-8224 | Sequence 8224, A |
| 134 | 72.5 | 4.3 | 1213 | 1 | US-08-308-872B-4 | Sequence 6478, Ap | 207 | 69.5 | 4.1 | 604 | 4 | US-09-248-796A-14489 | Sequence 14489, A |
| 135 | 72.5 | 4.3 | 1451 | 1 | US-09-134-001C-3561 | Sequence 15007, A | 208 | 69.5 | 4.1 | 777 | 2 | US-08-477-396A-4 | Sequence 4, Appli |
| 136 | 72.5 | 4.3 | 299 | 3 | US-09-949-016-7659 | Sequence 7659, Ap | 209 | 69.5 | 4.1 | 1199 | 4 | US-09-949-016-6989 | Sequence 6989, Ap |
| 137 | 72.5 | 4.3 | 3177 | 2 | US-09-404-627-2 | Sequence 2, Appli | 210 | 69.5 | 4.1 | 1203 | 4 | US-10-023-894-2 | Sequence 2, Appli |
| 138 | 72 | 4.3 | 3177 | 2 | US-08-477-451-4 | Sequence 4, Appli | 211 | 69.5 | 4.1 | 196 | 4 | US-09-949-016-10916 | Sequence 10916, A |
| 139 | 72 | 4.3 | 160 | 4 | US-09-248-796A-24377 | Sequence 24377, A | 212 | 69.5 | 4.1 | 196 | 4 | US-09-371-056-6 | Sequence 6, Appli |
| 140 | 72 | 4.3 | 257 | 4 | US-09-252-991A-18809 | Sequence 18809, A | 213 | 69.5 | 4.1 | 545 | 4 | US-09-949-016-6469 | Sequence 6469, Ap |
| 141 | 72 | 4.3 | 330 | 4 | US-09-543-681A-7860 | Sequence 7860, Ap | 214 | 69.5 | 4.1 | 558 | 4 | US-09-949-016-736 | Sequence 736, Ap |
| 142 | 72 | 4.3 | 336 | 4 | US-09-949-016-10000 | Sequence 10000, A | 215 | 69.5 | 4.1 | 635 | 3 | US-08-506-296B-59 | Sequence 59, App |
| 143 | 72 | 4.3 | 386 | 4 | US-08-339-152A-33 | Sequence 33, Appli | 216 | 69.5 | 4.1 | 635 | 4 | US-09-328-352-6078 | Sequence 6078, Ap |
| 144 | 71 | 4.2 | 429 | 1 | US-09-380-682-58 | Sequence 58, Appli | 217 | 69.5 | 4.1 | 637 | 4 | US-09-358-395A-58 | Sequence 58, Appli |
| 145 | 71 | 4.2 | 438 | 4 | US-09-426-627-6 | Sequence 6720, Ap | 218 | 69.5 | 4.1 | 637 | 4 | US-09-887-586A-58 | Sequence 58, Appli |
| 146 | 71 | 4.2 | 836 | 1 | US-08-426-627-6 | Sequence 6720, Ap | 219 | 69.5 | 4.1 | 637 | 4 | US-09-895-752-58 | Sequence 58, Appli |
| 147 | 71.5 | 4.2 | 1021 | 1 | US-09-252-991A-19205 | Sequence 19205, A | 220 | 69.5 | 4.1 | 637 | 4 | US-09-903-012B-58 | Sequence 58, Appli |
| 148 | 71.5 | 4.2 | 141 | 3 | US-08-513-974B-320 | Sequence 320, App | 221 | 69.5 | 4.1 | 637 | 4 | US-09-900-797-58 | Sequence 58, Appli |
| 149 | 71.5 | 4.2 | 141 | 3 | US-09-198-452A-875 | Sequence 875, App | 222 | 69.5 | 4.1 | 704 | 4 | US-09-590-656-2 | Sequence 2, Appli |
| 150 | 71 | 4.2 | 501 | 4 | US-09-438-185A-818 | Sequence 818, App | 223 | 69.5 | 4.1 | 704 | 4 | US-09-733-764-2 | Sequence 7, Appli |
| 151 | 70.5 | 4.2 | 525 | 4 | US-09-949-016-6353 | Sequence 6353, Ap | 224 | 69.5 | 4.1 | 895 | 4 | US-09-489-039A-12499 | Sequence 12499, A |
| 152 | 70.5 | 4.2 | 575 | 4 | US-09-134-000C-4457 | Sequence 4457, Ap | 225 | 69.5 | 4.1 | 977 | 4 | US-09-590-656-1 | Sequence 1, Appli |
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| 154 | 70.5 | 4.2 | 605 | 3 | US-08-477-346-49 | Sequence 49, Appli | 227 | 69.5 | 4.1 | 1064 | 4 | US-09-733-764-1 | Sequence 1, Appli |
| 155 | 70.5 | 4.2 | 605 | 3 | US-08-487-089-49 | Sequence 49, Appli | 228 | 69.5 | 4.1 | 1124 | 1 | US-08-323-474-2 | Sequence 2, Appli |
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| 158 | 70.5 | 4.2 | 677 | 4 | US-09-252-991A-25571 | Sequence 25571, A | 231 | 69.5 | 4.1 | 1260 | 3 | US-08-506-296B-21 | Sequence 21, Appli |
| 159 | 70.5 | 4.2 | 680 | 3 | US-08-211-430-2 | Sequence 2, Appli | 232 | 69.5 | 4.1 | 1293 | 4 | US-09-170-4960-292 | Sequence 292, App |
| 160 | 70.5 | 4.2 | 680 | 3 | US-08-761-136-1 | Sequence 1, Appli | 233 | 69.5 | 4.1 | 1822 | 4 | US-09-364-425B-57 | Sequence 57, Appli |
| 161 | 70.5 | 4.2 | 680 | 3 | US-09-576-967-1 | Sequence 1, Appli | 234 | 69.5 | 4.1 | 2037 | 4 | US-09-949-016-7999 | Sequence 7999, Ap |
| 162 | 70.5 | 4.2 | 680 | 4 | US-09-576-967-1 | Sequence 1, Appli | 235 | 69.5 | 4.1 | 2037 | 4 | US-09-543-681A-5538 | Sequence 5538, Ap |

| | | | | | | | | | | | | | |
|-----|------|-----|------|---|----------------------|--------------------|-----|------|-----|------|---|----------------------|-------------------|
| 247 | 69 | 4.1 | 3878 | 4 | US-09-914-259-11 | Sequence 11, Appl | 320 | 67.5 | 4.0 | 638 | 3 | US-09-347-488-2 | Sequence 2, Appl |
| 248 | 68.5 | 4.0 | 131 | 4 | US-09-328-352-4847 | Sequence 4847, Ap | 321 | 67.5 | 4.0 | 639 | 3 | US-09-376-856-2 | Sequence 2, Appl |
| 249 | 68.5 | 4.0 | 258 | 4 | US-09-270-767-43689 | Sequence 43689, Ap | 322 | 67.5 | 4.0 | 641 | 4 | US-09-167-206-4 | Sequence 4, Appl |
| 250 | 68.5 | 4.0 | 290 | 4 | US-09-328-352-6785 | Sequence 6785, Ap | 323 | 67.5 | 4.0 | 647 | 4 | US-09-389-956-6 | Sequence 6, Appl |
| 251 | 68.5 | 4.0 | 329 | 4 | US-09-248-796A-22243 | Sequence 22243, A | 324 | 67.5 | 4.0 | 728 | 4 | US-09-489-039A-13409 | Sequence 13409, A |
| 252 | 68.5 | 4.0 | 297 | 4 | US-09-248-796A-14761 | Sequence 14761, A | 325 | 67.5 | 4.0 | 760 | 1 | US-08-230-431A-2 | Sequence 2, Appl |
| 253 | 68.5 | 4.0 | 339 | 4 | US-09-270-767-41384 | Sequence 41384, A | 326 | 67.5 | 4.0 | 760 | 1 | US-08-619-280A-2 | Sequence 2, Appl |
| 254 | 68.5 | 4.0 | 339 | 4 | US-09-270-767-56600 | Sequence 56600, A | 327 | 67.5 | 4.0 | 760 | 2 | US-08-940-391-2 | Sequence 2, Appl |
| 255 | 68.5 | 4.0 | 443 | 4 | US-09-489-039A-8591 | Sequence 8591, Ap | 328 | 67.5 | 4.0 | 818 | 4 | US-09-248-796A-18342 | Sequence 18342, A |
| 256 | 68.5 | 4.0 | 710 | 4 | US-09-248-796A-14405 | Sequence 14405, A | 329 | 67.5 | 4.0 | 968 | 4 | US-09-248-796A-17547 | Sequence 17547, A |
| 257 | 68.5 | 4.0 | 737 | 1 | US-08-185-432-2 | Sequence 2, Appl | 330 | 67.5 | 4.0 | 1180 | 3 | US-09-224-024-28 | Sequence 28, Appl |
| 258 | 68.5 | 4.0 | 737 | 1 | US-08-185-432-4 | Sequence 4, Appl | 331 | 67.5 | 4.0 | 1180 | 5 | PCT-US94-07902-98 | Sequence 28, Appl |
| 259 | 68.5 | 4.0 | 737 | 4 | US-09-866-028-15 | Sequence 15, Appl | 332 | 67.5 | 4.0 | 1342 | 2 | US-08-484-438-9 | Sequence 9, Appl |
| 260 | 68.5 | 4.0 | 1022 | 4 | US-09-944-457-15 | Sequence 15, Appl | 333 | 67.5 | 4.0 | 1380 | 4 | US-09-949-016-11688 | Sequence 11688, A |
| 261 | 68.5 | 4.0 | 1022 | 4 | US-09-949-016-9041 | Sequence 8564, Ap | 334 | 67.5 | 4.0 | 1792 | 2 | US-08-962-284-4 | Sequence 4, Appl |
| 262 | 68.5 | 4.0 | 1022 | 4 | US-09-949-016-9041 | Sequence 9041, Ap | 335 | 67.5 | 4.0 | 1895 | 2 | US-08-619-554-4 | Sequence 4, Appl |
| 263 | 68.5 | 4.0 | 1071 | 2 | US-08-975-527-1 | Sequence 1, Appl | 336 | 67.5 | 4.0 | 2227 | 3 | US-08-478-886-4 | Sequence 4, Appl |
| 264 | 68.5 | 4.0 | 1102 | 4 | US-09-358-383C-36 | Sequence 36, Appl | 337 | 67.5 | 4.0 | 2227 | 3 | US-09-653-499-4 | Sequence 4, Appl |
| 265 | 68.5 | 4.0 | 1150 | 4 | US-09-462-136-6 | Sequence 6, Appl | 338 | 67.5 | 4.0 | 2227 | 4 | US-10-135-988-4 | Sequence 4, Appl |
| 266 | 68.5 | 4.0 | 1454 | 3 | US-08-392-459-22 | Sequence 22, Appl | 339 | 67.5 | 4.0 | 257 | 4 | US-09-248-796A-14623 | Sequence 14623, A |
| 267 | 68.5 | 4.0 | 1454 | 5 | PCT-US91-08255-22 | Sequence 22, Appl | 340 | 67 | 4.0 | 283 | 4 | US-09-198-452A-492 | Sequence 492, Ap |
| 268 | 68.5 | 4.0 | 1454 | 5 | PCT-US91-08255-22 | Sequence 22, Appl | 341 | 67 | 4.0 | 283 | 4 | US-09-438-185A-462 | Sequence 462, Ap |
| 269 | 68.5 | 4.0 | 1454 | 5 | PCT-US93-04384-43 | Sequence 43, Appl | 342 | 67 | 4.0 | 312 | 4 | US-09-599-360B-96 | Sequence 96, Appl |
| 270 | 68.5 | 4.0 | 1454 | 5 | PCT-US93-04384-45 | Sequence 45, Appl | 343 | 67 | 4.0 | 313 | 4 | US-09-148-545-233 | Sequence 233, Ap |
| 271 | 68.5 | 4.0 | 1454 | 5 | PCT-US93-04384-45 | Sequence 45, Appl | 344 | 67 | 4.0 | 404 | 4 | US-09-248-796A-18878 | Sequence 18878, A |
| 272 | 68.5 | 4.0 | 1454 | 5 | PCT-US93-04384-48 | Sequence 48, Appl | 345 | 67 | 4.0 | 411 | 4 | US-09-134-000C-4279 | Sequence 4279, Ap |
| 273 | 68.5 | 4.0 | 1602 | 4 | US-09-270-767-44170 | Sequence 44170, A | 346 | 67 | 4.0 | 439 | 4 | US-09-248-796A-15955 | Sequence 15955, A |
| 274 | 68 | 4.0 | 167 | 4 | US-09-711-164-465 | Sequence 465, App | 347 | 67 | 4.0 | 455 | 4 | US-09-710-279-2648 | Sequence 2648, Ap |
| 275 | 68 | 4.0 | 172 | 4 | US-09-248-796A-21509 | Sequence 21509, A | 348 | 67 | 4.0 | 535 | 4 | US-09-489-039A-11461 | Sequence 11461, A |
| 276 | 68 | 4.0 | 174 | 4 | US-09-489-039A-9228 | Sequence 9228, Ap | 349 | 67 | 4.0 | 543 | 4 | US-09-252-931A-10375 | Sequence 30775, A |
| 277 | 68 | 4.0 | 174 | 4 | US-09-489-039A-10069 | Sequence 10069, A | 350 | 67 | 4.0 | 557 | 1 | US-08-309-341-4 | Sequence 4, Appl |
| 278 | 68 | 4.0 | 174 | 4 | US-09-489-039A-11218 | Sequence 11218, A | 351 | 67 | 4.0 | 557 | 1 | US-08-608-267-4 | Sequence 4, Appl |
| 279 | 68 | 4.0 | 174 | 4 | US-09-489-039A-11342 | Sequence 11342, A | 352 | 67 | 4.0 | 557 | 1 | US-08-608-224-4 | Sequence 4, Appl |
| 280 | 68 | 4.0 | 174 | 4 | US-09-489-039A-11497 | Sequence 11497, A | 353 | 67 | 4.0 | 557 | 2 | US-08-967-149-4 | Sequence 4, Appl |
| 281 | 68 | 4.0 | 174 | 4 | US-09-489-039A-11926 | Sequence 11926, A | 354 | 67 | 4.0 | 557 | 2 | US-09-902-540-12677 | Sequence 12677, A |
| 282 | 68 | 4.0 | 174 | 4 | US-09-489-039A-12078 | Sequence 12078, A | 355 | 67 | 4.0 | 580 | 4 | US-09-482-273-127 | Sequence 127, App |
| 283 | 68 | 4.0 | 174 | 4 | US-09-489-039A-12619 | Sequence 12619, A | 356 | 67 | 4.0 | 612 | 4 | US-09-949-016-6941 | Sequence 6941, Ap |
| 284 | 68 | 4.0 | 185 | 4 | US-09-562-737-112 | Sequence 112, App | 357 | 67 | 4.0 | 661 | 4 | US-09-949-016-11084 | Sequence 11084, A |
| 285 | 68 | 4.0 | 287 | 4 | US-09-949-016-11191 | Sequence 4167, Ap | 358 | 67 | 4.0 | 665 | 4 | US-09-134-000C-6451 | Sequence 6451, Ap |
| 286 | 68 | 4.0 | 299 | 3 | US-09-134-001C-1167 | Sequence 3101, Ap | 359 | 67 | 4.0 | 710 | 4 | US-09-248-796A-18842 | Sequence 18842, A |
| 287 | 68 | 4.0 | 334 | 4 | US-09-543-681A-6301 | Sequence 32, Appl | 360 | 67 | 4.0 | 792 | 4 | US-09-248-796A-15074 | Sequence 4, Appl |
| 288 | 68 | 4.0 | 337 | 4 | US-09-457-646-32 | Sequence 32, Appl | 361 | 67 | 4.0 | 835 | 4 | US-08-938-291A-4 | Sequence 4, Appl |
| 289 | 68 | 4.0 | 337 | 4 | US-09-516-065-32 | Sequence 45912, A | 362 | 67 | 4.0 | 974 | 3 | US-09-589-619-4 | Sequence 4, Appl |
| 290 | 68 | 4.0 | 370 | 4 | US-09-270-767-45912 | Sequence 8, Appl | 363 | 67 | 4.0 | 974 | 4 | US-09-589-619-4 | Sequence 8, Appl |
| 291 | 68 | 4.0 | 375 | 4 | US-09-311-021-8 | Sequence 12, Appl | 364 | 67 | 4.0 | 1001 | 4 | US-09-949-016-9932 | Sequence 217, App |
| 292 | 68 | 4.0 | 452 | 4 | US-08-809-802-12 | Sequence 12, Appl | 365 | 67 | 4.0 | 1056 | 4 | US-08-026-138E-1 | Sequence 27, Appl |
| 293 | 68 | 4.0 | 456 | 4 | US-09-482-273-227 | Sequence 4415, Ap | 366 | 67 | 4.0 | 1464 | 1 | US-09-051-019-2 | Sequence 2, Appl |
| 294 | 68 | 4.0 | 456 | 4 | US-09-328-352-4415 | Sequence 36, Appl | 367 | 67 | 4.0 | 2289 | 3 | US-09-180-422B-27 | Sequence 1, Appl |
| 295 | 68 | 4.0 | 457 | 4 | US-09-482-273-189 | Sequence 36, Appl | 368 | 67 | 4.0 | 4536 | 4 | US-09-079-030-1 | Sequence 1, Appl |
| 296 | 68 | 4.0 | 612 | 2 | US-08-933-750C-36 | Sequence 6932, Ap | 369 | 67 | 4.0 | 4563 | 4 | US-09-108-006C-1 | Sequence 842, App |
| 297 | 68 | 4.0 | 613 | 3 | US-09-328-352-6932 | Sequence 12514, A | 370 | 67 | 4.0 | 4563 | 4 | US-09-270-767-42095 | Sequence 25095, A |
| 298 | 68 | 4.0 | 613 | 4 | US-09-489-039A-12514 | Sequence 20267, A | 371 | 67 | 4.0 | 4563 | 4 | US-09-248-796A-15040 | Sequence 1892, Ap |
| 299 | 68 | 4.0 | 729 | 4 | US-09-248-796A-20267 | Sequence 3, Appl | 372 | 66.5 | 3.9 | 137 | 4 | US-09-710-279-1892 | Sequence 1140, Ap |
| 300 | 68 | 4.0 | 748 | 4 | US-08-015-985-3 | Sequence 1, Appl | 373 | 66.5 | 3.9 | 290 | 4 | US-08-562-535C-4 | Sequence 4, Appl |
| 301 | 68 | 4.0 | 793 | 1 | US-08-280-597-3 | Sequence 1, Appl | 374 | 66.5 | 3.9 | 303 | 2 | US-08-742-605D-4 | Sequence 4, Appl |
| 302 | 68 | 4.0 | 802 | 1 | US-08-015-985-1 | Sequence 7356, Ap | 375 | 66.5 | 3.9 | 329 | 2 | US-09-259-234-4 | Sequence 4, Appl |
| 303 | 68 | 4.0 | 802 | 1 | US-09-280-597-1 | Sequence 6968, A | 376 | 66.5 | 3.9 | 334 | 4 | US-09-134-000C-4461 | Sequence 1461, Ap |
| 304 | 68 | 4.0 | 807 | 4 | US-09-949-016-7356 | Sequence 10620, A | 377 | 66.5 | 3.9 | 342 | 4 | US-09-489-039A-12340 | Sequence 12340, A |
| 305 | 68 | 4.0 | 1005 | 4 | US-09-949-016-6968 | Sequence 11668, A | 378 | 66.5 | 3.9 | 359 | 4 | US-09-710-279-2742 | Sequence 2742, Ap |
| 306 | 68 | 4.0 | 1005 | 4 | US-09-949-016-10620 | Sequence 20, Appl | 379 | 66.5 | 3.9 | 431 | 4 | US-09-543-681A-6326 | Sequence 15344, A |
| 307 | 68 | 4.0 | 75 | 4 | US-09-556-877-20 | Sequence 20, Appl | 380 | 66.5 | 3.9 | 442 | 4 | US-09-248-796A-15434 | Sequence 81219, A |
| 308 | 67.5 | 4.0 | 216 | 4 | US-09-288-594A-20 | Sequence 20, Appl | 381 | 66.5 | 3.9 | 512 | 4 | US-09-543-681A-8138 | Sequence 16453, A |
| 309 | 67.5 | 4.0 | 216 | 4 | US-09-620-412C-20 | Sequence 20, Appl | 382 | 66.5 | 3.9 | 522 | 4 | US-09-248-796A-16453 | Sequence 1, Appl |
| 310 | 67.5 | 4.0 | 216 | 4 | US-09-410-568-20 | Sequence 20, Appl | 383 | 66.5 | 3.9 | 928 | 4 | US-09-636-872A-1 | Sequence 1, Appl |
| 311 | 67.5 | 4.0 | 216 | 4 | US-09-598-419-20 | Sequence 61214, A | 384 | 66.5 | 3.9 | 928 | 4 | US-09-636-872A-1 | Sequence 1, Appl |
| 312 | 67.5 | 4.0 | 216 | 4 | US-09-543-681A-4525 | Sequence 4525, Ap | 385 | 66.5 | 3.9 | 928 | 4 | US-09-986-552-1 | Sequence 1, Appl |
| 313 | 67.5 | 4.0 | 486 | 4 | US-09-512-935-38 | Sequence 38, Appl | 386 | 66.5 | 3.9 | 928 | 4 | US-09-636-596C-1 | Sequence 4, Appl |
| 314 | 67.5 | 4.0 | 530 | 4 | US-09-134-000C-5782 | Sequence 45693, A | 387 | 66.5 | 3.9 | 928 | 4 | US-10-023-894-4 | Sequence 4, Appl |
| 315 | 67.5 | 4.0 | 565 | 4 | US-09-270-767-45693 | Sequence 4599, Ap | 388 | 66.5 | 3.9 | 928 | 4 | | |
| 316 | 67.5 | 4.0 | 580 | 4 | | | 389 | 66.5 | 3.9 | | | | |
| 317 | 67.5 | 4.0 | 633 | 4 | | | 390 | 66.5 | 3.9 | | | | |
| 318 | 67.5 | 4.0 | | | | | 391 | 66.5 | 3.9 | | | | |
| 319 | 67.5 | 4.0 | | | | | 392 | 66.5 | 3.9 | | | | |

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|-----|------|-----|------|---|----------------------|--------------------|-----|------|-----|------|---|----------------------|-------------------|
| 393 | 66.5 | 3.9 | 928 | 4 | US-10-306-686-1 | Sequence 1, Appli | 466 | 65.5 | 3.9 | 482 | 4 | US-09-949-016-9805 | Sequence 9805, Ap |
| 394 | 66.5 | 3.9 | 986 | 4 | US-09-248-19088 | Sequence 19088, A | 467 | 65.5 | 3.9 | 505 | 3 | US-09-382-256-16 | Sequence 16, Appl |
| 395 | 66.5 | 3.9 | 998 | 4 | US-09-540-736-3801 | Sequence 3801, Ap | 468 | 65.5 | 3.9 | 505 | 3 | US-09-395-115-16 | Sequence 16, Appl |
| 396 | 66.5 | 3.9 | 1072 | 4 | US-09-248-796A-16400 | Sequence 16400, A | 469 | 65.5 | 3.9 | 505 | 3 | US-08-123-934A-8 | Sequence 8, Appli |
| 397 | 66.5 | 3.9 | 1116 | 4 | US-09-949-016-10408 | Sequence 10408, A | 470 | 65.5 | 3.9 | 505 | 3 | US-08-436-265-16 | Sequence 16, Appl |
| 398 | 66.5 | 3.9 | 1339 | 4 | US-09-949-016-10448 | Sequence 10448, A | 471 | 65.5 | 3.9 | 505 | 3 | US-09-679-187-16 | Sequence 16, Appl |
| 399 | 66.5 | 3.9 | 1454 | 5 | PCT-US93-04384-16 | Sequence 16, Appl | 472 | 65.5 | 3.9 | 505 | 4 | US-09-874-628-8 | Sequence 8, Appli |
| 400 | 66.5 | 3.9 | 1478 | 4 | US-09-949-016-8315 | Sequence 8315, Ap | 473 | 65.5 | 3.9 | 505 | 4 | US-09-267-963D-16 | Sequence 16, Appl |
| 401 | 66.5 | 3.9 | 1478 | 4 | US-09-976-594-757 | Sequence 757, App | 474 | 65.5 | 3.9 | 505 | 5 | PCT-US94-10080-8 | Sequence 8, Appli |
| 402 | 66.5 | 3.9 | 1977 | 4 | US-09-919-039-367 | Sequence 367, App | 475 | 65.5 | 3.9 | 587 | 1 | US-07-955-905A-23 | Sequence 23, Appl |
| 403 | 66.5 | 3.9 | 2109 | 3 | US-08-646-695-6 | Sequence 6, Appli | 476 | 65.5 | 3.9 | 626 | 4 | US-09-248-796A-16472 | Sequence 16472, A |
| 404 | 66.5 | 3.9 | 2109 | 5 | PCT-US96-06053-6 | Sequence 6, Appli | 477 | 65.5 | 3.9 | 694 | 4 | US-09-949-016-1246 | Sequence 7246, Ap |
| 405 | 66.5 | 3.9 | 3898 | 2 | US-08-876-991-2 | Sequence 2, Appli | 478 | 65.5 | 3.9 | 694 | 4 | US-09-489-039A-9066 | Sequence 9066, Ap |
| 406 | 66.5 | 3.9 | 3898 | 2 | US-09-059-853-2 | Sequence 2, Appli | 479 | 65.5 | 3.9 | 755 | 4 | US-09-949-016-10644 | Sequence 10644, A |
| 407 | 66.5 | 3.9 | 144 | 4 | US-09-270-767-34852 | Sequence 34852, A | 480 | 65.5 | 3.9 | 798 | 4 | US-09-642-024-5 | Sequence 5, Appli |
| 408 | 66.5 | 3.9 | 144 | 4 | US-09-270-767-50069 | Sequence 50069, A | 481 | 65.5 | 3.9 | 1024 | 4 | US-09-562-737-47 | Sequence 47, Appl |
| 409 | 66.5 | 3.9 | 295 | 4 | US-09-585-858-51 | Sequence 51, Appl | 482 | 65.5 | 3.9 | 1127 | 3 | US-08-937-195-3 | Sequence 3, Appli |
| 410 | 66.5 | 3.9 | 295 | 4 | US-10-270-878-51 | Sequence 51, Appl | 483 | 65.5 | 3.9 | 1127 | 3 | US-08-915-152-3 | Sequence 3, Appli |
| 411 | 66.5 | 3.9 | 301 | 4 | US-09-198-452A-898 | Sequence 898, App | 484 | 65.5 | 3.9 | 1127 | 4 | US-09-915-152-3 | Sequence 3, Appli |
| 412 | 66.5 | 3.9 | 331 | 4 | US-09-489-847-309 | Sequence 309, App | 485 | 65.5 | 3.9 | 1127 | 5 | US-09-376-463-3 | Sequence 3, Appli |
| 413 | 66.5 | 3.9 | 338 | 4 | US-09-385-219A-12 | Sequence 12, Appl | 486 | 65.5 | 3.9 | 1127 | 5 | PCT-US96-07627-3 | Sequence 3, Appli |
| 414 | 66.5 | 3.9 | 339 | 4 | US-09-949-016-7998 | Sequence 7998, Ap | 487 | 65.5 | 3.9 | 1171 | 4 | US-09-248-796A-16043 | Sequence 16043, A |
| 415 | 66.5 | 3.9 | 346 | 2 | US-08-613-220B-4 | Sequence 4, Appl | 488 | 65.5 | 3.9 | 1326 | 4 | US-09-949-016-6806 | Sequence 6806, Ap |
| 416 | 66.5 | 3.9 | 363 | 4 | US-09-252-991A-6726 | Sequence 26726, A | 489 | 65.5 | 3.9 | 1338 | 4 | US-09-949-016-6029 | Sequence 6029, Ap |
| 417 | 66.5 | 3.9 | 366 | 4 | US-09-079-030-219 | Sequence 219, App | 490 | 65.5 | 3.9 | 1454 | 3 | US-08-392-459-32 | Sequence 32, Appl |
| 418 | 66.5 | 3.9 | 396 | 4 | US-09-248-796A-20351 | Sequence 20351, A | 491 | 65.5 | 3.9 | 1454 | 5 | US-09-854-799-32 | Sequence 32, Appl |
| 419 | 66.5 | 3.9 | 404 | 2 | US-08-504-459-8 | Sequence 8, Appli | 492 | 65.5 | 3.9 | 1454 | 5 | PCT-US91-09525-32 | Sequence 32, Appl |
| 420 | 66.5 | 3.9 | 413 | 4 | US-09-902-540-15607 | Sequence 15607, A | 493 | 65.5 | 3.9 | 1454 | 5 | PCT-US93-04384-12 | Sequence 12, Appl |
| 421 | 66.5 | 3.9 | 419 | 4 | US-09-270-767-45469 | Sequence 45469, A | 494 | 65.5 | 3.9 | 1454 | 5 | PCT-US93-04384-44 | Sequence 44, Appl |
| 422 | 66.5 | 3.9 | 432 | 4 | US-09-248-796A-24125 | Sequence 24125, A | 495 | 65.5 | 3.9 | 1454 | 5 | PCT-US93-04384-46 | Sequence 46, Appl |
| 423 | 66.5 | 3.9 | 457 | 4 | US-09-248-796A-15756 | Sequence 15756, A | 496 | 65.5 | 3.9 | 1454 | 5 | PCT-US93-04384-47 | Sequence 47, Appl |
| 424 | 66.5 | 3.9 | 492 | 4 | US-09-248-796A-16231 | Sequence 16231, A | 497 | 65.5 | 3.9 | 3066 | 3 | US-08-952-127-12 | Sequence 12, Appl |
| 425 | 66.5 | 3.9 | 532 | 2 | US-08-948-564-10 | Sequence 10, Appl | 498 | 65.5 | 3.8 | 215 | 4 | US-09-270-767-12271 | Sequence 12271, A |
| 426 | 66.5 | 3.9 | 572 | 2 | US-08-745-934-1 | Sequence 1, Appli | 499 | 65.5 | 3.8 | 254 | 4 | US-09-543-681A-7333 | Sequence 7333, Ap |
| 427 | 66.5 | 3.9 | 623 | 4 | US-09-949-016-7573 | Sequence 7573, Ap | 500 | 65.5 | 3.8 | 288 | 4 | US-09-248-796A-21210 | Sequence 21210, A |
| 428 | 66.5 | 3.9 | 676 | 4 | US-09-248-796A-17893 | Sequence 17893, A | 501 | 65.5 | 3.8 | 328 | 4 | US-09-583-110-9898 | Sequence 16494, A |
| 429 | 66.5 | 3.9 | 779 | 1 | US-08-426-627-4 | Sequence 4, Appli | 502 | 65.5 | 3.8 | 334 | 4 | US-09-107-433-0097 | Sequence 3389, Ap |
| 430 | 66.5 | 3.9 | 779 | 4 | US-08-426-627-24 | Sequence 24, Appl | 503 | 65.5 | 3.8 | 365 | 3 | US-09-043-627-8 | Sequence 8, Appli |
| 431 | 66.5 | 3.9 | 779 | 4 | US-09-461-912A-39 | Sequence 39, Appl | 504 | 65.5 | 3.8 | 432 | 4 | US-09-248-796A-19960 | Sequence 19960, A |
| 432 | 66.5 | 3.9 | 895 | 4 | US-09-614-912-194 | Sequence 194, App | 505 | 65.5 | 3.8 | 432 | 4 | US-09-328-352-7223 | Sequence 7223, Ap |
| 433 | 66.5 | 3.9 | 937 | 2 | US-08-469-537A-105 | Sequence 105, App | 506 | 65.5 | 3.8 | 441 | 4 | US-09-438-185A-890 | Sequence 890, App |
| 434 | 66.5 | 3.9 | 1052 | 4 | US-09-949-016-11508 | Sequence 11508, A | 507 | 65.5 | 3.8 | 446 | 4 | US-09-583-110-1634 | Sequence 4634, Ap |
| 435 | 66.5 | 3.9 | 1091 | 4 | US-09-583-110-3823 | Sequence 3823, Ap | 508 | 65.5 | 3.8 | 468 | 4 | US-09-107-433-1560 | Sequence 4660, Ap |
| 436 | 66.5 | 3.9 | 1101 | 4 | US-09-107-433-4859 | Sequence 4859, Ap | 509 | 65.5 | 3.8 | 480 | 2 | US-08-828-488-8 | Sequence 8, Appli |
| 437 | 66.5 | 3.9 | 1218 | 4 | US-09-438-185A-8337 | Sequence 8337, App | 510 | 65.5 | 3.8 | 480 | 3 | US-09-299-689A-8 | Sequence 8, Appli |
| 438 | 66.5 | 3.9 | 1436 | 4 | US-09-578-063-78 | Sequence 78, Appl | 511 | 65.5 | 3.8 | 480 | 3 | US-09-702-705-336 | Sequence 336, App |
| 439 | 66.5 | 3.9 | 1770 | 4 | US-09-538-092-253 | Sequence 263, App | 512 | 65.5 | 3.8 | 480 | 4 | US-09-736-457-336 | Sequence 336, App |
| 440 | 66.5 | 3.9 | 1809 | 3 | US-09-012-515A-12 | Sequence 12, Appl | 513 | 65.5 | 3.8 | 480 | 4 | US-09-614-124B-336 | Sequence 336, App |
| 441 | 66.5 | 3.9 | 1809 | 3 | US-08-360-144A-12 | Sequence 12, Appl | 514 | 65.5 | 3.8 | 480 | 4 | US-09-671-325-336 | Sequence 336, App |
| 442 | 66.5 | 3.9 | 1809 | 3 | US-09-012-504A-12 | Sequence 12, Appl | 515 | 65.5 | 3.8 | 480 | 4 | US-09-589-184-336 | Sequence 336, App |
| 443 | 66.5 | 3.9 | 1809 | 4 | US-09-012-399A-12 | Sequence 12, Appl | 516 | 65.5 | 3.8 | 480 | 4 | US-09-658-824-336 | Sequence 336, App |
| 444 | 66.5 | 3.9 | 2020 | 1 | US-07-551-531-2 | Sequence 2, Appli | 517 | 65.5 | 3.8 | 487 | 4 | US-09-949-016-10509 | Sequence 10509, A |
| 445 | 66.5 | 3.9 | 2485 | 5 | PCT-US94-00198-1 | Sequence 1, Appli | 518 | 65.5 | 3.8 | 487 | 4 | US-09-949-016-8278 | Sequence 8278, Ap |
| 446 | 66.5 | 3.9 | 2485 | 5 | PCT-US94-00198-2 | Sequence 2, Appli | 519 | 65.5 | 3.8 | 522 | 4 | US-09-549-519-34 | Sequence 34, Appl |
| 447 | 66.5 | 3.9 | 2549 | 3 | US-08-471-112A-3 | Sequence 3, Appli | 520 | 65.5 | 3.8 | 523 | 4 | US-09-549-519-35 | Sequence 35, Appl |
| 448 | 66.5 | 3.9 | 2549 | 3 | US-08-265-967C-1 | Sequence 1, Appli | 521 | 65.5 | 3.8 | 530 | 4 | US-09-949-016-6085 | Sequence 6085, Ap |
| 449 | 66.5 | 3.9 | 2549 | 4 | US-08-305-790B-2 | Sequence 2, Appli | 522 | 65.5 | 3.8 | 554 | 4 | US-09-949-016-8533 | Sequence 8532, Ap |
| 450 | 66.5 | 3.9 | 2549 | 4 | US-09-950-634-3 | Sequence 3, Appli | 523 | 65.5 | 3.8 | 554 | 4 | US-09-949-016-8533 | Sequence 8533, Ap |
| 451 | 66.5 | 3.9 | 2549 | 5 | US-09-538-093-1112 | Sequence 1112, Ap | 524 | 65.5 | 3.8 | 554 | 4 | US-09-949-016-9420 | Sequence 9420, Ap |
| 452 | 66.5 | 3.9 | 2549 | 5 | PCT-US95-06722-12 | Sequence 12, Appl | 525 | 65.5 | 3.8 | 554 | 4 | US-09-949-016-9421 | Sequence 9421, Ap |
| 453 | 66.5 | 3.9 | 2818 | 1 | US-08-510-284-1 | Sequence 1, Appli | 526 | 65.5 | 3.8 | 600 | 4 | US-09-543-681A-1496 | Sequence 1496, Ap |
| 454 | 66.5 | 3.9 | 2818 | 1 | US-08-411-389-2 | Sequence 2, Appli | 527 | 65.5 | 3.8 | 605 | 4 | US-09-543-681A-1496 | Sequence 1496, Ap |
| 455 | 66.5 | 3.9 | 2818 | 2 | US-08-449-933-2 | Sequence 2, Appli | 528 | 65.5 | 3.8 | 650 | 4 | US-09-620-405B-469 | Sequence 469, App |
| 456 | 66.5 | 3.9 | 2818 | 3 | US-07-966-049A-2 | Sequence 2, Appli | 529 | 65.5 | 3.8 | 650 | 4 | US-09-620-405B-469 | Sequence 469, App |
| 457 | 66.5 | 3.9 | 3898 | 3 | US-08-750-717-2 | Sequence 2, Appli | 530 | 65.5 | 3.8 | 650 | 4 | US-09-433-826B-469 | Sequence 469, App |
| 458 | 66.5 | 3.9 | 233 | 1 | US-08-015-985-11 | Sequence 11, Appl | 531 | 65.5 | 3.8 | 650 | 4 | US-09-604-287A-469 | Sequence 469, App |
| 459 | 66.5 | 3.9 | 233 | 4 | US-09-280-597-11 | Sequence 11, Appl | 532 | 65.5 | 3.8 | 650 | 4 | US-09-834-759-469 | Sequence 469, App |
| 460 | 66.5 | 3.9 | 327 | 4 | US-09-270-767-43979 | Sequence 43979, A | 533 | 65.5 | 3.8 | 650 | 4 | US-09-590-751A-469 | Sequence 469, App |
| 461 | 66.5 | 3.9 | 350 | 4 | US-09-270-767-42267 | Sequence 42267, A | 534 | 65.5 | 3.8 | 667 | 4 | US-09-551-621-469 | Sequence 469, App |
| 462 | 66.5 | 3.9 | 431 | 1 | US-08-311-023-2 | Sequence 2, Appli | 535 | 65.5 | 3.8 | 743 | 4 | US-09-902-540-16440 | Sequence 16440, A |
| 463 | 66.5 | 3.9 | 448 | 4 | US-09-198-452A-216 | Sequence 216, App | 536 | 65.5 | 3.8 | 743 | 4 | US-09-620-405B-494 | Sequence 494, App |
| 464 | 66.5 | 3.9 | 455 | 3 | US-08-91A-375C-62 | Sequence 62, Appl | 537 | 65.5 | 3.8 | 817 | 4 | US-09-710-879-2948 | Sequence 2948, Ap |
| 465 | 66.5 | 3.9 | 457 | 4 | US-09-438-185A-199 | Sequence 199, App | 538 | 65.5 | 3.8 | 818 | 4 | US-09-538-092-323 | Sequence 323, App |

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|-----|------|-----|------|---|----------------------|--------------------|-----|------|-----|------|---|----------------------|--------------------|
| 539 | 65 | 3.8 | 880 | 4 | US-09-538-092-601 | Sequence 601, App | 612 | 64.5 | 3.8 | 1403 | 4 | US-09-262-537-6 | Sequence 6, App11 |
| 540 | 65 | 3.8 | 886 | 3 | US-09-134-001C-4496 | Sequence 4496, Ap | 613 | 64.5 | 3.8 | 1957 | 4 | US-08-669-656A-2 | Sequence 2, App11 |
| 541 | 65 | 3.8 | 928 | 4 | US-09-336-946B-2 | Sequence 2, App11 | 614 | 64.5 | 3.8 | 2227 | 3 | US-08-475-886-2 | Sequence 2, App11 |
| 542 | 65 | 3.8 | 928 | 4 | US-09-336-946B-4 | Sequence 4, App11 | 615 | 64.5 | 3.8 | 2227 | 3 | US-08-475-886-6 | Sequence 6, App11 |
| 543 | 65 | 3.8 | 928 | 4 | US-09-993-170-58 | Sequence 58, App1 | 615 | 64.5 | 3.8 | 2227 | 3 | US-08-397-232-2 | Sequence 2, App11 |
| 544 | 65 | 3.8 | 1002 | 4 | US-09-620-405B-475 | Sequence 475, App | 616 | 64.5 | 3.8 | 2227 | 3 | US-08-397-232-4 | Sequence 4, App11 |
| 545 | 65 | 3.8 | 1002 | 4 | US-09-604-287A-475 | Sequence 475, App | 617 | 64.5 | 3.8 | 2227 | 3 | US-09-171-387-2 | Sequence 2, App11 |
| 546 | 65 | 3.8 | 1002 | 4 | US-09-834-759-475 | Sequence 475, App | 618 | 64.5 | 3.8 | 2227 | 3 | US-09-653-499-2 | Sequence 2, App11 |
| 547 | 65 | 3.8 | 1002 | 4 | US-09-590-751A-475 | Sequence 475, App | 619 | 64.5 | 3.8 | 2227 | 4 | US-09-653-499-6 | Sequence 6, App11 |
| 548 | 65 | 3.8 | 1002 | 4 | US-09-551-621-475 | Sequence 475, App | 620 | 64.5 | 3.8 | 2227 | 4 | US-10-135-988-2 | Sequence 2, App11 |
| 549 | 65 | 3.8 | 1019 | 1 | US-08-296-014A-4 | Sequence 4, App11 | 621 | 64.5 | 3.8 | 2227 | 4 | US-10-135-988-6 | Sequence 6, App11 |
| 550 | 65 | 3.8 | 1019 | 2 | US-08-596-405-4 | Sequence 4, App11 | 622 | 64.5 | 3.8 | 2227 | 4 | US-09-219-983A-7 | Sequence 7, App11 |
| 551 | 65 | 3.8 | 1019 | 2 | US-08-877-620-4 | Sequence 4, App11 | 623 | 64 | 3.8 | 203 | 4 | US-09-248-796A-15374 | Sequence 15374, A |
| 552 | 65 | 3.8 | 1019 | 4 | US-09-287-368-4 | Sequence 4, App11 | 624 | 64 | 3.8 | 324 | 4 | US-09-248-796A-15351 | Sequence 15351, A |
| 553 | 65 | 3.8 | 1019 | 4 | US-09-626-795-4 | Sequence 4, App11 | 625 | 64 | 3.8 | 350 | 4 | US-09-248-796A-16614 | Sequence 16614, A |
| 554 | 65 | 3.8 | 1048 | 4 | US-08-887-534A-85 | Sequence 85, App1 | 626 | 64 | 3.8 | 413 | 4 | US-09-252-991A-26309 | Sequence 26309, A |
| 555 | 65 | 3.8 | 1048 | 4 | US-09-527-431-85 | Sequence 85, App1 | 627 | 64 | 3.8 | 418 | 4 | US-09-743-742B-5 | Sequence 5, App11 |
| 556 | 65 | 3.8 | 1048 | 4 | US-09-446-861-85 | Sequence 85, App1 | 628 | 64 | 3.8 | 418 | 4 | US-09-826-509-535 | Sequence 535, App |
| 557 | 65 | 3.8 | 1049 | 2 | US-08-817-090B-2 | Sequence 85, App1 | 629 | 64 | 3.8 | 466 | 4 | US-09-620-405B-472 | Sequence 472, App |
| 558 | 65 | 3.8 | 1065 | 4 | US-09-328-352-8064 | Sequence 8064, Ap | 630 | 64 | 3.8 | 466 | 4 | US-09-433-826B-472 | Sequence 472, App |
| 559 | 65 | 3.8 | 1095 | 4 | US-09-834-759-493 | Sequence 493, App | 631 | 64 | 3.8 | 466 | 4 | US-09-604-287A-472 | Sequence 472, App |
| 560 | 65 | 3.8 | 1095 | 4 | US-08-726-214-16 | Sequence 16, App1 | 632 | 64 | 3.8 | 466 | 4 | US-09-590-751A-472 | Sequence 472, App |
| 561 | 65 | 3.8 | 1248 | 3 | US-08-864-785-2 | Sequence 12, App1 | 633 | 64 | 3.8 | 466 | 4 | US-09-551-621-472 | Sequence 472, App |
| 562 | 65 | 3.8 | 1253 | 1 | US-08-252-966B-12 | Sequence 12, App1 | 634 | 64 | 3.8 | 466 | 4 | US-09-489-039A-13282 | Sequence 13282, A |
| 563 | 65 | 3.8 | 1253 | 1 | US-08-864-785-2 | Sequence 12, App1 | 635 | 64 | 3.8 | 574 | 4 | US-09-949-016-11325 | Sequence 11325, A |
| 564 | 65 | 3.8 | 1261 | 1 | US-08-252-966B-18 | Sequence 18, App1 | 637 | 64 | 3.8 | 594 | 4 | US-09-650-324A-59 | Sequence 59, App1 |
| 565 | 65 | 3.8 | 1261 | 1 | US-08-755-587-185 | Sequence 185, App | 638 | 64 | 3.8 | 730 | 4 | US-09-071-035-364 | Sequence 364, App |
| 566 | 65 | 3.8 | 1909 | 4 | US-09-590-968B-2 | Sequence 2, App11 | 639 | 64 | 3.8 | 766 | 4 | US-09-071-035-362 | Sequence 362, App |
| 567 | 64.5 | 3.8 | 1117 | 4 | US-09-248-796A-16571 | Sequence 16571, A | 640 | 64 | 3.8 | 776 | 4 | US-09-134-000C-5717 | Sequence 5717, App |
| 568 | 64.5 | 3.8 | 214 | 4 | US-09-248-796A-21132 | Sequence 21132, A | 641 | 64 | 3.8 | 817 | 4 | US-09-248-796A-19402 | Sequence 19402, A |
| 569 | 64.5 | 3.8 | 214 | 1 | US-07-739-642-12 | Sequence 12, App1 | 642 | 64 | 3.8 | 844 | 4 | US-09-949-016-9638 | Sequence 9438, App |
| 570 | 64.5 | 3.8 | 214 | 1 | US-07-739-642-12 | Sequence 12, App1 | 643 | 64 | 3.8 | 878 | 3 | US-09-735-934A-2 | Sequence 2, App11 |
| 571 | 64.5 | 3.8 | 214 | 1 | US-07-739-642-12 | Sequence 12, App1 | 644 | 64 | 3.8 | 878 | 3 | US-10-060-332-2 | Sequence 2, App11 |
| 572 | 64.5 | 3.8 | 228 | 4 | US-09-593-887-24 | Sequence 24, App1 | 645 | 64 | 3.8 | 878 | 4 | US-10-333-657-2 | Sequence 2, App11 |
| 573 | 64.5 | 3.8 | 254 | 4 | US-09-902-540-10099 | Sequence 10099, A | 646 | 64 | 3.8 | 931 | 4 | US-09-079-592-11 | Sequence 11, App1 |
| 574 | 64.5 | 3.8 | 296 | 4 | US-09-949-016-11136 | Sequence 11136, A | 647 | 64 | 3.8 | 987 | 1 | US-08-436-044-6 | Sequence 6, App11 |
| 575 | 64.5 | 3.8 | 312 | 3 | US-09-328-352-4582 | Sequence 4582, Ap | 648 | 64 | 3.8 | 987 | 2 | US-08-436-054-6 | Sequence 6, App11 |
| 576 | 64.5 | 3.8 | 312 | 3 | US-09-216-295-21 | Sequence 21, App1 | 649 | 64 | 3.8 | 987 | 5 | PCT-US95-08812-6 | Sequence 6, App11 |
| 577 | 64.5 | 3.8 | 371 | 3 | US-09-104-308-1 | Sequence 1, App11 | 650 | 64 | 3.8 | 987 | 5 | US-09-949-016-7235 | Sequence 7235, App |
| 578 | 64.5 | 3.8 | 371 | 3 | US-09-321-981-1 | Sequence 1, App11 | 651 | 64 | 3.8 | 990 | 4 | US-08-836-335-2 | Sequence 2, App11 |
| 579 | 64.5 | 3.8 | 371 | 4 | US-09-739-861A-1 | Sequence 1, App11 | 652 | 64 | 3.8 | 1011 | 3 | US-09-457-571-2 | Sequence 2, App11 |
| 580 | 64.5 | 3.8 | 371 | 4 | US-09-795-583-1 | Sequence 1, App11 | 653 | 64 | 3.8 | 1011 | 3 | US-08-480-474-11 | Sequence 11, App1 |
| 581 | 64.5 | 3.8 | 371 | 4 | US-09-632-570-21 | Sequence 21, App1 | 654 | 64 | 3.8 | 1078 | 3 | US-09-949-016-6874 | Sequence 6874, App |
| 582 | 64.5 | 3.8 | 371 | 4 | US-09-632-575-51 | Sequence 51, App1 | 655 | 64 | 3.8 | 1165 | 4 | US-09-949-016-11392 | Sequence 11392, A |
| 583 | 64.5 | 3.8 | 386 | 1 | US-08-758-213-1 | Sequence 1, App11 | 656 | 64 | 3.8 | 1165 | 4 | US-08-222-616-24 | Sequence 24, App1 |
| 584 | 64.5 | 3.8 | 386 | 2 | US-08-692-787-48 | Sequence 48, App1 | 657 | 64 | 3.8 | 1276 | 1 | US-08-446-648-24 | Sequence 24, App1 |
| 585 | 64.5 | 3.8 | 386 | 3 | US-09-097-199-48 | Sequence 5, App11 | 658 | 64 | 3.8 | 1276 | 5 | PCT-US95-04228-24 | Sequence 24, App1 |
| 586 | 64.5 | 3.8 | 386 | 3 | US-09-321-981-5 | Sequence 5, App11 | 659 | 64 | 3.8 | 1276 | 5 | US-08-836-335-10 | Sequence 10, App1 |
| 587 | 64.5 | 3.8 | 386 | 4 | US-09-739-861A-5 | Sequence 5, App11 | 660 | 64 | 3.8 | 1984 | 3 | US-09-457-571-10 | Sequence 10, App1 |
| 588 | 64.5 | 3.8 | 386 | 4 | US-09-795-583-5 | Sequence 5, App11 | 661 | 64 | 3.8 | 1984 | 4 | US-08-737-248-9 | Sequence 9, App11 |
| 589 | 64.5 | 3.8 | 386 | 4 | US-09-949-016-6022 | Sequence 235, App | 662 | 64 | 3.8 | 199 | 3 | US-09-134-001C-4727 | Sequence 4727, App |
| 590 | 64.5 | 3.8 | 404 | 4 | US-09-482-273-235 | Sequence 7294, Ap | 663 | 64 | 3.8 | 223 | 2 | US-08-771-455-2 | Sequence 2, App11 |
| 591 | 64.5 | 3.8 | 480 | 4 | US-09-107-532A-7294 | Sequence 2, App11 | 664 | 64 | 3.8 | 223 | 2 | US-08-889-425-2 | Sequence 2, App11 |
| 592 | 64.5 | 3.8 | 515 | 2 | US-09-146-283-2 | Sequence 2, App11 | 665 | 64 | 3.8 | 262 | 3 | US-09-949-016-6754 | Sequence 6754, App |
| 593 | 64.5 | 3.8 | 515 | 3 | US-08-579-823A-2 | Sequence 2, App11 | 666 | 64 | 3.8 | 374 | 4 | US-09-543-681A-5052 | Sequence 5052, App |
| 594 | 64.5 | 3.8 | 515 | 3 | US-09-344-195-2 | Sequence 2, App11 | 667 | 64 | 3.8 | 374 | 4 | US-08-846-762-85 | Sequence 85, App1 |
| 595 | 64.5 | 3.8 | 524 | 4 | US-09-252-991A-27006 | Sequence 27006, A | 668 | 64 | 3.8 | 374 | 4 | US-09-328-352-7608 | Sequence 7608, App |
| 596 | 64.5 | 3.8 | 543 | 4 | US-09-252-991A-27586 | Sequence 46218, A | 669 | 64 | 3.8 | 374 | 4 | US-09-107-532A-1894 | Sequence 48290, A |
| 597 | 64.5 | 3.8 | 553 | 4 | US-09-270-767-46218 | Sequence 46218, A | 670 | 64 | 3.8 | 435 | 4 | US-09-270-767-462290 | Sequence 48290, A |
| 598 | 64.5 | 3.8 | 568 | 4 | US-09-520-822A-3 | Sequence 9861, App | 671 | 64 | 3.8 | 435 | 4 | US-09-270-767-462290 | Sequence 48290, A |
| 599 | 64.5 | 3.8 | 568 | 4 | US-09-489-039A-8861 | Sequence 11109, A | 672 | 64 | 3.8 | 435 | 4 | US-09-270-767-462290 | Sequence 48290, A |
| 600 | 64.5 | 3.8 | 878 | 4 | US-09-949-016-11109 | Sequence 11109, A | 673 | 64 | 3.8 | 435 | 4 | US-09-270-767-462290 | Sequence 48290, A |
| 601 | 64.5 | 3.8 | 913 | 1 | US-08-220-151-6 | Sequence 6, App11 | 674 | 64 | 3.8 | 435 | 4 | US-09-270-767-462290 | Sequence 48290, A |
| 602 | 64.5 | 3.8 | 913 | 1 | US-08-413-118-6 | Sequence 6, App11 | 675 | 64 | 3.8 | 435 | 4 | US-09-270-767-462290 | Sequence 48290, A |
| 603 | 64.5 | 3.8 | 913 | 6 | US-08-473-446-6 | Sequence 6, App11 | 676 | 64 | 3.8 | 435 | 4 | US-09-270-767-462290 | Sequence 48290, A |
| 604 | 64.5 | 3.8 | 913 | 6 | US-08-473-446-6 | Sequence 6, App11 | 677 | 64 | 3.8 | 435 | 4 | US-09-270-767-462290 | Sequence 48290, A |
| 605 | 64.5 | 3.8 | 913 | 6 | US-08-473-446-6 | Sequence 6, App11 | 678 | 64 | 3.8 | 435 | 4 | US-09-270-767-462290 | Sequence 48290, A |
| 606 | 64.5 | 3.8 | 913 | 6 | US-08-473-446-6 | Sequence 6, App11 | 679 | 64 | 3.8 | 435 | 4 | US-09-270-767-462290 | Sequence 48290, A |
| 607 | 64.5 | 3.8 | 1052 | 3 | US-08-863-118-2 | Sequence 2, App11 | 680 | 64 | 3.8 | 501 | 4 | US-09-905-125A-185 | Sequence 185, App |
| 608 | 64.5 | 3.8 | 1261 | 3 | US-08-937-236-3 | Sequence 3, App11 | 681 | 64 | 3.8 | 501 | 4 | US-09-905-125A-185 | Sequence 185, App |
| 609 | 64.5 | 3.8 | 1291 | 3 | US-08-569-214-3 | Sequence 3, App11 | 682 | 64 | 3.8 | 501 | 4 | US-09-905-125A-185 | Sequence 185, App |
| 610 | 64.5 | 3.8 | 1291 | 3 | US-08-937-236-2 | Sequence 2, App11 | 683 | 64 | 3.8 | 501 | 4 | US-09-905-125A-185 | Sequence 185, App |
| 611 | 64.5 | 3.8 | 1295 | 3 | US-08-569-214-2 | Sequence 2, App11 | 684 | 64 | 3.8 | 501 | 4 | US-09-905-125A-185 | Sequence 185, App |

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| 685 | 63.5 | 3.7 | 501 | 4 | US-09-909-064-185 | Sequence 185, App | 758 | 63 | 3.7 | 552 | 3 | US-08-851-843A-4 | Sequence 4, Appli |
| 686 | 63.5 | 3.7 | 501 | 4 | US-09-905-381A-185 | Sequence 185, App | 759 | 63 | 3.7 | 552 | 3 | US-08-854-050-4 | Sequence 4, Appli |
| 687 | 63.5 | 3.7 | 501 | 4 | US-09-906-618-185 | Sequence 185, App | 760 | 63 | 3.7 | 552 | 3 | US-09-430-323-4 | Sequence 4, Appli |
| 688 | 63.5 | 3.7 | 502 | 4 | US-09-252-991A-20651 | Sequence 20651, A | 761 | 63 | 3.7 | 552 | 4 | US-09-766-253-4 | Sequence 4, Appli |
| 689 | 63.5 | 3.7 | 505 | 1 | US-08-220-603A-10 | Sequence 10, Appli | 762 | 63 | 3.7 | 562 | 6 | 5258502-2 | Patent No. 5258502 |
| 690 | 63.5 | 3.7 | 522 | 3 | US-08-821-984-10 | Sequence 10, Appli | 763 | 63 | 3.7 | 562 | 6 | 5258502-2 | Patent No. 5258502 |
| 691 | 63.5 | 3.7 | 522 | 3 | US-09-329-749-10 | Sequence 10, Appli | 764 | 63 | 3.7 | 621 | 4 | US-09-385-219A-56 | Sequence 56, Appli |
| 692 | 63.5 | 3.7 | 522 | 4 | US-09-502-264-10 | Sequence 10, Appli | 765 | 63 | 3.7 | 621 | 4 | US-09-949-016-11582 | Sequence 11582, A |
| 693 | 63.5 | 3.7 | 540 | 4 | US-09-107-532A-5467 | Sequence 5467, Ap | 766 | 63 | 3.7 | 638 | 4 | US-09-900-540-11575 | Sequence 11575, A |
| 694 | 63.5 | 3.7 | 567 | 1 | US-08-361-873A-2 | Sequence 2, Appli | 767 | 63 | 3.7 | 641 | 1 | US-08-441-139-4 | Sequence 139-4 |
| 695 | 63.5 | 3.7 | 567 | 2 | US-08-483-926A-1 | Sequence 1, Appli | 768 | 63 | 3.7 | 746 | 4 | US-09-248-796A-15023 | Sequence 15023, A |
| 696 | 63.5 | 3.7 | 567 | 2 | US-08-854-768-1 | Sequence 1, Appli | 769 | 63 | 3.7 | 756 | 4 | US-09-248-796A-14736 | Sequence 14736, A |
| 697 | 63.5 | 3.7 | 567 | 2 | US-08-445-520B-9 | Sequence 9, Appli | 770 | 63 | 3.7 | 770 | 1 | US-08-369-796-12 | Sequence 12, Appli |
| 698 | 63.5 | 3.7 | 567 | 2 | US-08-737-045-1 | Sequence 1, Appli | 771 | 63 | 3.7 | 770 | 2 | US-08-850-091-12 | Sequence 12, Appli |
| 699 | 63.5 | 3.7 | 567 | 3 | US-08-451-946B-8 | Sequence 8, Appli | 772 | 63 | 3.7 | 770 | 2 | US-08-820-754-12 | Sequence 12, Appli |
| 700 | 63.5 | 3.7 | 567 | 3 | US-08-446-938B-8 | Sequence 8, Appli | 773 | 63 | 3.7 | 770 | 3 | US-08-956-652-12 | Sequence 12, Appli |
| 701 | 63.5 | 3.7 | 567 | 3 | US-08-311-703A-8 | Sequence 8, Appli | 774 | 63 | 3.7 | 770 | 3 | US-08-956-869-12 | Sequence 12, Appli |
| 702 | 63.5 | 3.7 | 567 | 3 | US-08-446-939B-8 | Sequence 8, Appli | 775 | 63 | 3.7 | 770 | 3 | US-08-948-547-12 | Sequence 12, Appli |
| 703 | 63.5 | 3.7 | 567 | 3 | US-09-183-543-8 | Sequence 8, Appli | 776 | 63 | 3.7 | 770 | 3 | US-08-948-547-12 | Sequence 12, Appli |
| 704 | 63.5 | 3.7 | 567 | 3 | US-08-446-936A-8 | Sequence 8, Appli | 777 | 63 | 3.7 | 770 | 3 | US-09-364-970-3 | Sequence 3, Appli |
| 705 | 63.5 | 3.7 | 567 | 4 | US-09-239-864A-11 | Sequence 11, Appli | 778 | 63 | 3.7 | 770 | 3 | US-08-956-653A-12 | Sequence 12, Appli |
| 706 | 63.5 | 3.7 | 567 | 4 | US-09-878-905-11 | Sequence 11, Appli | 779 | 63 | 3.7 | 770 | 4 | US-08-212-185-12 | Sequence 12, Appli |
| 707 | 63.5 | 3.7 | 567 | 4 | US-09-267-963D-36 | Sequence 36, Appli | 780 | 63 | 3.7 | 770 | 5 | PCT-US95-17025-12 | Sequence 12, Appli |
| 708 | 63.5 | 3.7 | 567 | 4 | PCT-US92-09326-4 | Sequence 4, Appli | 781 | 63 | 3.7 | 787 | 4 | US-09-825-294-207 | Sequence 207, App |
| 709 | 63.5 | 3.7 | 572 | 5 | PCT-US91-08177-11 | Sequence 11, Appli | 782 | 63 | 3.7 | 787 | 4 | US-09-970-966-207 | Sequence 207, App |
| 710 | 63.5 | 3.7 | 593 | 4 | US-09-270-767-41549 | Sequence 41549, A | 783 | 63 | 3.7 | 793 | 4 | US-09-313-942-12 | Sequence 32, Appli |
| 711 | 63.5 | 3.7 | 661 | 4 | US-09-540-236-3743 | Sequence 3743, Ap | 784 | 63 | 3.7 | 801 | 4 | US-09-248-796A-18375 | Sequence 18375, A |
| 712 | 63.5 | 3.7 | 839 | 4 | US-09-949-041-10846 | Sequence 10846, A | 785 | 63 | 3.7 | 846 | 3 | US-08-885-221-55 | Sequence 55, Appli |
| 713 | 63.5 | 3.7 | 871 | 3 | US-09-245-041-19 | Sequence 19, Appli | 786 | 63 | 3.7 | 846 | 3 | US-09-107-847-2 | Sequence 2, Appli |
| 714 | 63.5 | 3.7 | 871 | 4 | US-09-358-055B-19 | Sequence 19, Appli | 787 | 63 | 3.7 | 846 | 3 | US-09-496-672-55 | Sequence 55, Appli |
| 715 | 63.5 | 3.7 | 871 | 4 | US-09-893-238-19 | Sequence 19, Appli | 788 | 63 | 3.7 | 851 | 1 | US-08-369-796-12 | Sequence 12, Appli |
| 716 | 63.5 | 3.7 | 926 | 1 | US-08-159-340A-2 | Sequence 2, Appli | 789 | 63 | 3.7 | 851 | 2 | US-08-852-091-2 | Sequence 2, Appli |
| 717 | 63.5 | 3.7 | 1041 | 3 | US-08-898-978-2 | Sequence 2, Appli | 790 | 63 | 3.7 | 851 | 2 | US-08-820-754-2 | Sequence 2, Appli |
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| 719 | 63.5 | 3.7 | 1350 | 3 | US-09-245-041-17 | Sequence 17, Appli | 792 | 63 | 3.7 | 851 | 3 | US-08-956-652-2 | Sequence 2, Appli |
| 720 | 63.5 | 3.7 | 1350 | 4 | US-09-358-055B-17 | Sequence 17, Appli | 793 | 63 | 3.7 | 851 | 3 | US-09-012-710-2 | Sequence 2, Appli |
| 721 | 63.5 | 3.7 | 1350 | 4 | US-09-893-238-17 | Sequence 17, Appli | 794 | 63 | 3.7 | 851 | 3 | US-08-948-547-2 | Sequence 2, Appli |
| 722 | 63.5 | 3.7 | 1391 | 4 | US-09-538-092-250 | Sequence 250, App | 795 | 63 | 3.7 | 851 | 3 | US-09-087-465-4 | Sequence 4, Appli |
| 723 | 63.5 | 3.7 | 1463 | 1 | US-08-220-603A-11 | Sequence 11, Appli | 796 | 63 | 3.7 | 851 | 3 | US-09-364-970-2 | Sequence 2, Appli |
| 724 | 63.5 | 3.7 | 1487 | 4 | US-09-489-039A-12113 | Sequence 12113, A | 797 | 63 | 3.7 | 851 | 3 | US-09-556-273-2 | Sequence 2, Appli |
| 725 | 63.5 | 3.7 | 1956 | 3 | US-08-843-417-2 | Sequence 2, Appli | 798 | 63 | 3.7 | 851 | 3 | US-08-956-653A-2 | Sequence 2, Appli |
| 726 | 63.5 | 3.7 | 1956 | 4 | US-09-527-013-2 | Sequence 2, Appli | 799 | 63 | 3.7 | 851 | 4 | US-09-972-800A-4 | Sequence 4, Appli |
| 727 | 63.5 | 3.7 | 1956 | 4 | US-08-669-656A-8 | Sequence 8, Appli | 800 | 63 | 3.7 | 851 | 4 | US-08-212-185-2 | Sequence 2, Appli |
| 728 | 63.5 | 3.7 | 2132 | 4 | US-08-669-656A-6 | Sequence 6, Appli | 801 | 63 | 3.7 | 851 | 5 | PCT-US95-17025-2 | Sequence 2, Appli |
| 729 | 63.5 | 3.7 | 2227 | 4 | US-10-104-966-12 | Sequence 12, Appli | 802 | 63 | 3.7 | 852 | 1 | US-08-276-099A-13 | Sequence 13, Appli |
| 730 | 63.5 | 3.7 | 2813 | 3 | US-08-896-449A-2 | Sequence 2, Appli | 803 | 63 | 3.7 | 852 | 1 | US-08-781-890-13 | Sequence 13, Appli |
| 731 | 63.5 | 3.7 | 2813 | 3 | US-09-133-652-2 | Sequence 2, Appli | 804 | 63 | 3.7 | 856 | 4 | US-09-152-060-77 | Sequence 77, Appli |
| 732 | 63.5 | 3.7 | 2813 | 4 | US-09-886-900A-2 | Sequence 2, Appli | 805 | 63 | 3.7 | 939 | 4 | US-09-248-796A-16082 | Sequence 16082, A |
| 733 | 63.5 | 3.7 | 2813 | 4 | US-09-662-478C-2 | Sequence 2, Appli | 806 | 63 | 3.7 | 1014 | 4 | US-10-101-464A-807 | Sequence 807, App |
| 734 | 63.5 | 3.7 | 3730 | 4 | US-09-949-016-9908 | Sequence 9908, Ap | 807 | 63 | 3.7 | 1045 | 4 | US-09-949-016-11112 | Sequence 11112, A |
| 735 | 63.5 | 3.7 | 166 | 3 | US-08-916-576B-6 | Sequence 6, Appli | 808 | 63 | 3.7 | 1151 | 4 | US-09-023-905A-4 | Sequence 4, Appli |
| 736 | 63 | 3.7 | 166 | 4 | US-10-078-337-6 | Sequence 4293, Ap | 809 | 63 | 3.7 | 1162 | 2 | US-08-599-455B-43 | Sequence 43, Appli |
| 737 | 63 | 3.7 | 203 | 4 | US-09-328-335-4293 | Sequence 8937, Ap | 810 | 63 | 3.7 | 1162 | 3 | US-09-059-781B-43 | Sequence 43, Appli |
| 738 | 63 | 3.7 | 204 | 4 | US-09-489-039A-8937 | Sequence 27421, A | 811 | 63 | 3.7 | 1162 | 3 | US-09-137-132-43 | Sequence 43, Appli |
| 739 | 63 | 3.7 | 225 | 4 | US-09-252-991A-27421 | Sequence 27421, A | 812 | 63 | 3.7 | 1162 | 3 | US-08-864-564A-43 | Sequence 43, Appli |
| 740 | 63 | 3.7 | 259 | 4 | US-09-328-352-4873 | Sequence 8048, Ap | 813 | 63 | 3.7 | 1162 | 4 | US-09-094-410-43 | Sequence 43, Appli |
| 741 | 63 | 3.7 | 307 | 4 | US-09-489-039A-8048 | Sequence 14618, A | 814 | 63 | 3.7 | 1162 | 4 | US-08-708-123D-43 | Sequence 43, Appli |
| 742 | 63 | 3.7 | 314 | 4 | US-09-248-796A-14618 | Sequence 6587, Ap | 815 | 63 | 3.7 | 1162 | 4 | US-08-638-524B-43 | Sequence 43, Appli |
| 743 | 63 | 3.7 | 320 | 4 | US-09-949-016-6587 | Sequence 6587, Ap | 816 | 63 | 3.7 | 1172 | 1 | US-08-313-288B-19 | Sequence 19, Appli |
| 744 | 63 | 3.7 | 323 | 4 | US-09-489-039A-8083 | Sequence 8083, Ap | 817 | 63 | 3.7 | 1172 | 4 | US-09-949-016-6333 | Sequence 6333, Ap |
| 745 | 63 | 3.7 | 331 | 4 | US-09-270-767-41873 | Sequence 41873, A | 818 | 63 | 3.7 | 1172 | 4 | US-09-949-016-10545 | Sequence 10545, A |
| 746 | 63 | 3.7 | 335 | 1 | US-08-085-122-13 | Sequence 23, Appli | 819 | 63 | 3.7 | 1453 | 1 | US-08-308-872B-6 | Sequence 8, Appli |
| 747 | 63 | 3.7 | 335 | 4 | US-08-442-108B-23 | Sequence 118, App | 820 | 63 | 3.7 | 1493 | 3 | US-09-433-890-8 | Sequence 4, Appli |
| 748 | 63 | 3.7 | 335 | 4 | US-09-543-681A-4369 | Sequence 4369, Ap | 821 | 63 | 3.7 | 1593 | 3 | US-08-638-829-4 | Sequence 4, Appli |
| 749 | 63 | 3.7 | 384 | 4 | US-09-152-060-118 | Sequence 976, App | 822 | 63 | 3.7 | 2362 | 1 | US-09-999-016-8985 | Sequence 8885, Ap |
| 750 | 63 | 3.7 | 385 | 4 | US-09-198-452A-976 | Sequence 976, App | 823 | 63 | 3.7 | 3056 | 1 | US-08-508-836A-8 | Sequence 8, Appli |
| 751 | 63 | 3.7 | 391 | 4 | US-09-438-185A-905 | Sequence 905, App | 824 | 63 | 3.7 | 3056 | 2 | US-08-629-001A-3 | Sequence 3, Appli |
| 752 | 63 | 3.7 | 393 | 4 | US-09-634-238-274 | Sequence 274, App | 825 | 63 | 3.7 | 3056 | 3 | US-08-642-274D-3 | Sequence 3, Appli |
| 753 | 63 | 3.7 | 398 | 4 | US-09-489-039A-10213 | Sequence 10213, A | 826 | 63 | 3.7 | 3056 | 3 | US-08-952-127-3 | Sequence 3, Appli |
| 754 | 63 | 3.7 | 413 | 3 | US-09-134-001C-40582 | Sequence 4058, Ap | 827 | 63 | 3.7 | 3056 | 3 | US-08-952-014C-3 | Sequence 3, Appli |
| 755 | 63 | 3.7 | 485 | 4 | US-09-949-016-10882 | Sequence 10882, A | 828 | 63 | 3.7 | 4544 | 1 | US-08-469-486-52 | Sequence 52, Appli |
| 756 | 63 | 3.7 | 488 | 4 | US-09-949-016-9120 | Sequence 9120, Ap | 829 | 63 | 3.7 | 4544 | 2 | US-08-469-658-52 | Sequence 52, Appli |
| 757 | 63 | 3.7 | 551 | 4 | US-09-543-681A-4462 | Sequence 4462, Ap | 830 | 62.5 | 3.7 | 151 | 4 | US-09-270-767-37639 | Sequence 37639, A |

| | | | | | | | | | | | | | |
|-----|------|-----|------|---|----------------------|--------------------|-----|------|-----|------|---|----------------------|-------------------|
| 831 | 62.5 | 3.7 | 151 | 4 | US-09-270-767-52856 | Sequence 52856, A | 904 | 62.5 | 3.7 | 1454 | 4 | US-09-854-799-26 | Sequence 26, Appl |
| 832 | 62.5 | 3.7 | 176 | 4 | US-09-328-352-5939 | Sequence 5939, Ap | 905 | 62.5 | 3.7 | 1454 | 5 | PCR-US91-08525-26 | Sequence 26, Appl |
| 833 | 62.5 | 3.7 | 180 | 4 | US-09-328-352-5939 | Sequence 5939, Ap | 906 | 62.5 | 3.7 | 1454 | 5 | PCR-US91-08525-26 | Sequence 26, Appl |
| 834 | 62.5 | 3.7 | 191 | 4 | US-09-621-976-4640 | Sequence 4640, Ap | 907 | 62.5 | 3.7 | 1827 | 4 | US-09-443-780C-14 | Sequence 14, Appl |
| 835 | 62.5 | 3.7 | 205 | 4 | US-09-248-796A-22069 | Sequence 22069, A | 908 | 62.5 | 3.7 | 1827 | 4 | US-09-443-780C-14 | Sequence 14, Appl |
| 836 | 62.5 | 3.7 | 286 | 4 | US-09-248-796A-22818 | Sequence 22818, A | 909 | 62.5 | 3.7 | 2475 | 3 | US-09-413-814-48 | Sequence 48, Appl |
| 837 | 62.5 | 3.7 | 288 | 4 | US-09-270-767-35019 | Sequence 35019, A | 910 | 62.5 | 3.7 | 2492 | 3 | US-09-991-258-3 | Sequence 3, Appl |
| 838 | 62.5 | 3.7 | 288 | 4 | US-09-270-767-50236 | Sequence 50236, A | 911 | 62.5 | 3.7 | 2710 | 1 | US-08-480-604A-6 | Sequence 6, Appl |
| 839 | 62.5 | 3.7 | 291 | 4 | US-09-393-634-64 | Sequence 64, Appl | 912 | 62.5 | 3.7 | 2710 | 2 | US-08-405-496A-6 | Sequence 6, Appl |
| 840 | 62.5 | 3.7 | 291 | 4 | US-09-949-016-6919 | Sequence 6919, Ap | 913 | 62.5 | 3.7 | 2710 | 3 | US-08-915-136-6 | Sequence 6, Appl |
| 841 | 62.5 | 3.7 | 291 | 4 | US-09-949-016-8213 | Sequence 8213, Ap | 914 | 62.5 | 3.7 | 2710 | 3 | US-08-957-310-6 | Sequence 6, Appl |
| 842 | 62.5 | 3.7 | 322 | 4 | US-09-270-767-42152 | Sequence 42152, A | 915 | 62.5 | 3.7 | 2710 | 4 | US-10-011-366-6 | Sequence 6, Appl |
| 843 | 62.5 | 3.7 | 359 | 4 | US-09-646-028-16 | Sequence 16, Appl | 916 | 62.5 | 3.7 | 2710 | 4 | US-09-084-517-6 | Sequence 6, Appl |
| 844 | 62.5 | 3.7 | 375 | 4 | US-09-538-092-159 | Sequence 159, App | 917 | 62.5 | 3.7 | 4861 | 4 | US-09-919-497-8 | Sequence 7, Appl |
| 845 | 62.5 | 3.7 | 400 | 4 | US-09-668-097A-16 | Sequence 16, Appl | 918 | 62.5 | 3.7 | 174 | 4 | US-09-489-039A-10650 | Sequence 10650, A |
| 846 | 62.5 | 3.7 | 411 | 4 | US-09-253-701-1 | Sequence 1, Appl | 919 | 62 | 3.7 | 185 | 4 | US-09-248-796A-20284 | Sequence 20284, A |
| 847 | 62.5 | 3.7 | 412 | 4 | US-09-646-403-5 | Sequence 5, Appl | 920 | 62 | 3.7 | 200 | 4 | US-09-107-532A-5545 | Sequence 5545, Ap |
| 848 | 62.5 | 3.7 | 437 | 3 | US-08-486-099-91 | Sequence 91, Appl | 921 | 62 | 3.7 | 251 | 2 | US-08-665-647-7 | Sequence 7, Appl |
| 849 | 62.5 | 3.7 | 437 | 3 | US-08-360-107A-101 | Sequence 101, App | 922 | 62 | 3.7 | 267 | 3 | US-09-489-039A-9036 | Sequence 9036, Ap |
| 850 | 62.5 | 3.7 | 437 | 3 | US-08-484-223B-91 | Sequence 91, Appl | 923 | 62 | 3.7 | 282 | 3 | US-08-812-586-49 | Sequence 49, Appl |
| 851 | 62.5 | 3.7 | 437 | 3 | US-08-919-597-91 | Sequence 91, Appl | 924 | 62 | 3.7 | 282 | 4 | US-09-535-892A-46 | Sequence 46, Appl |
| 852 | 62.5 | 3.7 | 437 | 3 | US-08-475-668A-91 | Sequence 91, Appl | 925 | 62 | 3.7 | 293 | 2 | US-08-919-145-2 | Sequence 2, Appl |
| 853 | 62.5 | 3.7 | 437 | 3 | US-08-485-551A-91 | Sequence 91, Appl | 926 | 62 | 3.7 | 293 | 2 | US-09-344-889-2 | Sequence 2, Appl |
| 854 | 62.5 | 3.7 | 437 | 3 | US-08-471-913A-91 | Sequence 91, Appl | 927 | 62 | 3.7 | 308 | 2 | US-09-047-026A-23 | Sequence 23, Appl |
| 855 | 62.5 | 3.7 | 437 | 3 | US-08-485-264A-91 | Sequence 91, Appl | 928 | 62 | 3.7 | 341 | 4 | US-09-399-081A-6 | Sequence 6, Appl |
| 856 | 62.5 | 3.7 | 437 | 3 | US-08-474-349A-91 | Sequence 91, Appl | 929 | 62 | 3.7 | 347 | 4 | US-09-248-796A-19101 | Sequence 19101, A |
| 857 | 62.5 | 3.7 | 437 | 4 | US-08-255-208A-27 | Sequence 27, Appl | 930 | 62 | 3.7 | 378 | 2 | US-08-904-031-4 | Sequence 4, Appl |
| 858 | 62.5 | 3.7 | 437 | 4 | US-08-470-896-91 | Sequence 91, Appl | 931 | 62 | 3.7 | 385 | 4 | US-09-248-796A-14377 | Sequence 14377, A |
| 859 | 62.5 | 3.7 | 437 | 4 | US-08-485-546A-91 | Sequence 91, Appl | 932 | 62 | 3.7 | 386 | 4 | US-09-949-016-10095 | Sequence 10095, A |
| 860 | 62.5 | 3.7 | 437 | 4 | US-08-487-266A-91 | Sequence 91, Appl | 933 | 62 | 3.7 | 407 | 4 | US-09-521-335-13 | Sequence 13, Appl |
| 861 | 62.5 | 3.7 | 449 | 4 | US-09-984-880-2 | Sequence 2, Appl | 934 | 62 | 3.7 | 412 | 4 | US-09-107-433-3327 | Sequence 3327, Ap |
| 862 | 62.5 | 3.7 | 449 | 4 | US-10-277-032-2 | Sequence 18, Appl | 935 | 62 | 3.7 | 422 | 4 | US-09-489-039A-12413 | Sequence 12413, A |
| 863 | 62.5 | 3.7 | 453 | 1 | US-08-417-330A-18 | Sequence 18, Appl | 936 | 62 | 3.7 | 423 | 4 | US-09-824-551-2 | Sequence 2, Appl |
| 864 | 62.5 | 3.7 | 498 | 4 | US-09-438-185A-126 | Sequence 26, Appl | 937 | 62 | 3.7 | 427 | 3 | US-08-969-125-9 | Sequence 9, Appl |
| 865 | 62.5 | 3.7 | 513 | 5 | PCR-US91-02714-26 | Sequence 26, Appl | 938 | 62 | 3.7 | 427 | 4 | US-09-545-002-9 | Sequence 9, Appl |
| 866 | 62.5 | 3.7 | 572 | 5 | PCR-US91-08177-19 | Sequence 19, Appl | 939 | 62 | 3.7 | 427 | 3 | US-09-949-016-6094 | Sequence 6094, Ap |
| 867 | 62.5 | 3.7 | 574 | 4 | US-09-567-458A-4 | Sequence 4, Appl | 940 | 62 | 3.7 | 443 | 3 | US-09-155-855-1 | Sequence 1, Appl |
| 868 | 62.5 | 3.7 | 574 | 6 | 5223254-2 | Patent No. 5223254 | 941 | 62 | 3.7 | 443 | 3 | US-09-155-855-2 | Sequence 2, Appl |
| 869 | 62.5 | 3.7 | 574 | 6 | 5223254-2 | Patent No. 5223254 | 942 | 62 | 3.7 | 443 | 3 | US-09-543-744-1 | Sequence 1, Appl |
| 870 | 62.5 | 3.7 | 613 | 4 | US-09-438-833-6 | Sequence 6, Appl | 943 | 62 | 3.7 | 443 | 3 | US-09-543-744-2 | Sequence 2, Appl |
| 871 | 62.5 | 3.7 | 626 | 4 | US-09-949-016-6213 | Sequence 6213, Ap | 944 | 62 | 3.7 | 443 | 3 | US-09-929-060-1 | Sequence 1, Appl |
| 872 | 62.5 | 3.7 | 639 | 4 | US-09-107-532A-304 | Sequence 304, Ap | 945 | 62 | 3.7 | 443 | 4 | US-09-929-060-2 | Sequence 2, Appl |
| 873 | 62.5 | 3.7 | 641 | 4 | US-09-248-796A-17974 | Sequence 17974, A | 946 | 62 | 3.7 | 446 | 4 | US-09-902-540-13447 | Sequence 13447, A |
| 874 | 62.5 | 3.7 | 664 | 4 | US-09-949-016-7850 | Sequence 7850, Ap | 947 | 62 | 3.7 | 467 | 3 | US-09-155-855-3 | Sequence 3, Appl |
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| 877 | 62.5 | 3.7 | 688 | 3 | US-09-146-249A-28 | Sequence 28, Appl | 950 | 62 | 3.7 | 468 | 4 | US-09-149-476-387 | Sequence 387, App |
| 878 | 62.5 | 3.7 | 688 | 3 | US-08-206-188B-28 | Sequence 28, Appl | 951 | 62 | 3.7 | 469 | 4 | US-09-252-991A-30596 | Sequence 30596, A |
| 879 | 62.5 | 3.7 | 716 | 2 | US-08-372-652-4 | Sequence 4, Appl | 952 | 62 | 3.7 | 477 | 4 | US-09-543-744A-8129 | Sequence 8129, Ap |
| 880 | 62.5 | 3.7 | 716 | 5 | PCR-US95-16311-4 | Sequence 4, Appl | 953 | 62 | 3.7 | 480 | 4 | US-09-107-532A-6160 | Sequence 6160, Ap |
| 881 | 62.5 | 3.7 | 807 | 4 | US-09-132-769-3 | Sequence 3, Appl | 954 | 62 | 3.7 | 489 | 4 | US-09-134-000C-4888 | Sequence 4888, Ap |
| 882 | 62.5 | 3.7 | 905 | 2 | US-08-574-959A-9 | Sequence 9, Appl | 955 | 62 | 3.7 | 509 | 4 | US-09-328-352-5785 | Sequence 5785, Ap |
| 883 | 62.5 | 3.7 | 905 | 3 | US-08-357-014-9 | Sequence 9, Appl | 956 | 62 | 3.7 | 549 | 4 | US-09-673-335A-208 | Sequence 208, App |
| 884 | 62.5 | 3.7 | 920 | 3 | US-08-930-996A-8 | Sequence 8, Appl | 957 | 62 | 3.7 | 549 | 4 | US-09-673-335A-564 | Sequence 564, App |
| 885 | 62.5 | 3.7 | 1011 | 4 | US-09-489-039A-11808 | Sequence 11808, A | 958 | 62 | 3.7 | 571 | 4 | US-09-248-796A-22498 | Sequence 22498, A |
| 886 | 62.5 | 3.7 | 1038 | 3 | US-08-334-179A-8 | Sequence 8, Appl | 959 | 62 | 3.7 | 579 | 4 | US-09-922-364A-19 | Sequence 19, Appl |
| 887 | 62.5 | 3.7 | 1052 | 3 | US-08-863-118-1 | Sequence 1, Appl | 960 | 62 | 3.7 | 579 | 4 | US-09-254-590-19 | Sequence 19, Appl |
| 888 | 62.5 | 3.7 | 1052 | 3 | US-09-377-310-2 | Sequence 2, Appl | 961 | 62 | 3.7 | 579 | 4 | US-10-115-415-19 | Sequence 19, Appl |
| 889 | 62.5 | 3.7 | 1091 | 6 | 5516630-2 | Patent No. 5516630 | 962 | 62 | 3.7 | 579 | 4 | US-10-116-260-19 | Sequence 19, Appl |
| 890 | 62.5 | 3.7 | 1091 | 6 | 5516630-2 | Patent No. 5516630 | 963 | 62 | 3.7 | 580 | 4 | US-09-922-364A-2 | Sequence 2, Appl |
| 891 | 62.5 | 3.7 | 1096 | 4 | US-09-252-991A-19328 | Sequence 19328, A | 964 | 62 | 3.7 | 580 | 4 | US-09-254-590-2 | Sequence 2, Appl |
| 892 | 62.5 | 3.7 | 1101 | 3 | US-08-331-625A-52 | Sequence 52, Appl | 965 | 62 | 3.7 | 580 | 4 | US-10-115-415-2 | Sequence 2, Appl |
| 893 | 62.5 | 3.7 | 1101 | 4 | US-09-494-151-52 | Sequence 52, Appl | 966 | 62 | 3.7 | 580 | 4 | US-10-116-260-2 | Sequence 2, Appl |
| 894 | 62.5 | 3.7 | 1166 | 4 | US-09-972-484-52 | Sequence 52, Appl | 967 | 62 | 3.7 | 580 | 4 | US-10-116-260-2 | Sequence 2, Appl |
| 895 | 62.5 | 3.7 | 1383 | 4 | US-10-101-464A-900 | Sequence 900, App | 968 | 62 | 3.7 | 580 | 4 | US-10-115-671-2 | Sequence 2, Appl |
| 896 | 62.5 | 3.7 | 1443 | 1 | US-09-540-236-3580 | Sequence 3580, App | 969 | 62 | 3.7 | 592 | 2 | US-08-366-490-2 | Sequence 2, Appl |
| 897 | 62.5 | 3.7 | 1443 | 1 | US-08-308-872B-2 | Sequence 2, Appl | 970 | 62 | 3.7 | 600 | 4 | US-08-860-483A-2 | Sequence 2, Appl |
| 898 | 62.5 | 3.7 | 1452 | 3 | US-08-331-625A-2 | Sequence 2, Appl | 971 | 62 | 3.7 | 601 | 4 | US-09-519-232-10 | Sequence 20, Appl |
| 899 | 62.5 | 3.7 | 1452 | 3 | US-09-494-151-2 | Sequence 2, Appl | 972 | 62 | 3.7 | 601 | 4 | US-09-519-232-10 | Sequence 20, Appl |
| 900 | 62.5 | 3.7 | 1452 | 3 | US-09-972-484-2 | Sequence 2, Appl | 973 | 62 | 3.7 | 604 | 4 | US-09-134-000C-5256 | Sequence 5256, Ap |
| 901 | 62.5 | 3.7 | 1452 | 5 | PCR-US93-04384-18 | Sequence 18, Appl | 974 | 62 | 3.7 | 609 | 4 | US-09-949-016-7747 | Sequence 7747, Ap |
| 902 | 62.5 | 3.7 | 1452 | 5 | PCR-US93-04692-2 | Sequence 2, Appl | 975 | 62 | 3.7 | 609 | 4 | US-09-949-016-7748 | Sequence 7748, Ap |
| 903 | 62.5 | 3.7 | 1454 | 3 | US-08-392-459-26 | Sequence 26, Appl | 976 | 62 | 3.7 | 609 | 4 | US-09-949-016-7749 | Sequence 7749, Ap |

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|------|------|-----|------|---|----------------------|-------------------|------|------|-----|------|---|----------------------|-------------------|
| 977 | 62 | 3.7 | 609 | 4 | US-09-949-016-7750 | Sequence 7750, Ap | 1050 | 61.5 | 3.6 | 705 | 4 | US-09-854-133-186 | Sequence 186, App |
| 978 | 62 | 3.7 | 609 | 4 | US-09-949-016-7751 | Sequence 7751, Ap | 1051 | 61.5 | 3.6 | 734 | 1 | US-08-276-099A-16 | Sequence 16, Appl |
| 979 | 62 | 3.7 | 609 | 4 | US-09-949-016-7752 | Sequence 7752, Ap | 1052 | 61.5 | 3.6 | 734 | 1 | US-08-781-880-16 | Sequence 16, Appl |
| 980 | 62 | 3.7 | 609 | 4 | US-09-949-016-7753 | Sequence 7753, Ap | 1053 | 61.5 | 3.6 | 738 | 4 | US-09-107-532A-5095 | Sequence 5096, Ap |
| 981 | 62 | 3.7 | 609 | 4 | US-09-949-016-7754 | Sequence 7754, Ap | 1054 | 61.5 | 3.6 | 820 | 4 | US-09-248-796A-15055 | Sequence 15055, A |
| 982 | 62 | 3.7 | 610 | 4 | US-09-198-452A-899 | Sequence 899, App | 1055 | 61.5 | 3.6 | 828 | 1 | US-08-261-304-2 | Sequence 2, Appl |
| 983 | 62 | 3.7 | 700 | 4 | US-09-134-000C-6262 | Sequence 6262, Ap | 1056 | 61.5 | 3.6 | 835 | 2 | US-08-968-751-4 | Sequence 4, Appl |
| 984 | 62 | 3.7 | 708 | 4 | US-09-443-780C-16 | Sequence 16, Appl | 1057 | 61.5 | 3.6 | 897 | 4 | US-09-849-602-18 | Sequence 18, Appl |
| 985 | 62 | 3.7 | 708 | 4 | US-09-079-723-110 | Sequence 110, App | 1058 | 61.5 | 3.6 | 958 | 4 | US-09-270-767-6021 | Sequence 46021, A |
| 986 | 62 | 3.7 | 708 | 4 | US-09-079-723-110 | Sequence 110, App | 1059 | 61.5 | 3.6 | 997 | 4 | US-09-747-371-3 | Sequence 3, Appl |
| 987 | 62 | 3.7 | 724 | 4 | US-09-900-920-62 | Sequence 62, Appl | 1060 | 61.5 | 3.6 | 1003 | 4 | US-09-949-016-10627 | Sequence 10627, A |
| 988 | 62 | 3.7 | 791 | 4 | US-09-543-681A-5446 | Sequence 5446, Ap | 1061 | 61.5 | 3.6 | 1041 | 4 | US-09-270-767-32619 | Sequence 32619, A |
| 989 | 62 | 3.7 | 796 | 4 | US-09-107-532A-7065 | Sequence 7065, Ap | 1062 | 61.5 | 3.6 | 1041 | 4 | US-09-270-767-47836 | Sequence 47836, A |
| 990 | 62 | 3.7 | 835 | 4 | US-09-949-016-9685 | Sequence 9685, Ap | 1063 | 61.5 | 3.6 | 1094 | 4 | US-10-160-719A-26 | Sequence 26, Appl |
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| 995 | 62 | 3.7 | 988 | 1 | US-08-162-809-14 | Sequence 14, Appl | 1068 | 61.5 | 3.6 | 1485 | 4 | US-09-543-681A-5367 | Sequence 5367, Ap |
| 996 | 62 | 3.7 | 1122 | 1 | US-08-619-198-3 | Sequence 3, Appl | 1069 | 61.5 | 3.6 | 1492 | 4 | US-09-697-898-5 | Sequence 5, Appl |
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| 998 | 62 | 3.7 | 1139 | 1 | US-09-113-825-4 | Sequence 4, Appl | 1071 | 61.5 | 3.6 | 1989 | 3 | US-08-457-571-12 | Sequence 12, Appl |
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| 1003 | 62 | 3.7 | 1479 | 3 | US-08-840-062-4 | Sequence 4, Appl | 1076 | 61.5 | 3.6 | 2472 | 4 | US-09-538-092-1312 | Sequence 1312, Ap |
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| 1005 | 62 | 3.7 | 2465 | 2 | US-09-100-804-3 | Sequence 3, Appl | 1078 | 61.5 | 3.6 | 3084 | 4 | US-09-562-702A-12 | Sequence 12, Appl |
| 1006 | 62 | 3.7 | 2466 | 3 | US-09-080-855-12 | Sequence 12, Appl | 1079 | 61.5 | 3.6 | 3106 | 4 | US-09-562-702A-10 | Sequence 10, Appl |
| 1007 | 62 | 3.7 | 2466 | 3 | US-09-566-076-11 | Sequence 11, Appl | 1080 | 61.5 | 3.6 | 3178 | 4 | US-09-479-467A-4 | Sequence 4, Appl |
| 1008 | 62 | 3.7 | 2466 | 3 | PCT-US94-09943-2 | Sequence 2, Appl | 1081 | 61.5 | 3.6 | 3838 | 4 | US-09-949-016-10853 | Sequence 10853, A |
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| 1010 | 62 | 3.7 | 2474 | 4 | US-08-305-790B-4 | Sequence 4, Appl | 1083 | 61.5 | 3.6 | 7257 | 3 | US-09-568-102-5 | Sequence 5, Appl |
| 1011 | 62 | 3.7 | 2485 | 4 | US-09-290-640-46 | Sequence 46, Appl | 1084 | 61.5 | 3.6 | 7257 | 3 | US-09-567-969-5 | Sequence 5, Appl |
| 1012 | 62 | 3.7 | 2485 | 4 | US-09-665-615B-46 | Sequence 46, Appl | 1085 | 61.5 | 3.6 | 7257 | 3 | US-09-568-480-5 | Sequence 5, Appl |
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| 1015 | 62 | 3.7 | 2703 | 1 | US-08-899-232-4 | Sequence 4, Appl | 1088 | 61.5 | 3.6 | 7257 | 3 | US-09-567-899-5 | Sequence 5, Appl |
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| 1019 | 61.5 | 3.6 | 90 | 2 | US-08-442-108B-5 | Sequence 5, Appl | 1092 | 61 | 3.6 | 173 | 4 | US-09-248-796A-18321 | Sequence 18321, A |
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| 1022 | 61.5 | 3.6 | 142 | 4 | US-09-976-594-358 | Sequence 358, App | 1095 | 61 | 3.6 | 213 | 3 | US-09-599-360B-121 | Sequence 121, App |
| 1023 | 61.5 | 3.6 | 142 | 4 | US-08-849-303-20 | Sequence 20, Appl | 1096 | 61 | 3.6 | 223 | 4 | US-09-387-418A-19 | Sequence 19, Appl |
| 1024 | 61.5 | 3.6 | 183 | 3 | US-09-710-279-1092 | Sequence 1092, Ap | 1097 | 61 | 3.6 | 222 | 4 | US-09-270-767-45500 | Sequence 45500, A |
| 1025 | 61.5 | 3.6 | 183 | 3 | US-09-134-001C-3411 | Sequence 3411, Ap | 1098 | 61 | 3.6 | 223 | 4 | US-09-387-418A-22 | Sequence 22, Appl |
| 1026 | 61.5 | 3.6 | 191 | 4 | US-09-270-767-45117 | Sequence 45117, A | 1099 | 61 | 3.6 | 229 | 3 | US-09-387-418A-18 | Sequence 18, Appl |
| 1027 | 61.5 | 3.6 | 245 | 4 | US-09-107-433-2979 | Sequence 2979, Ap | 1100 | 61 | 3.6 | 229 | 3 | US-09-387-418A-28 | Sequence 28, Appl |
| 1028 | 61.5 | 3.6 | 270 | 3 | US-09-364-230-28 | Sequence 28, Appl | 1101 | 61 | 3.6 | 229 | 3 | US-09-387-418A-30 | Sequence 30, Appl |
| 1029 | 61.5 | 3.6 | 364 | 4 | US-09-540-236-3729 | Sequence 3729, Ap | 1102 | 61 | 3.6 | 229 | 3 | US-09-387-418A-31 | Sequence 31, Appl |
| 1030 | 61.5 | 3.6 | 371 | 4 | US-09-354-123-10 | Sequence 10, Appl | 1103 | 61 | 3.6 | 229 | 3 | US-09-387-418A-14 | Sequence 14, Appl |
| 1031 | 61.5 | 3.6 | 445 | 4 | US-08-937-834-5 | Sequence 5, Appl | 1104 | 61 | 3.6 | 236 | 3 | US-09-387-418A-15 | Sequence 15, Appl |
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| 1035 | 61.5 | 3.6 | 498 | 5 | US-09-198-452A-143 | Sequence 143, App | 1108 | 61 | 3.6 | 271 | 3 | US-09-387-418A-9 | Sequence 9, Appl |
| 1036 | 61.5 | 3.6 | 498 | 5 | PCT-US94-01101-2 | Sequence 2, Appl | 1109 | 61 | 3.6 | 274 | 3 | US-09-188-930-336 | Sequence 336, App |
| 1037 | 61.5 | 3.6 | 500 | 2 | US-08-987-519-1 | Sequence 1, Appl | 1110 | 61 | 3.6 | 274 | 4 | US-09-312-283C-336 | Sequence 336, App |
| 1038 | 61.5 | 3.6 | 505 | 4 | US-08-657-749D-25 | Sequence 25, Appl | 1111 | 61 | 3.6 | 279 | 4 | US-09-107-532A-6807 | Sequence 6807, Ap |
| 1039 | 61.5 | 3.6 | 506 | 3 | US-09-066-047-7 | Sequence 7, Appl | 1112 | 61 | 3.6 | 296 | 1 | US-07-783-705A-5 | Sequence 5, Appl |
| 1040 | 61.5 | 3.6 | 517 | 4 | US-09-198-452A-298 | Sequence 298, App | 1113 | 61 | 3.6 | 314 | 4 | US-09-438-185A-555 | Sequence 555, App |
| 1041 | 61.5 | 3.6 | 517 | 4 | US-09-438-185A-287 | Sequence 287, App | 1114 | 61 | 3.6 | 322 | 2 | US-08-622-354-3 | Sequence 3, Appl |
| 1042 | 61.5 | 3.6 | 523 | 4 | US-09-549-519-36 | Sequence 36, Appl | 1115 | 61 | 3.6 | 325 | 4 | US-09-248-796A-27766 | Sequence 27766, A |
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| 1044 | 61.5 | 3.6 | 540 | 4 | US-09-302-626B-168 | Sequence 168, App | 1117 | 61 | 3.6 | 327 | 3 | US-09-665-615B-66 | Sequence 66, Appl |
| 1045 | 61.5 | 3.6 | 566 | 4 | US-09-252-991A-26887 | Sequence 26887, A | 1118 | 61 | 3.6 | 328 | 4 | US-09-513-597A-2 | Sequence 2, Appl |
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| 1047 | 61.5 | 3.6 | 637 | 4 | US-09-360-545-69 | Sequence 69, Appl | 1120 | 61 | 3.6 | 360 | 3 | US-09-043-627-2 | Sequence 2, Appl |
| 1048 | 61.5 | 3.6 | 640 | 4 | US-09-302-626B-20 | Sequence 20, Appl | 1121 | 61 | 3.6 | 366 | 4 | US-09-270-767-42127 | Sequence 42127, A |
| 1049 | 61.5 | 3.6 | 705 | 4 | US-09-370-838-186 | Sequence 186, App | 1122 | 61 | 3.6 | 368 | 1 | US-08-185-851A-4 | Sequence 4, Appl |

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|------|----|-----|-----|---|----------------------|---------------------|------|------|-----|------|---|----------------------|--------------------|
| 1123 | 61 | 3.6 | 368 | 2 | US-08-525-742-4 | Sequence 4, Appli | 1196 | 61 | 3.6 | 837 | 1 | US-07-923-976-2 | Sequence 2, Appli |
| 1124 | 61 | 3.6 | 370 | 4 | US-09-248-796A-15625 | Sequence 15625, A | 1197 | 61 | 3.6 | 847 | 4 | US-10-162-012-2 | Sequence 4, Appli |
| 1125 | 61 | 3.6 | 381 | 2 | US-09-193-887-2 | Sequence 2, Appli | 1198 | 61 | 3.6 | 860 | 4 | US-07-946-295-4 | Sequence 4, Appli |
| 1126 | 61 | 3.6 | 387 | 2 | US-08-484-575A-7 | Sequence 7, Appli | 1199 | 61 | 3.6 | 870 | 2 | US-08-266-311-1 | Sequence 1, Appli |
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| 1128 | 61 | 3.6 | 387 | 3 | US-08-479-869-7 | Sequence 7, Appli | 1201 | 61 | 3.6 | 870 | 2 | US-08-467-557A-1 | Sequence 1, Appli |
| 1129 | 61 | 3.6 | 387 | 3 | US-08-486-414-7 | Sequence 7, Appli | 1202 | 61 | 3.6 | 879 | 4 | US-09-914-259-18 | Sequence 38, Appli |
| 1130 | 61 | 3.6 | 387 | 5 | PCT-US94-01826A-7 | Sequence 7, Appli | 1203 | 61 | 3.6 | 952 | 4 | US-09-270-767-141680 | Sequence 4, Appli |
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| 1132 | 61 | 3.6 | 402 | 4 | US-09-513-597A-13 | Sequence 13, Appli | 1205 | 61 | 3.6 | 976 | 4 | US-09-538-082-1339 | Sequence 1339, Ap |
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| 1134 | 61 | 3.6 | 425 | 4 | US-09-270-767-51905 | Sequence 51905, A | 1207 | 61 | 3.6 | 1183 | 4 | US-09-532-310B-5 | Sequence 5, Appli |
| 1135 | 61 | 3.6 | 430 | 4 | US-09-912-935-35 | Sequence 35, Appli | 1208 | 61 | 3.6 | 1487 | 3 | US-08-840-062-7 | Sequence 7, Appli |
| 1136 | 61 | 3.6 | 431 | 2 | US-09-252-991A-22471 | Sequence 22471, A | 1209 | 61 | 3.6 | 1722 | 4 | US-09-194-612A-1 | Sequence 1, Appli |
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| 1138 | 61 | 3.6 | 443 | 3 | US-08-980-514-1 | Sequence 1, Appli | 1211 | 61 | 3.6 | 2141 | 4 | US-09-946-016-10918 | Sequence 10918, A |
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| 1142 | 61 | 3.6 | 475 | 2 | US-08-272-255-13 | Sequence 13, Appli | 1215 | 61 | 3.6 | 3056 | 4 | US-08-984-090-2 | Sequence 2, Appli |
| 1143 | 61 | 3.6 | 475 | 5 | PCT-US95-08565-13 | Sequence 13, Appli | 1216 | 61 | 3.6 | 3057 | 4 | US-09-360-416-3 | Sequence 3, Appli |
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| 1146 | 61 | 3.6 | 486 | 4 | US-09-914-259-35 | Sequence 35, Appli | 1219 | 60.5 | 3.6 | 173 | 4 | US-09-270-767-51097 | Sequence 51097, A |
| 1147 | 61 | 3.6 | 486 | 4 | US-09-976-594-278 | Sequence 278, Appli | 1220 | 60.5 | 3.6 | 193 | 1 | US-08-159-340A-3 | Sequence 3, Appli |
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| 1149 | 61 | 3.6 | 503 | 4 | US-09-248-796A-15409 | Sequence 15409, A | 1222 | 60.5 | 3.6 | 262 | 6 | 5194375-4 | Sequence 42765, A |
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| 1151 | 61 | 3.6 | 519 | 4 | US-09-107-532A-7778 | Sequence 6778, Ap | 1224 | 60.5 | 3.6 | 264 | 4 | US-09-270-767-33115 | Sequence 33115, A |
| 1152 | 61 | 3.6 | 548 | 1 | US-08-333-358-2 | Sequence 2, Appli | 1225 | 60.5 | 3.6 | 264 | 4 | US-09-270-767-48332 | Sequence 48332, A |
| 1153 | 61 | 3.6 | 548 | 1 | US-08-463-694-2 | Sequence 2, Appli | 1226 | 60.5 | 3.6 | 273 | 4 | US-09-252-991A-23086 | Sequence 23086, A |
| 1154 | 61 | 3.6 | 548 | 1 | US-08-694-501-2 | Sequence 2, Appli | 1227 | 60.5 | 3.6 | 282 | 4 | US-09-248-796A-14879 | Sequence 14879, A |
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| 1156 | 61 | 3.6 | 552 | 4 | US-09-106-194-3 | Sequence 3, Appli | 1229 | 60.5 | 3.6 | 328 | 3 | US-09-253-516-28 | Sequence 28, Appli |
| 1157 | 61 | 3.6 | 557 | 1 | US-08-309-341-2 | Sequence 2, Appli | 1230 | 60.5 | 3.6 | 328 | 4 | US-09-961-403-2 | Sequence 2, Appli |
| 1158 | 61 | 3.6 | 557 | 1 | US-08-608-267-2 | Sequence 2, Appli | 1231 | 60.5 | 3.6 | 334 | 4 | US-09-328-352-7591 | Sequence 7591, Ap |
| 1159 | 61 | 3.6 | 557 | 1 | US-08-608-452-2 | Sequence 2, Appli | 1232 | 60.5 | 3.6 | 338 | 4 | US-08-426-630-18 | Sequence 38, Appli |
| 1160 | 61 | 3.6 | 557 | 1 | US-08-608-224-2 | Sequence 2, Appli | 1233 | 60.5 | 3.6 | 347 | 4 | US-09-949-016-9849 | Sequence 9849, Ap |
| 1161 | 61 | 3.6 | 557 | 1 | US-08-967-149-2 | Sequence 2, Appli | 1234 | 60.5 | 3.6 | 355 | 4 | US-09-498-520A-8 | Sequence 8, Appli |
| 1162 | 61 | 3.6 | 584 | 1 | US-08-426-819A-36 | Sequence 36, Appli | 1235 | 60.5 | 3.6 | 366 | 4 | US-09-830-433A-4 | Sequence 4, Appli |
| 1163 | 61 | 3.6 | 599 | 1 | US-08-442-548-18 | Sequence 18, Appli | 1236 | 60.5 | 3.6 | 381 | 4 | US-09-248-796A-20906 | Sequence 20906, A |
| 1164 | 61 | 3.6 | 599 | 1 | US-08-765-464-18 | Sequence 18, Appli | 1237 | 60.5 | 3.6 | 393 | 4 | US-08-956-171B-5248 | Sequence 5248, Ap |
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| 1166 | 61 | 3.6 | 622 | 1 | US-08-426-819A-35 | Sequence 35, Appli | 1239 | 60.5 | 3.6 | 393 | 4 | US-08-781-986A-5248 | Sequence 5248, Ap |
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| 1168 | 61 | 3.6 | 643 | 4 | US-09-949-016-6660 | Sequence 19, Appli | 1241 | 60.5 | 3.6 | 422 | 3 | US-09-625-188-12 | Sequence 12, Appli |
| 1169 | 61 | 3.6 | 643 | 5 | PCT-US93-00031-19 | Sequence 19, Appli | 1242 | 60.5 | 3.6 | 433 | 2 | US-08-466-120-2 | Sequence 2, Appli |
| 1170 | 61 | 3.6 | 666 | 1 | US-08-083-590A-17 | Sequence 36, Appli | 1243 | 60.5 | 3.6 | 433 | 5 | PCT-US94-07266-2 | Sequence 2, Appli |
| 1171 | 61 | 3.6 | 666 | 2 | US-08-346-128-36 | Sequence 17, Appli | 1244 | 60.5 | 3.6 | 443 | 4 | US-09-252-991A-20035 | Sequence 20035, A |
| 1172 | 61 | 3.6 | 666 | 3 | US-08-532-384-17 | Sequence 17, Appli | 1245 | 60.5 | 3.6 | 446 | 4 | US-09-328-352-6527 | Sequence 6527, Ap |
| 1173 | 61 | 3.6 | 681 | 4 | US-09-134-000C-3371 | Sequence 14, Appli | 1246 | 60.5 | 3.6 | 446 | 4 | US-09-248-796A-16004 | Sequence 16004, A |
| 1174 | 61 | 3.6 | 706 | 4 | US-10-087-400C-14 | Sequence 4, Appli | 1247 | 60.5 | 3.6 | 476 | 3 | US-08-378-313-34 | Sequence 34, Appli |
| 1175 | 61 | 3.6 | 708 | 2 | US-08-576-165-2 | Sequence 2, Appli | 1248 | 60.5 | 3.6 | 490 | 4 | US-09-949-016-10949 | Sequence 10949, A |
| 1176 | 61 | 3.6 | 716 | 4 | US-09-816-093-4 | Sequence 4, Appli | 1249 | 60.5 | 3.6 | 491 | 1 | US-08-489-733-5 | Sequence 5, Appli |
| 1177 | 61 | 3.6 | 721 | 4 | US-09-815-048-2 | Sequence 2, Appli | 1250 | 60.5 | 3.6 | 491 | 2 | US-08-993-581B-5 | Sequence 5, Appli |
| 1178 | 61 | 3.6 | 726 | 6 | 5208144-37 | Sequence 2, Appli | 1251 | 60.5 | 3.6 | 499 | 4 | US-09-900-540-16020 | Sequence 16020, A |
| 1179 | 61 | 3.6 | 726 | 6 | 5208144-37 | Sequence 2, Appli | 1252 | 60.5 | 3.6 | 501 | 3 | US-09-111-730-1 | Sequence 1, Appli |
| 1180 | 61 | 3.6 | 732 | 3 | US-09-815-048-4 | Sequence 4, Appli | 1253 | 60.5 | 3.6 | 507 | 2 | US-08-408-122-2 | Sequence 2, Appli |
| 1181 | 61 | 3.6 | 735 | 3 | US-09-115-704-2 | Sequence 2, Appli | 1254 | 60.5 | 3.6 | 507 | 2 | US-08-408-122-2 | Sequence 2, Appli |
| 1182 | 61 | 3.6 | 735 | 4 | US-09-636-791A-13 | Sequence 13, Appli | 1255 | 60.5 | 3.6 | 514 | 4 | US-09-270-767-59153 | Sequence 59153, A |
| 1183 | 61 | 3.6 | 735 | 4 | US-09-780-115-2 | Sequence 2, Appli | 1256 | 60.5 | 3.6 | 514 | 4 | US-09-270-767-52396 | Sequence 52396, A |
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| 1186 | 61 | 3.6 | 773 | 4 | US-09-889-914B-2 | Sequence 2, Appli | 1259 | 60.5 | 3.6 | 534 | 4 | US-09-248-796A-15081 | Sequence 15081, A |
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| 1188 | 61 | 3.6 | 803 | 4 | US-09-154-750A-85 | Sequence 85, Appli | 1261 | 60.5 | 3.6 | 552 | 4 | US-09-356-643B-11 | Sequence 11, Appli |
| 1189 | 61 | 3.6 | 803 | 4 | US-09-665-479A-12 | Sequence 12, Appli | 1262 | 60.5 | 3.6 | 552 | 4 | US-10-053-510-11 | Sequence 11, Appli |
| 1190 | 61 | 3.6 | 803 | 4 | US-09-949-016-6383 | Sequence 6383, Ap | 1263 | 60.5 | 3.6 | 553 | 2 | US-08-661-052-16 | Sequence 16, Appli |
| 1191 | 61 | 3.6 | 807 | 4 | US-09-132-769-1 | Sequence 1, Appli | 1264 | 60.5 | 3.6 | 553 | 3 | US-09-188-082-16 | Sequence 16, Appli |
| 1192 | 61 | 3.6 | 807 | 4 | US-09-640-173-186 | Sequence 186, App | 1265 | 60.5 | 3.6 | 553 | 3 | US-09-364-088-16 | Sequence 16, Appli |
| 1193 | 61 | 3.6 | 807 | 4 | US-09-713-550-186 | Sequence 186, App | 1266 | 60.5 | 3.6 | 553 | 3 | US-09-102-716-16 | Sequence 16, Appli |
| 1194 | 61 | 3.6 | 807 | 4 | US-09-825-294-186 | Sequence 186, App | 1267 | 60.5 | 3.6 | 573 | 3 | US-09-330-740A-8 | Sequence 8, Appli |
| 1195 | 61 | 3.6 | 807 | 4 | US-09-970-966-186 | Sequence 186, App | 1268 | 60.5 | 3.6 | 594 | 3 | US-08-826-964-2 | Sequence 2, Appli |

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| 1272 | 60.5 | 3.6 | 625 | 4 | US-09-438-185A-346 | Sequence 346, App | 1345 | 60 | 3.5 | 109 | 4 | US-09-621-976-4797 | Sequence 4797, Ap |
| 1273 | 60.5 | 3.6 | 630 | 4 | US-09-583-110-4711 | Sequence 4711, Ap | 1346 | 60 | 3.5 | 110 | 4 | US-09-489-039A-10081 | Sequence 10081, A |
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| 1294 | 60.5 | 3.6 | 922 | 4 | US-09-854-856-38 | Sequence 38, Appl | 1367 | 60 | 3.5 | 162 | 3 | US-09-249-451-63 | Sequence 63, Appl |
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| 1296 | 60.5 | 3.6 | 954 | 4 | US-09-854-856-22 | Sequence 22, Appl | 1369 | 60 | 3.5 | 162 | 3 | US-09-249-461-63 | Sequence 63, Appl |
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| 1311 | 60.5 | 3.6 | 1582 | 3 | US-08-476-900A-9 | Sequence 9, Appl1 | 1384 | 60 | 3.5 | 301 | 2 | US-08-656-906-25 | Sequence 25, Appl |
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| 1314 | 60.5 | 3.6 | 1582 | 3 | US-09-208-716-5 | Sequence 5, Appl1 | 1387 | 60 | 3.5 | 327 | 6 | US-09-854-856-18 | Sequence 18, Appl1 |
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| 1316 | 60.5 | 3.6 | 1939 | 4 | US-09-854-856-48 | Sequence 48, Appl | 1389 | 60 | 3.5 | 331 | 2 | US-09-215-087-1 | Sequence 1, Appl1 |
| 1317 | 60.5 | 3.6 | 1971 | 4 | US-09-854-856-32 | Sequence 32, Appl | 1390 | 60 | 3.5 | 331 | 3 | US-09-331-959-1 | Sequence 1, Appl1 |
| 1318 | 60.5 | 3.6 | 1999 | 4 | US-09-854-856-16 | Sequence 16, Appl | 1391 | 60 | 3.5 | 355 | 4 | US-09-949-016-10717 | Sequence 10717, A |
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| 1322 | 60.5 | 3.6 | 2032 | 4 | US-09-854-856-42 | Sequence 42, Appl | 1395 | 60 | 3.5 | 376 | 3 | US-09-902-540-9957 | Sequence 9957, Ap |
| 1323 | 60.5 | 3.6 | 2048 | 4 | US-09-854-856-62 | Sequence 62, Appl | 1396 | 60 | 3.5 | 380 | 4 | US-09-316-080-5 | Sequence 5, Appl1 |
| 1324 | 60.5 | 3.6 | 2064 | 4 | US-09-854-856-26 | Sequence 26, Appl | 1397 | 60 | 3.5 | 380 | 4 | US-09-949-016-8534 | Sequence 8534, Ap |
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| 1330 | 60.5 | 3.6 | 2157 | 4 | US-09-854-856-52 | Sequence 52, Appl | 1403 | 60 | 3.5 | 398 | 4 | US-09-489-039A-13159 | Sequence 13159, A |
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| 1334 | 60.5 | 3.6 | 2183 | 2 | US-08-348-891A-7 | Sequence 7, Appl1 | 1407 | 60 | 3.5 | 428 | 4 | US-09-538-092-828 | Sequence 828, App |
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| 1340 | 60.5 | 3.6 | 2294 | 4 | US-09-854-856-50 | Sequence 50, Appl | 1413 | 60 | 3.5 | 468 | 4 | US-09-949-016-9259 | Sequence 9259, Ap |
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1491 59.5 3.5 313 4 US-09-248-796A-19461 Sequence 19461, A
1492 59.5 3.5 321 4 US-09-688-019-2 Sequence 2, Ap11
1493 59.5 3.5 324 4 US-09-328-352-7234 Sequence 7234, Ap
1494 59.5 3.5 325 2 US-08-800-264A-8 Sequence 8, Ap11
1495 59.5 3.5 325 2 US-09-018-628-8 Sequence 8, Ap11
1496 59.5 3.5 325 3 US-09-273-378-8 Sequence 8, Ap11
1497 59.5 3.5 325 3 US-09-209-605-8 Sequence 8, Ap11
1498 59.5 3.5 328 4 US-09-270-767-44241 Sequence 44241, A
1499 59.5 3.5 334 4 US-09-535-909-6 Sequence 6, Ap11
1500 59.5 3.5 342 4 US-09-248-796A-15115 Sequence 15115, A

ALIGNMENTS

RESULT 1
US-09-976-594-818
; Sequence 818, Application US/0976594
; Patent No. 6673549
; GENERAL INFORMATION:
; APPLICANT: Fumess, Michael
; APPLICANT: Buchbinder, Jenny
; TITLE OF INVENTION: GENES EXPRESSED IN C3A LIVER CELL CULTURES TREATED WITH STEROIDS
; FILE REFERENCE: PA-0041 US
; CURRENT APPLICATION NUMBER: US/0976,594
; CURRENT FILING DATE: 2001-10-12
; PRIOR APPLICATION NUMBER: 60/240,409
; PRIOR FILING DATE: 2000-10-12
; NUMBER OF SEQ ID NOS: 1143
; SOFTWARE: PERL Program
; SEQ ID NO 818
; LENGTH: 323
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID No. 6673549 2454013CD1
US-09-976-594-818

Query Match 100.0%; Score 1694; DB 4; Length 323;
Beet Local Similarity 100.0%; Pred. No. 7.3e-162;
Matches 323; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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/ Sequence 476, Application US/09149476
/ Patent No. 6420526
/ GENERAL INFORMATION:
/ APPLICANT: Rosen et al.
/ TITLE OF INVENTION: 186 Human Secreted proteins
/ FILE REFERENCE: P2002PI
/ CURRENT FILING DATE: US/09/149,476
/ EARLIER APPLICATION NUMBER: PCT/US98/04493
/ EARLIER FILING DATE: 1998-03-06
/ EARLIER APPLICATION NUMBER: 60/040,162
/ EARLIER FILING DATE: 1997-03-07
/ EARLIER APPLICATION NUMBER: 60/040,333
/ EARLIER FILING DATE: 1997-03-07
/ EARLIER APPLICATION NUMBER: 60/038,621
/ EARLIER FILING DATE: 1997-03-07
/ EARLIER APPLICATION NUMBER: 60/040,626
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/ EARLIER APPLICATION NUMBER: 60/047,596
/ EARLIER FILING DATE: 1997-05-23
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/ EARLIER APPLICATION NUMBER: 60/047,632
/ EARLIER FILING DATE: 1997-05-23
/ EARLIER APPLICATION NUMBER: 60/047,601
/ EARLIER FILING DATE: 1997-05-23
/ EARLIER APPLICATION NUMBER: 60/043,580
/ EARLIER FILING DATE: 1997-04-11
/ EARLIER APPLICATION NUMBER: 60/043,568
/ EARLIER FILING DATE: 1997-04-11
/ EARLIER APPLICATION NUMBER: 60/043,314
/ EARLIER FILING DATE: 1997-04-11
/ EARLIER APPLICATION NUMBER: 60/043,569
/ EARLIER FILING DATE: 1997-04-11
/ EARLIER APPLICATION NUMBER: 60/043,311
/ EARLIER FILING DATE: 1997-04-11
/ EARLIER APPLICATION NUMBER: 60/043,671
/ EARLIER FILING DATE: 1997-04-11
/ EARLIER APPLICATION NUMBER: 60/043,674
/ EARLIER FILING DATE: 1997-04-11
/ EARLIER APPLICATION NUMBER: 60/043,669
/ EARLIER FILING DATE: 1997-04-11
/ EARLIER APPLICATION NUMBER: 60/043,312
/ EARLIER FILING DATE: 1997-04-11
/ EARLIER APPLICATION NUMBER: 60/043,313
/ EARLIER FILING DATE: 1997-04-11
/ EARLIER APPLICATION NUMBER: 60/043,672
/ EARLIER FILING DATE: 1997-04-11
/ EARLIER APPLICATION NUMBER: 60/043,315
/ EARLIER FILING DATE: 1997-04-11
/ EARLIER APPLICATION NUMBER: 60/048,974
/ EARLIER FILING DATE: 1997-06-06
/ EARLIER APPLICATION NUMBER: 60/056,886
/ EARLIER FILING DATE: 1997-08-22
/ EARLIER APPLICATION NUMBER: 60/056,877
/ EARLIER FILING DATE: 1997-08-22
/ EARLIER APPLICATION NUMBER: 60/056,889
/ EARLIER FILING DATE: 1997-08-22
/ EARLIER APPLICATION NUMBER: 60/056,893
/ EARLIER FILING DATE: 1997-08-22
/ EARLIER APPLICATION NUMBER: 60/056,630
/ EARLIER FILING DATE: 1997-08-22
/ EARLIER APPLICATION NUMBER: 60/056,878
/ EARLIER FILING DATE: 1997-08-22
/ EARLIER APPLICATION NUMBER: 60/056,662
/ EARLIER FILING DATE: 1997-08-22
/ EARLIER APPLICATION NUMBER: 60/056,872
/ EARLIER FILING DATE: 1997-08-22
/ EARLIER APPLICATION NUMBER: 60/056,882
/ EARLIER FILING DATE: 1997-08-22
/ EARLIER APPLICATION NUMBER: 60/056,637
/ EARLIER FILING DATE: 1997-08-22
/ EARLIER APPLICATION NUMBER: 60/056,903
/ EARLIER FILING DATE: 1997-08-22
/ EARLIER APPLICATION NUMBER: 60/056,888
/ EARLIER FILING DATE: 1997-08-22
/ EARLIER APPLICATION NUMBER: 60/056,879
/ EARLIER FILING DATE: 1997-08-22
/ EARLIER APPLICATION NUMBER: 60/056,880
/ EARLIER FILING DATE: 1997-08-22
/ EARLIER APPLICATION NUMBER: 60/056,894
/ EARLIER FILING DATE: 1997-08-22
/ EARLIER APPLICATION NUMBER: 60/056,911
/ EARLIER FILING DATE: 1997-08-22
/ EARLIER APPLICATION NUMBER: 60/056,636
/ EARLIER FILING DATE: 1997-08-22
/ EARLIER APPLICATION NUMBER: 60/056,874
/ EARLIER FILING DATE: 1997-08-22
/ EARLIER APPLICATION NUMBER: 60/056,910
/ EARLIER FILING DATE: 1997-08-22
/ EARLIER APPLICATION NUMBER: 60/056,864
/ EARLIER FILING DATE: 1997-08-22
/ EARLIER APPLICATION NUMBER: 60/056,631
/ EARLIER FILING DATE: 1997-08-22
/ EARLIER APPLICATION NUMBER: 60/056,845
/ EARLIER FILING DATE: 1997-08-22
/ EARLIER APPLICATION NUMBER: 60/056,892
/ EARLIER FILING DATE: 1997-08-22
/ EARLIER APPLICATION NUMBER: 60/057,761
/ EARLIER FILING DATE: 1997-08-22
/ EARLIER APPLICATION NUMBER: 60/047,595
/ EARLIER FILING DATE: 1997-05-23
/ EARLIER APPLICATION NUMBER: 60/047,599
/ EARLIER FILING DATE: 1997-05-23

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|--|
| EARLIER APPLICATION NUMBER: 60/047,568 |
| EARLIER FILING DATE: 1997-05-23 |
| EARLIER APPLICATION NUMBER: 60/047,565 |
| EARLIER FILING DATE: 1997-05-23 |
| EARLIER APPLICATION NUMBER: 60/047,566 |
| EARLIER FILING DATE: 1997-05-23 |
| EARLIER APPLICATION NUMBER: 60/047,550 |
| EARLIER FILING DATE: 1997-05-23 |
| EARLIER APPLICATION NUMBER: 60/047,594 |
| EARLIER FILING DATE: 1997-05-23 |
| EARLIER APPLICATION NUMBER: 60/047,589 |
| EARLIER FILING DATE: 1997-05-23 |
| EARLIER APPLICATION NUMBER: 60/047,553 |
| EARLIER FILING DATE: 1997-05-23 |
| EARLIER APPLICATION NUMBER: 60/047,614 |
| EARLIER FILING DATE: 1997-05-23 |
| EARLIER APPLICATION NUMBER: 60/043,578 |
| EARLIER FILING DATE: 1997-04-11 |
| EARLIER APPLICATION NUMBER: 60/043,576 |
| EARLIER FILING DATE: 1997-04-11 |
| EARLIER APPLICATION NUMBER: 60/047,501 |
| EARLIER FILING DATE: 1997-05-23 |
| EARLIER APPLICATION NUMBER: 60/043,670 |
| EARLIER FILING DATE: 1997-04-11 |
| EARLIER APPLICATION NUMBER: 60/056,632 |
| EARLIER FILING DATE: 1997-08-22 |
| EARLIER APPLICATION NUMBER: 60/056,664 |
| EARLIER FILING DATE: 1997-08-22 |
| EARLIER APPLICATION NUMBER: 60/056,875 |
| EARLIER FILING DATE: 1997-08-22 |
| EARLIER APPLICATION NUMBER: 60/056,862 |
| EARLIER FILING DATE: 1997-08-22 |
| EARLIER APPLICATION NUMBER: 60/056,887 |
| EARLIER FILING DATE: 1997-08-22 |
| EARLIER APPLICATION NUMBER: 60/056,908 |
| EARLIER FILING DATE: 1997-08-22 |
| EARLIER APPLICATION NUMBER: 60/048,964 |
| EARLIER FILING DATE: 1997-06-06 |
| EARLIER APPLICATION NUMBER: 60/057,650 |
| EARLIER FILING DATE: 1997-09-05 |
| EARLIER APPLICATION NUMBER: 60/056,884 |
| EARLIER FILING DATE: 1997-08-22 |
| EARLIER APPLICATION NUMBER: 60/057,669 |
| EARLIER FILING DATE: 1997-09-05 |
| EARLIER APPLICATION NUMBER: 60/049,610 |
| EARLIER FILING DATE: 1997-06-13 |
| EARLIER APPLICATION NUMBER: 60/061,060 |
| EARLIER FILING DATE: 1997-10-02 |

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|-----------------------|-------|--|------|---------------------------------|
| Query Match | 74.5% | Score 1262.5 | DB 4 | Length 273 |
| Best Local Similarity | 93.5% | Pred. No. 26-133 | | |
| Matches | 246 | Conservative | 1 | Mismatches 13; Indels 3; Gaps 3 |
| QY | 1 | MAARKGSIWNTQTGLPPLLLITLMAAGSGTGAEEAFDSVYGDTASCHRAQCLTYPLHT | 60 | |
| Db | 1 | MAARKGSIWNTQTGLPPLLLITLMAAGSGTGAEEAFDSVYGDTASCHRAQCLTYPLHT | 60 | |
| QY | 61 | YPKEBEIYACORGCHLFSICQFVDDGIDILNRTKLECESACTEAVESQSDQVYACHLGQCNQ | 120 | |
| Db | 61 | YPKEBEIYACORGCHLFSICQFVDDGIDILNRTKLECESACTEAVESQSDQVYACHLGQCNQ | 120 | |
| QY | 121 | LPFAELIREQOLSLMPKXHLPLTLVLVSSFWSDMDMDASQFTTSSMTPLQDDPKIYVF | 180 | |
| Db | 121 | LPFAELIREQOLSLMPKXHLPLTLVLVSSFWSDMDMDASQFTTSSMTPLQDDPKIYVF | 180 | |
| QY | 181 | QSKP-EIQYAPHLEQEP-TNIRESSLKQSYLQ-NRNSQAHNPLLEDESDGFLIRCLSLN | 237 | |

Db 181 XSKRPRAAPHLEBQALPNLXXSLSTKMSXXSKMRNSQAHNPLEDGESEGFRLCLSLN 240

OY 238 SGHILTTTLVLSSVMVLWLCAT 260

Db : 241 SGHILTTTLVLSSVMVLWLCAT 263

```

RESULT 3
US-09-513-999C-4172
: Sequence 4172, Application US/09513999C
: Patent No. 6783961
: GENERAL INFORMATION:
: APPLICANT: Dumas Milne Edwards, J.B.
: APPLICANT: Duclert, A.
: APPLICANT: Giordano, J.Y.
: TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins
: Patent No. 6783961
: FILE REFERENCE: 59_US2.REG
: CURRENT APPLICATION NUMBER: US/09/513,999C
: CURRENT FILING DATE: 2000-02-24
: PRIOR APPLICATION NUMBER: US 60/122,487
: PRIOR FILING DATE: 1999-02-26
: NUMBER OF SEQ ID NOS: 36681
: SOFTWARE: Patent.pm
: SEQ ID NO 4172
: LENGTH: 132
: TYPE: PRT
: ORGANISM: Homo sapiens
: FEATURE:
: NAME/KEY: SIGNAL
: LOCATION: -31..-1
: OTHER INFORMATION: score 9.1
: OTHER INFORMATION: seq LLLLLLALAGSGG/TA
US-09-513-999C-4172

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| | | | | |
|-----------------------|-----------------|--------------------|-----------|-------------|
| Query Match | 41.7%; | Score 707; | DB 4; | Length 132; |
| Best Local Similarity | 100.0%; | Pred. No. 2.2e-71; | | |
| Matches 132; | Conservative 0; | Mismatches 0; | Indels 0; | Gaps 0 |

| | | | |
|----|-----|---|---|
| QY | 1 | MAAPKGSILWVRITQLG.PPILLLITMALAGSGTASABAFDSVLTGPTASCHRACOLTYPLHT | 60 |
| | | 1 | MAAPKGSILWVRITQLG.PPILLLITMALAGSGTASABAFDSVLTGPTASCHRACOLTYPLHT |
| Db | 1 | MAAPKGSILWVRITQLG.PPILLLITMALAGSGTASABAFDSVLTGPTASCHRACOLTYPLHT | 60 |
| QY | 61 | YPKBEELVACORGCRLFSICQFVDDGIDILNNTKLECECSACTEAYSQSDQEOYACHLGCONQ | 120 |
| | | 61 | YPKBEELVACORGCRLFSICQFVDDGIDILNNTKLECECSACTEAYSQSDQEOYACHLGCONQ |
| Db | 61 | YPKBEELVACORGCRLFSICQFVDDGIDILNNTKLECECSACTEAYSQSDQEOYACHLGCONQ | 120 |
| QY | 121 | LPFAELROEQLM | 132 |
| | | 121 | LPFAELROEQLM |
| Db | 121 | LPFAELROEQLM | 132 |

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RESULT 4
; Sequence 11519, Application US/03949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 11519
; LENGTH: 963

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; TYPE: PRT
; ORGANISM: Human
US-09-949-016-11519

Query Match
  Best Local Similarity 19.4%; Score 96; DB 4; Length 963;
  Matches 78; Conservative 44; Mismatches 130; Indels 150; Gaps 20;

QY 31 GFAAEPDSVGLDPTASCHRAQOLYPLHTYPKKEELVACQ-----RGRRLPSI 79
DB 561 GKTCKALBSCALGD-----HGCE-----HSCVSSDSFVCCQCEGYILREDKTRKRDV 610
QY 80 CQFVDDGIDILNRTKLECSACTEAYSOSDEQYAC-----HL 115
DB 611 COAIDHG-----CEHICV-----NSDDSYTCCLBGFRLAEDGKRCRRKDVCKSTHH 657
QY 116 GCQN-----QLEPAILRQEQMLSLMPKMHLLFPLTLVRSFMSDMWDSAS 160
DB 658 GGEHICVNNNGNSYICKCSGFFVLAEDGRCKCTEGPIDLVFVIDGSXSLGENEFVVKQ 717
QY 161 FITSWTFYLAQDDKIVLPQSKPE-----IQVAPHLEQEPPTNLRESSLSKMSYLOWRN 214
DB 718 FVT-----GIISLTLSPKARVGLQYSTQVHTFT-LRNFNSAK-----DMKK 761
QY 215 SOAHNPFLEDSG-----FLRCLSLNSGWLITTLTVLSVMVL-----WIC 257
DB 762 AVAHMKYMGKSGMTGLAKMFERSGFTQGBARPLSTRVPRAIYFTDGRADVDSEWAS 821
QY 258 CAT-----VATAVEQYV-----PSEKLSIYG-DLEFANE--OKLNR----- 290
DB 822 KAKANGITMYAVGVGKALIEELQELASPTNHLFYAEDPSTMDISIKLKKGICEALD 881
QY 291 -----YPASSL-VVRSKTEHD-----BEAGPLPTKNLAHS 321
DB 882 SDGRDSPAGELPKTVQOPTVQHRVLPFEDNMLNSTQKLSHS 923

RESULT 5
US-09-949-016-11520
; Sequence 11520, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CLO01307
; CURRENT APPLICATION NUMBER: US/09/949,016
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11520
; LENGTH: 963
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-11520

Query Match
  Best Local Similarity 19.4%; Score 96; DB 4; Length 963;
  Matches 78; Conservative 44; Mismatches 130; Indels 150; Gaps 20;

QY 31 GFAAEPDSVGLDPTASCHRAQOLYPLHTYPKKEELVACQ-----RGRRLPSI 79
DB 561 GKTCKALBSCALGD-----HGCE-----HSCVSSDSFVCCQCEGYILREDKTRKRDV 610
QY 80 CQFVDDGIDILNRTKLECSACTEAYSOSDEQYAC-----HL 115
DB 611 COAIDHG-----CEHICV-----NSDDSYTCCLBGFRLAEDGKRCRRKDVCKSTHH 657
QY 116 GCQN-----QLEPAILRQEQMLSLMPKMHLLFPLTLVRSFMSDMWDSAS 160
DB 658 GGEHICVNNNGNSYICKCSGFFVLAEDGRCKCTEGPIDLVFVIDGSXSLGENEFVVKQ 717
QY 161 FITSWTFYLAQDDKIVLPQSKPE-----IQVAPHLEQEPPTNLRESSLSKMSYLOWRN 214
DB 718 FVT-----GIISLTLSPKARVGLQYSTQVHTFT-LRNFNSAK-----DMKK 761
QY 215 SOAHNPFLEDSG-----FLRCLSLNSGWLITTLTVLSVMVL-----WIC 257
DB 762 AVAHMKYMGKSGMTGLAKMFERSGFTQGBARPLSTRVPRAIYFTDGRADVDSEWAS 821
QY 258 CAT-----VATAVEQYV-----PSEKLSIYG-DLEFANE--OKLNR----- 290
DB 822 KAKANGITMYAVGVGKALIEELQELASPTNHLFYAEDPSTMDISIKLKKGICEALD 881
QY 291 -----YPASSL-VVRSKTEHD-----BEAGPLPTKNLAHS 321
DB 882 SDGRDSPAGELPKTVQOPTVQHRVLPFEDNMLNSTQKLSHS 923
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QY 116 GCQN-----QLEPAILRQEQMLSLMPKMHLLFPLTLVRSFMSDMWDSAS 160
DB 658 GGEHICVNNNGNSYICKCSGFFVLAEDGRCKCTEGPIDLVFVIDGSXSLGENEFVVKQ 717
QY 161 FITSWTFYLAQDDKIVLPQSKPE-----IQVAPHLEQEPPTNLRESSLSKMSYLOWRN 214
DB 718 FVT-----GIISLTLSPKARVGLQYSTQVHTFT-LRNFNSAK-----DMKK 761
QY 215 SOAHNPFLEDSG-----FLRCLSLNSGWLITTLTVLSVMVL-----WIC 257
DB 762 AVAHMKYMGKSGMTGLAKMFERSGFTQGBARPLSTRVPRAIYFTDGRADVDSEWAS 821
QY 258 CAT-----VATAVEQYV-----PSEKLSIYG-DLEFANE--OKLNR----- 290
DB 822 KAKANGITMYAVGVGKALIEELQELASPTNHLFYAEDPSTMDISIKLKKGICEALD 881
QY 291 -----YPASSL-VVRSKTEHD-----BEAGPLPTKNLAHS 321
DB 882 SDGRDSPAGELPKTVQOPTVQHRVLPFEDNMLNSTQKLSHS 923

RESULT 6
US-09-907-794A-34
; Sequence 34, Application US/09907794A
; Patent No. 6635468
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gottlieb, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Grimaldi, Paul J.
; APPLICANT: Guiney, Austin L.
; APPLICANT: Hillman, Kenneth J.
; APPLICANT: Kijavlin, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoliti, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: 10466-14
; CURRENT APPLICATION NUMBER: US/09/907,794A
; PRIOR FILING DATE: 2001-07-17
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: US 60/143,048
; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: US 60/145,698
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: US 60/146,222
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: PCT/US99/20594
; PRIOR FILING DATE: 1999-09-08
; PRIOR APPLICATION NUMBER: PCT/US99/20944
; PRIOR FILING DATE: 1999-09-13
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/21547
; PRIOR FILING DATE: 1999-09-15
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: PRIOR APPLICATION NUMBER: PCT/US99/23089
: PRIOR FILING DATE: 1999-10-05
: PRIOR APPLICATION NUMBER: PCT/US99/28214
: PRIOR FILING DATE: 1999-11-29
: PRIOR APPLICATION NUMBER: PCT/US99/28313
: PRIOR FILING DATE: 1999-11-30
: PRIOR APPLICATION NUMBER: PCT/US99/28564
: PRIOR FILING DATE: 1999-12-02
: PRIOR APPLICATION NUMBER: PCT/US99/28565
: PRIOR FILING DATE: 1999-12-02
: PRIOR APPLICATION NUMBER: PCT/US99/30095
: PRIOR FILING DATE: 1999-12-16
: PRIOR APPLICATION NUMBER: PCT/US99/30911
: PRIOR FILING DATE: 1999-12-20
: PRIOR APPLICATION NUMBER: PCT/US99/30999
: PRIOR FILING DATE: 1999-12-20
: PRIOR APPLICATION NUMBER: PCT/US00/00219
: PRIOR FILING DATE: 2000-01-05
: NUMBER OF SEQ ID NOS: 423
: SEQ ID NO 34
: LENGTH: 915
: TYPE: PRT
: ORGANISM: Homo sapiens
US-09-907-794A-34

Query Match      5.6%; Score 95.5; DB 4; Length 915;
Best Local Similarity 18.0%; Pred. No. 0.29; Indels 131; Gaps 15;
Matches 65; Conservative 47; Mismatches 118;

QY 31 GTAAAEAFDSVLCGTASCHRAQOLTYPLHTYKKEELVACQ-----RCGRFSI 79
Db 479 GKTCAKUDSCALGD-----HGCE-----HSCVSSSDSFVCCFEGYILREBCKTRKRDV 528
QY 80 CQFVDDGIDLNRKTLKECSACTEAYSQSDQYAC-----HL 115
Db 529 COADIDHG-----CEHICV-----NSDSYTCCECLGFLAEDGKCRKRDVCKSTHH 575
QY 116 GCON-----QLPFAELRBOQLMSLMPKHHLLPRLVLVSFMSDDMSQOS 160
Db 576 GCEHICVNNNGSYICKSEGVLAEDGRCKCKTEGPIDLVFDGSSJLSEBNEFVVKQ 635
QY 161 FITSWTFYLOADGDKIVIFQSKPE-----IOVAPHLEOEPYTLRESSLKMSYLOQRN 214
Db 636 FVT-----GIIDSLTISPPAAVGLQISYQVHTFT-LRNNSAK-----DMKK 679
QY 215 SQARNFLDEDSG-----FLRCLSLNSGMLITTLVLVSVMLLMICATVATAVEQY 268
Db 680 AVAHMKYWGKSGMTGLAKHMFERSFTQEG-----ARPLSTR 717
QY 269 VPSKLSIYGD-----LEFMNEQKLNRYPASSLVVVRSKTEDEHESGPIPTKYNLAHS 321
Db 718 VPRALV-VFTDGRADVSEWASKAKANGITMYAVGKALIEELQETIASSEPTNHLRYA 776
QY 322 E 322
Db 777 E 777

RESULT 7
US-09-905-125A-34
: Sequence 34, Application US/09905125A
: Patent NO. 6664376
: GENERAL INFORMATION:
: APPLICANT: Genentech, Inc.
: APPLICANT: Ashkenazi, Avi
: APPLICANT: Botstein, David
: APPLICANT: Desnoyers, Luc
: APPLICANT: Eaton, Dan L.
: APPLICANT: Ferrara, Napoleone
: APPLICANT: Filvaroft, Ellen
: APPLICANT: Fong, Sherman
: APPLICANT: Geo, Wei-Qiang
: APPLICANT: Gerber, Hanspeter
```

```

: APPLICANT: Gerritsen, Mary E.
: APPLICANT: Goddard, A.
: APPLICANT: Goddard, Paul J.
: APPLICANT: Grimaldi, Christopher J.
: APPLICANT: Gutney, Austin L.
: APPLICANT: Hillan, Kenneth J.
: APPLICANT: Kijavlin, Ivar J.
: APPLICANT: Mather, Jennie P.
: APPLICANT: Pan, James
: APPLICANT: Paoli, Nicholas F.
: APPLICANT: Roy, Margaret Ann
: APPLICANT: Stewart, Timothy A.
: APPLICANT: Tumas, Daniel
: APPLICANT: Williams, P. Mickey
: APPLICANT: Wood, William, I
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: 10466-14
CURRENT FILING DATE: 2001-07-12
PRIOR APPLICATION NUMBER: US/09/905,125A
PRIOR FILING DATE: 2000-02-22
PRIOR APPLICATION NUMBER: PCT/US00/04414
PRIOR FILING DATE: 2000-02-22
PRIOR APPLICATION NUMBER: US 60/143,048
PRIOR FILING DATE: 1999-07-07
PRIOR APPLICATION NUMBER: US 60/145,698
PRIOR FILING DATE: 1999-07-26
PRIOR APPLICATION NUMBER: US 60/146,222
PRIOR FILING DATE: 1999-07-28
PRIOR APPLICATION NUMBER: PCT/US99/20594
PRIOR FILING DATE: 1999-09-08
PRIOR APPLICATION NUMBER: PCT/US99/20944
PRIOR FILING DATE: 1999-09-13
PRIOR APPLICATION NUMBER: PCT/US99/21090
PRIOR FILING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: PCT/US99/21547
PRIOR FILING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: PCT/US99/23089
PRIOR FILING DATE: 1999-10-05
PRIOR APPLICATION NUMBER: PCT/US99/28214
PRIOR FILING DATE: 1999-11-29
PRIOR APPLICATION NUMBER: PCT/US99/28313
PRIOR FILING DATE: 1999-11-30
PRIOR APPLICATION NUMBER: PCT/US99/28564
PRIOR FILING DATE: 1999-12-02
PRIOR APPLICATION NUMBER: PCT/US99/28565
PRIOR FILING DATE: 1999-12-02
PRIOR APPLICATION NUMBER: PCT/US99/30095
PRIOR FILING DATE: 1999-12-16
PRIOR APPLICATION NUMBER: PCT/US99/30911
PRIOR FILING DATE: 1999-12-20
PRIOR APPLICATION NUMBER: PCT/US99/30999
PRIOR FILING DATE: 1999-12-20
PRIOR APPLICATION NUMBER: PCT/US00/00219
NUMBER OF SEQ ID NOS: 423
SEQ ID NO 34
LENGTH: 915
TYPE: PRT
: ORGANISM: Homo sapiens
US-09-905-125A-34

Query Match      5.6%; Score 95.5; DB 4; Length 915;
Best Local Similarity 18.0%; Pred. No. 0.29; Indels 131; Gaps 15;
Matches 65; Conservative 47; Mismatches 118;

QY 31 GTAAAEAFDSVLCGTASCHRAQOLTYPLHTYKKEELVACQ-----RCGRFSI 79
Db 479 GKTCAKUDSCALGD-----HGCE-----HSCVSSSDSFVCCFEGYILREBCKTRKRDV 528
QY 80 CQFVDDGIDLNRKTLKECSACTEAYSQSDQYAC-----HL 115
Db 529 COADIDHG-----CEHICV-----NSDSYTCCECLGFLAEDGKCRKRDVCKSTHH 575
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[illegible]

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: RESULT 8
: US-09-902-775A-34
: Sequence 34, Application US/09902775A
: Patent No. 6686451
: GENERAL INFORMATION:
: APPLICANT: Genentech, Inc.
: APPLICANT: Ashkenazi, Avi
: APPLICANT: Botstein, David
: APPLICANT: Desnovers, Luc
: APPLICANT: Eaton, Dan L.
: APPLICANT: Ferrara, Napoleone
: APPLICANT: Filvaroff, Ellen
: APPLICANT: Fong, Sherman
: APPLICANT: Gao, Wei-Qiang
: APPLICANT: Gerber, Hanspeter
: APPLICANT: Gerritsen, Mary E.
: APPLICANT: Goddard, A.
: APPLICANT: Godowski, Paul J.
: APPLICANT: Grimaldi, Christopher J.
: APPLICANT: Gurney, Austin L.
: APPLICANT: Hillan, Kenneth, J.
: APPLICANT: Kljavin, Ivar J.
: APPLICANT: Mather, Jennie P.
: APPLICANT: Pan, James
: APPLICANT: Paoni, Nicholas F.
: APPLICANT: Roy, Margaret Ann
: APPLICANT: Stewart, Timothy A.
: APPLICANT: Tumas, Daniel
: APPLICANT: Williams, P. Mickey
: APPLICANT: Wood, William, I.
: TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
: TITLE OF INVENTION: Acids Encoding the Same
: FILE REFERENCE: 10466-14
: CURRENT APPLICATION NUMBER: US/09/902,775A
: CURRENT FILING DATE: 2001-07-10
: PRIOR APPLICATION NUMBER: PCT/US00/04414
: PRIOR FILING DATE: 2000-02-22
: PRIOR APPLICATION NUMBER: US 60/143,048
: PRIOR FILING DATE: 1999-07-07
: PRIOR APPLICATION NUMBER: US 60/145,698
: PRIOR FILING DATE: 1999-07-26
: PRIOR APPLICATION NUMBER: US 60/146,222
: PRIOR FILING DATE: 1999-07-28
: PRIOR APPLICATION NUMBER: PCT/US99/20594
: PRIOR FILING DATE: 1999-09-08
: PRIOR APPLICATION NUMBER: PCT/US99/20944
: PRIOR FILING DATE: 1999-09-13
: PRIOR APPLICATION NUMBER: PCT/US99/21090
: PRIOR FILING DATE: 1999-09-15
: PRIOR APPLICATION NUMBER: PCT/US99/21547
: PRIOR FILING DATE: 1999-09-15
: PRIOR APPLICATION NUMBER: PCT/US99/23089

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? PRIOR FILING DATE: 1999-10-05
? PRIOR APPLICATION NUMBER: PCT/US99/28214
? PRIOR FILING DATE: 1999-11-29
? PRIOR APPLICATION NUMBER: PCT/US99/28313
? PRIOR FILING DATE: 1999-11-30
? PRIOR APPLICATION NUMBER: PCT/US99/28564
? PRIOR FILING DATE: 1999-12-02
? PRIOR APPLICATION NUMBER: PCT/US99/28565
? PRIOR FILING DATE: 1999-12-02
? PRIOR APPLICATION NUMBER: PCT/US99/30095
? PRIOR FILING DATE: 1999-12-16
? PRIOR APPLICATION NUMBER: PCT/US99/30911
? PRIOR FILING DATE: 1999-12-20
? PRIOR APPLICATION NUMBER: PCT/US99/30999
? PRIOR FILING DATE: 1999-12-20
? PRIOR APPLICATION NUMBER: PCT/US00/00219
? PRIOR FILING DATE: 2000-01-05
? NUMBER OF SEQ ID NOS: 423
? SEQ ID NO 34
? LENGTH: 915
? TYPE: PRT
? ORGANISM: Homo sapiens
US-09-902-775A-34

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| Query Match | 5.6%; | Score 95.5; | DB 4; | Length 915; |
| Best Local Similarity | 18.0%; | Pred. No. 0.29; | | |
| Matches | 65; | Conservative | 47; | Mismatches 118; Indels 131; Gaps 15 |

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| Qy | 31 | GTASAAPFDSVLSGPTASCHRAQCLTPLYLHTYPKKEELVACQ----- | RGCRLSFI | 79 |
| Db | 479 | GKTCAKLSDSCALGD-----HGCE-----HSCVSESDSFVCCCFEGYLIREDGKTCRRKDV | | 528 |
| Qy | 80 | CGPFDGGLDINRRTLCEGSACTEAYSQSDQYAC----- | HL | 115 |
| Db | 529 | CGALDHG-----CEHICV-----NSDSITCECEGFFLAEDGKCRKKDYCKSTHH | | 575 |
| Qy | 116 | GCON-----QLPFAELRQEOQLMSIMPKMHLFPPLYLVRFSFMDKDSAQ | | 160 |
| Db | 576 | GCEHICVNNNGNSYICKSGSEGFVLAEDGRCKCTEGPDLVFVLDGSKSLGEENFEVYKQ | | 635 |
| Qy | 161 | FITSWTFPLQADGKVIYQSKRE-----IQVAPHLEQPTLRESLSKMSYLQNRN | | 214 |
| Db | 636 | FVLT-----GIIDSLTISPKARVGLLOYSTOVHTEFT-LRNFSNAK---DMKK | | 679 |
| Qy | 215 | SOAHRNFLDEGSDG-----FLRCLSLNSGMITLTLVLVSVMILWICCATVATAVEQY | | 268 |
| Db | 680 | AVAMKMKMGKSGWGLAKHMFERSFLQGEG-----ARPLSTR | | 717 |
| Qy | 269 | VPSKSLSLTYGD-----LEPMNQKLRNYASSLVVVRKSTDEPHEAGPLPTKYNLAHS | | 321 |
| Db | 718 | VPRALV-VFTDGRAQDDVSEWASAKANGITMVAVGKALEELQETASEPNNKHLFYA | | 776 |
| Qy | 322 | E 322 | | |
| Db | 777 | E 777 | | |

| | |
|----------|---------------------------------------|
| RESULT 9 | US-09-906-700-34 |
| | : Sequence 34, Application us/0906700 |
| | : Patent No. 6723535 |
| | GENERAL INFORMATION: |
| | APPLICANT: Genentech, Inc. |
| | APPLICANT: Aethkenazi, Avi |
| | APPLICANT: Botsstein, David |
| | APPLICANT: Desnoyers, Luc |
| | APPLICANT: Baton, Dan L. |
| | APPLICANT: Ferrara, Napoleone |
| | APPLICANT: Filvaroff, Ellen |
| | APPLICANT: Fong, Sherman |
| | APPLICANT: Gao, Wei-Qiang |
| | APPLICANT: Gerber, Hanspeter |
| | APPLICANT: Gerritsen, Mary E. |

APPLICANT: Goddard, A.
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, Christopher J.
APPLICANT: Gurney, Austin L.
APPLICANT: Hillan, Kenneth, J.
APPLICANT: Kljavin, Ivar J.
APPLICANT: Mather, Jennie P.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: 1046-14
CURRENT APPLICATION NUMBER: US/09/906,700
CURRENT FILING DATE: 2000-09-18
PRIOR APPLICATION NUMBER: PCT/US00/04414
PRIOR FILING DATE: 2000-02-22
PRIOR APPLICATION NUMBER: US 60/143,048
PRIOR FILING DATE: 1999-07-07
PRIOR APPLICATION NUMBER: US 60/145,698
PRIOR FILING DATE: 1999-07-26
PRIOR APPLICATION NUMBER: US 60/146,222
PRIOR FILING DATE: 1999-07-28
PRIOR APPLICATION NUMBER: PCT/US99/20594
PRIOR FILING DATE: 1999-09-08
PRIOR APPLICATION NUMBER: PCT/US99/20944
PRIOR FILING DATE: 1999-09-13
PRIOR APPLICATION NUMBER: PCT/US99/21090
PRIOR FILING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: PCT/US99/21547
PRIOR FILING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: PCT/US99/23089
PRIOR FILING DATE: 1999-10-05
PRIOR APPLICATION NUMBER: PCT/US99/28214
PRIOR FILING DATE: 1999-11-29
PRIOR APPLICATION NUMBER: PCT/US99/28313
PRIOR FILING DATE: 1999-11-30
PRIOR APPLICATION NUMBER: PCT/US99/28564
PRIOR FILING DATE: 1999-12-02
PRIOR APPLICATION NUMBER: PCT/US99/28565
PRIOR FILING DATE: 1999-12-02
PRIOR APPLICATION NUMBER: PCT/US99/30095
PRIOR FILING DATE: 1999-12-16
PRIOR APPLICATION NUMBER: PCT/US99/30911
PRIOR FILING DATE: 1999-12-20
PRIOR APPLICATION NUMBER: PCT/US99/30999
PRIOR FILING DATE: 1999-12-20
PRIOR APPLICATION NUMBER: PCT/US00/00219
PRIOR FILING DATE: 2000-01-05
NUMBER OF SEQ ID NOS: 423
SEQ ID NO 34
LENGTH: 915
TYPE: PRT
ORGANISM: Homo sapiens
US-09-906-700-34

Query Match 5.6%; Score 95.5; DB 4; Length 915;
Best Local Similarity 18.0%; Pred. No. 0.29; Indels 111; Gaps 15;
Matches 65; Conservative 47; Mismatches 118

31 GTASAEAFDVLGDTASCHRAQCLTYPLATYPKKEELVACQ-----RGRRLPSI 79
479 GKTCAKLDSCALGD-----HGCE-----HSCVSSSDSFVCCCFEGYILREDOKTCRRKDV 528
80 CQFVDDGIDLNRKTLCEGSACTEANSQSDEQYAC-----HL 115
529 CQALIDHG-----CEHICV-----NSDDSTYTCLEGLFRLAEDGKRCRRDYCKSTTH 575
116 GCQN-----QLPFAELRQEQLMSLMPKQHLLEPLTLVRSFMSDMMDASQS 160

DB 576 GCEHICVNNNGNSYICKCEGFFVLAEDGRCKKCTEGPIDLVFVIDGSKSLGSENEPVKQ 635
QY 161 FITSWTFYTLQADGCKYIFOSKPE-----IQYAPHLEQEPYTNRESLSMSTLQWRN 214
DB 636 FVT-----GIDSLTISPPCARVGLQYSTOVHTFT- LRNNSAK-----DMKK 679
QY 215 SOAHNFLEDESDD-----FLNCLSNCGMILTTTLVLSVMVLLWICATVATAVEQY 268
DB 680 AVAHMKYKGSMTGLAKNHFERSFTGEG-----APPLSTR 717
QY 269 VPSEKSLYGD-----LEFMNEQKLNRYPASSLVVRSKTEDEHAGPLPTKYNLAHS 321
DB 718 VPRALVFTDGRADDVSNASAKANGITMYANGVKALBELLQELASEPTNGLFPA 776
QY 322 E 322
DB 777 E 777

RESULT 10
US-09-903-603a-34
Sequence 34, Application US/09903603A
Patent No. 6767995
GENERAL INFORMATION:
APPLICANT: Genentech, Inc.
APPLICANT: Ashkenazi, Avi
APPLICANT: Botstein, David
APPLICANT: Deenoyers, Luc
APPLICANT: Baton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Filvaroff, Ellen
APPLICANT: Fong, Sherman
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerdtzen, Mary B.
APPLICANT: Goddard, A.
APPLICANT: Godowski, Paul J.
APPLICANT: Gurney, Austin L.
APPLICANT: Hillan, Kenneth, J.
APPLICANT: Kljavin, Ivar J.
APPLICANT: Mather, Jennie P.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William, I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: GNE.16182C12
CURRENT APPLICATION NUMBER: US/09/903,603A
CURRENT FILING DATE: 2001-07-11
PRIOR APPLICATION NUMBER: PCT/US00/04414
PRIOR FILING DATE: 2000-02-22
PRIOR APPLICATION NUMBER: US 60/143,048
PRIOR FILING DATE: 1999-07-07
PRIOR APPLICATION NUMBER: US 60/145,698
PRIOR FILING DATE: 1999-07-26
PRIOR APPLICATION NUMBER: US 60/146,222
PRIOR FILING DATE: 1999-07-28
PRIOR APPLICATION NUMBER: PCT/US99/20594
PRIOR FILING DATE: 1999-09-08
PRIOR APPLICATION NUMBER: PCT/US99/20944
PRIOR FILING DATE: 1999-09-13
PRIOR APPLICATION NUMBER: PCT/US99/21090
PRIOR FILING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: PCT/US99/21547
PRIOR FILING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: PCT/US99/23089
PRIOR FILING DATE: 1999-10-05

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; PRIOR APPLICATION NUMBER: PCT/US99/28214
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: PCT/US99/28313
; PRIOR FILING DATE: 1999-11-30
; PRIOR APPLICATION NUMBER: PCT/US99/28564
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/28565
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: PCT/US99/30911
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US99/30999
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US00/00219
; PRIOR FILING DATE: 2000-01-05
; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 34
; LENGTH: 915
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-903-603A-34
```

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Query Match      5.6%; Score 95.5; DB 4; Length 915;
Best Local Similarity 18.0%; Pred. No. 0.29;
Matches 65; Conservative 47; Mismatches 118; Indels 131; Gaps 15;
```

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QY 31 GTASAEAFDSVLTGPTASCHRAQULYPLHYPKBEELVACO-----RGCRLSFI 79
DB 479 GKTCAKLDSCALGD-----HGCE-----HSCVSSSEDSFVQCCEGYTLREDGKTCRKDV 528
QY 80 CQFVDDGIDINRTKLECSACTEAYSSQSDQYAC-----HL 115
DB 529 CQALDHG-----CEHICV-----NSDDSYTCCELGFRFLAEDGKCRKDVCKSTHH 575
QY 116 GCQN-----OLPFAELROEQLMSLMPKMLLFPPLTVRSFWSMDMSAQS 160
DB 576 GEHENICVANNNGNSYICKCSERGFVLAEDGRCKCTEGPDLVAVGDSKSLGEENEVAVKQ 635
QY 161 FTTSWTFYLAQDDKTYIVFQSKPE-----IOVAPHLEQEPNTNRESLSMSTLQKRN 214
DB 636 FVT-----LITSLTSPRAARVGLQYSTQVTEFT-LRNFSAR-----DKK 679
QY 215 SQAHNFLEDESDG-----FLRCLSLNSGWLTTTLVLSVWVLWLCATVATAVEQY 268
DB 680 AVAHMKWKGKSGMTGLAKHMERSEFTQSEG-----APPLSTR 717
QY 269 VPSEKLSTYGD-----LEFANEQKLNRYPASSLVVRSKTEDEHEAGPLTKVNLAS 321
DB 718 VPRRAI-VFTDGRADQDVSEWASKAKANGITWYAVGVKALIEELQELIASSEFTNGLFYA 776
QY 322 E 322
DB 777 E 777
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RESULT 11
US-09-904-920A-34
; Sequence 34, Application US/09904920A
; Patent No. 6806352
```

```

; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gottard, A.
```

```

; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gunney, Austin L.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: KJavin, Ivar J.
; APPLICANT: Macher, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: 10466-14
; CURRENT APPLICATION NUMBER: US/09/904,920A
; PRIOR FILING DATE: 2001-07-13
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: US 60/143,048
; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: US 60/145,698
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: US 60/146,222
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: PCT/US99/20594
; PRIOR FILING DATE: 1999-09-08
; PRIOR APPLICATION NUMBER: PCT/US99/20944
; PRIOR FILING DATE: 1999-09-13
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/21547
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/23089
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: PCT/US99/28214
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: PCT/US99/28313
; PRIOR FILING DATE: 1999-11-30
; PRIOR APPLICATION NUMBER: PCT/US99/28564
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/28565
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: PCT/US99/30911
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US99/30999
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US00/00219
; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 34
; LENGTH: 915
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-904-920A-34
```

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Query Match      5.6%; Score 95.5; DB 4; Length 915;
Best Local Similarity 18.0%; Pred. No. 0.29;
Matches 65; Conservative 47; Mismatches 118; Indels 131; Gaps 15;
```

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QY 31 GTASAEAFDSVLTGPTASCHRAQULYPLHYPKBEELVACO-----RGCRLSFI 79
DB 479 GKTCAKLDSCALGD-----HGCE-----HSCVSSSEDSFVQCCEGYTLREDGKTCRKDV 528
QY 80 CQFVDDGIDINRTKLECSACTEAYSSQSDQYAC-----HL 115
DB 529 CQALDHG-----CEHICV-----NSDDSYTCCELGFRFLAEDGKCRKDVCKSTHH 575
QY 116 GCQN-----OLPFAELROEQLMSLMPKMLLFPPLTVRSFWSMDMSAQS 160
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Db 576 GCEHICVNNNGNSYICKSEGFVLAEDGRCKCTEGPIDLVFVIDGSKSLGEGNEFVVKQ 635
Qy 161 FITSMTFTYLAQDDKITYIFQSKPE-----IOYAPHLEQEPNTLRSSLSKMSYLOKRN 214
Db 636 FVT-----GIIDSLTISPPARVGLQYSTQVHTFT-LRNFSAR---DMKK 679
Qy 215 SOAHNFLEDGESD-----FLRCLSLNSGWLTTTLVLSVWVLMICATVATAVEQY 268
Db 660 AVAHMKYKXGKSGMTGLAKHMFERSFTQEG-----ARPLSTR 717
Qy 269 VPSEKLSIYGD-----LEFNNBQKLNRYPASSLVVRSKTEDEHAGPLPTKYNLAHS 321
Db 718 VPRRAI-VFTDGRADVDSEWASKAKANGITWYAVGVGKAIIEELQELIASPTNKLIFYA 776
Qy 322 E 322
Db 777 E 777

RESULT 12
US-09-909-064-34
; Sequence 34, Application US/09909064
; Patent No. 6818449
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnovers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: 10466-14
; CURRENT APPLICATION NUMBER: US/09/909,064
; PRIOR FILING DATE: 2001-07-18
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: US 60/143,048
; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: US 60/145,698
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: US 60/146,222
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: PCT/US99/20594
; PRIOR FILING DATE: 1999-09-08
; PRIOR APPLICATION NUMBER: PCT/US99/20944
; PRIOR FILING DATE: 1999-09-13
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/21547
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/23089
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: PCT/US99/28214

; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: PCT/US99/28313
; PRIOR FILING DATE: 1999-11-30
; PRIOR APPLICATION NUMBER: PCT/US99/28564
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/28565
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/30095
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; PRIOR APPLICATION NUMBER: PCT/US99/30911
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US99/30999
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US00/00219
; PRIOR FILING DATE: 2000-01-05
; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 34
; LENGTH: 915
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-909-064-34

Query Match 5.6%; Score 95.5; DB 4; Length 915;
Best Local Similarity 18.0%; Pred. No. 0.29;
Matches 65; Conservative 47; Mismatches 118; Indels 131; Gaps 15;

Qy 31 GTASAPADSVYGDPRASCHRAQULTYPLTYKEBELYACQ-----RGCRLPBI 79
Db 479 GRTCAKLNSCALGD-----HGCE-----HSCVSSSDSPVCCQCFEGYILREDGKTRKRDV 528
Qy 80 CQFVDGIDILNRTKLECSACTEAYSQSDEQYAC-----HL 115
Db 529 COAIDHG-----CHICY-----NSDDSTTCCLGFRLAEDGKCRKRDVCKSTH 575
Qy 116 GCQN-----QLPFAELROEQLSLMPKHLPLPLTVLSFMSDMMDSAGS 160.
Db 576 GCEHICVNNNGNSYICKSEGFVLAEDGRCKCTEGPIDLVFVIDGSKSLGEGNEFVVKQ 635
Qy 161 FITSMTFTYLAQDDKITYIFQSKPE-----IOYAPHLEQEPNTLRSSLSKMSYLOKRN 214
Db 636 FVT-----GIIDSLTISPPARVGLQYSTQVHTFT-LRNFSAR---DMKK 679
Qy 215 SOAHNFLEDGESD-----FLRCLSLNSGWLTTTLVLSVWVLMICATVATAVEQY 268
Db 660 AVAHMKYKXGKSGMTGLAKHMFERSFTQEG-----ARPLSTR 717
Qy 269 VPSEKLSIYGD-----LEFNNBQKLNRYPASSLVVRSKTEDEHAGPLPTKYNLAHS 321
Db 718 VPRRAI-VFTDGRADVDSEWASKAKANGITWYAVGVGKAIIEELQELIASPTNKLIFYA 776
Qy 322 E 322
Db 777 E 777

RESULT 13
US-09-905-381A-34
; Sequence 34, Application US/09905381A
; Patent No. 6818746
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnovers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.

```
APPLICANT: Grimaldi, Christopher J.
APPLICANT: Gurney, Austin L.
APPLICANT: Hillan, Kenneth J.
APPLICANT: Kljavin, Ivar J.
APPLICANT: Mather, Jennie P.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William, I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: 10466-14
CURRENT FILING DATE: 2001-07-13
PRIOR APPLICATION NUMBER: US/09/905,381A
PRIOR FILING DATE: 2000-02-22
PRIOR APPLICATION NUMBER: PCT/US00/04414
PRIOR FILING DATE: 2000-02-22
PRIOR APPLICATION NUMBER: US 60/143,048
PRIOR FILING DATE: 1999-07-07
PRIOR APPLICATION NUMBER: US 60/145,698
PRIOR FILING DATE: 1999-07-26
PRIOR APPLICATION NUMBER: US 60/146,222
PRIOR FILING DATE: 1999-07-28
PRIOR APPLICATION NUMBER: PCT/US99/20594
PRIOR FILING DATE: 1999-09-08
PRIOR APPLICATION NUMBER: PCT/US99/20944
PRIOR FILING DATE: 1999-09-13
PRIOR APPLICATION NUMBER: PCT/US99/21090
PRIOR FILING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: PCT/US99/21547
PRIOR FILING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: PCT/US99/23089
PRIOR FILING DATE: 1999-10-05
PRIOR APPLICATION NUMBER: PCT/US99/28214
PRIOR FILING DATE: 1999-11-29
PRIOR APPLICATION NUMBER: PCT/US99/28313
PRIOR FILING DATE: 1999-11-30
PRIOR APPLICATION NUMBER: PCT/US99/28564
PRIOR FILING DATE: 1999-12-02
PRIOR APPLICATION NUMBER: PCT/US99/28565
PRIOR FILING DATE: 1999-12-02
PRIOR APPLICATION NUMBER: PCT/US99/30095
PRIOR FILING DATE: 1999-12-16
PRIOR APPLICATION NUMBER: PCT/US99/30911
PRIOR FILING DATE: 1999-12-20
PRIOR APPLICATION NUMBER: PCT/US99/30999
PRIOR FILING DATE: 1999-12-20
PRIOR APPLICATION NUMBER: PCT/US00/00219
PRIOR FILING DATE: 2000-01-05
NUMBER OF SEQ ID NOS: 423
SEQ ID NO 34
LENGTH: 915
TYPE: PRT
ORGANISM: Homo sapiens
US-09-905-381A-34

Query Match      5.6%; Score 95.5; DB 4; Length 915;
Best Local Similarity 18.0%; Pred. No. 0.29;
Matches 65; Conservative 47; Mismatches 118; Indels 131; Gaps 15;

QY 31 GTASAPADSVLGDPTASGHRACQLTYPLHYPKREBELYAC-----RGCRLSFI 79
DB 479 GRTKAKLSDSCALGD-----HGCE-----HSCVSSSDSFVCCQCFEGYIILREBGTCKRRADV 528
QY 80 CQFVVDGIDILARKTKECESACTEAVSQSDQDYAC-----HL 115
DB 529 COAIDHG-----CHICV-----NSDSYTCCELEGFRLAEDGKCRKRDYCKSTHH 575
QY 116 GCQNN-----QLPFAELROEQMLMKPKHLLFPLTLVRSFMSDDMDSQOS 160
DB 576 GCCHICVNNNGNSYTCGSEBGFVLADGRRCKCKCTGPIDLVFLVIGSKSLGSENFENVVQK 635
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QY 161 FITSMTFVYLQADGKIVIFQSKPR-----IOYAPHLEQEPNLRBESSLSKMSYLOWRN 214
DB 636 FVT-----GIIDSLTISPKAAVGLLOYSOVHTFT-LRNNSNAK---DKK 679
QY 215 SOAHNPLEDESDG-----FLRCLSLNSGMILTTTLVLVSWVLWLICATVAVAEQY 268
DB 680 AVAHMKVKGKSWMTGLAKHMFERSFTQEG-----ARPLSTR 717
QY 269 VPSEKLSIYGD-----LEMEQKLNRYPASSLVYVRKSTEDHEEAGPLPTKVNLAHS 321
DB 718 VPRAL-VFTDGRADVDVSEWASRAKANGITMYAVGVKALBELQETASBPTKHLFYA 776
QY 322 E 322
DB 777 E 777

RESULT 14
US-09-906-618-34
Sequence 34, Application US/09906618
Patent No. 6828146
GENERAL INFORMATION:
APPLICANT: Genentech, Inc.
APPLICANT: Ashkenazi, Avi
APPLICANT: Botstein, David
APPLICANT: Deanoysers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Filvaroff, Ellen
APPLICANT: Fong, Sherman
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, A.
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, Christopher J.
APPLICANT: Gurney, Austin L.
APPLICANT: Hillan, Kenneth J.
APPLICANT: Kljavin, Ivar J.
APPLICANT: Mather, Jennie P.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William, I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: 10466-14
CURRENT FILING DATE: US/09/906,618
PRIOR APPLICATION NUMBER: PCT/US00/04414
PRIOR FILING DATE: 2000-02-22
PRIOR APPLICATION NUMBER: US 60/143,048
PRIOR FILING DATE: 1999-07-07
PRIOR APPLICATION NUMBER: US 60/145,698
PRIOR FILING DATE: 1999-07-26
PRIOR APPLICATION NUMBER: US 60/146,222
PRIOR FILING DATE: 1999-07-28
PRIOR APPLICATION NUMBER: PCT/US99/20594
PRIOR FILING DATE: 1999-09-08
PRIOR APPLICATION NUMBER: PCT/US99/20944
PRIOR FILING DATE: 1999-09-13
PRIOR APPLICATION NUMBER: PCT/US99/21090
PRIOR FILING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: PCT/US99/21547
PRIOR FILING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: PCT/US99/23089
PRIOR FILING DATE: 1999-10-05
PRIOR APPLICATION NUMBER: PCT/US99/28214
PRIOR FILING DATE: 1999-11-29
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; PRIOR APPLICATION NUMBER: PCT/US99/28313
; PRIOR FILING DATE: 1999-11-30
; PRIOR APPLICATION NUMBER: PCT/US99/28564
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/28565
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: PCT/US99/30911
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US99/30999
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US00/00219
; PRIOR FILING DATE: 2000-01-05
; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 34
; LENGTH: 915
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-906-618-34

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Query Match      5.6%; Score 95.5; DB 4; Length 915;
Best Local Similarity 18.0%; Pred. No. 0.29;
Matches 65; Conservative 47; Mismatches 118; Indels 131; Gaps 15;

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QY 31 GTASAEAFDSVIGDTASCHRAQQLTYPLTYPKREELVACQ-----RGCRLPSI 79
DB 479 GRTCKAKLDSALGD-----HGCE-----HSCVSSSDSFVCCQCFEGYILREDGKTCRRKDV 528
QY 80 CQFVDDGIDILNRTKLECSACTEAYSQSDQYAC-----HL 115
DB 529 COALDHG-----CEHICV-----NSDDSYTCCLGFRLAEDGKRCRRKDVCKSTH 575
QY 116 GCQN-----QLPFAELROQLMSLMPKXHLPLTLVRSFMSDMMSAQ 160
DB 576 GCEHICVNNNGNSYICKCEGFLVLAEDGRCKCTGEPIDLVFVINDGSKSLGEENFEVYKQ 635
QY 161 FITSSWTFYLAADGKIYIFOSKPE-----IOVAPHLEOEPNTLRSSLSKSYLOMKN 214
DB 636 FVT-----GIIDSLTISPKARVGLQYSTQVHTFT-LRNFRSAK-----DMKK 679
QY 215 SOAHNPLEDESDG-----FLRCLSLNSGWLITTLVLSVWLMLICATVATAVEQY 268
DB 680 AVAHMKYMGKSMGTGLAKHMERSTQEG-----ARPLSTR 717
QY 269 VPSEKLSIYGD-----LEFNNBOKLNRYPASSLVVRSKTEDHEBAGPLTKVNLAS 321
DB 718 VPRALVFTDGRADVDVSEWASKAKANGITWYAVGVKALIEBLQELIASBPTNGLPYA 776
QY 322 E 322
DB 777 E 777

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RESULT 15
US-09-949-016-6215
; Sequence 6215, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CLO01307
; CURRENT APPLICATION NUMBER: US/09/949,016
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0

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; SEQ ID NO 6215
; LENGTH: 956
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-6215

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Query Match      5.5%; Score 93.5; DB 4; Length 956;
Best Local Similarity 18.0%; Pred. No. 0.53;
Matches 65; Conservative 46; Mismatches 119; Indels 131; Gaps 15;

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QY 31 GTASAEAFDSVIGDTASCHRAQQLTYPLTYPKREELVACQ-----RGCRLPSI 79
DB 520 GRTCKAKLDSALGD-----HGCE-----HSCVSSSDSFVCCQCFEGYILREDGKTCRRKDV 569
QY 80 CQFVDDGIDILNRTKLECSACTEAYSQSDQYAC-----HL 115
DB 570 COALDHG-----CEHICV-----NSDDSYTCCLGFRLAEDGKRCRRKDVCKSTH 616
QY 116 GCQN-----QLPFAELROQLMSLMPKXHLPLTLVRSFMSDMMSAQ 160
DB 617 GCEHICVNNNGNSYICKCEGFLVLAEDGRCKCTGEPIDLVFVINDGSKSLGEENFEVYKQ 676
QY 161 FITSSWTFYLAADGKIYIFOSKPE-----IOVAPHLEOEPNTLRSSLSKSYLOMKN 214
DB 677 FVT-----GIIDSLTISPKARVGLQYSTQVHTFT-LRNFRSAK-----DMKK 720
QY 215 SOAHNPLEDESDG-----FLRCLSLNSGWLITTLVLSVWLMLICATVATAVEQY 268
DB 721 AVAHMKYMGKSMGTGLAKHMERSTQEG-----ARPLSTR 758
QY 269 VPSEKLSIYGD-----LEFNNBOKLNRYPASSLVVRSKTEDHEBAGPLTKVNLAS 321
DB 759 VPRALVFTDGRADVDVSEWASKAKANGITWYAVGVKALIEBLQELIASBPTNGLPYA 817
QY 322 E 322
DB 818 E 818

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Search completed: March 28, 2005, 13:10:28
Job time : 41 secs

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GenCore version 5.1.6
OM protein - protein search, using sw model
Run on: March 28, 2005, 13:08:15 ; Search time 68 Seconds
(without alignments)
1837.112 Million cell updates/sec

Title: US-09-978-299a-330
Perfect score: 1694
Sequence: 1 MAARKSLWVRVTLGLPPL.....EDHEAGPLPKVNLHSEI 323
Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5
Total number of hits satisfying chosen parameters: 2105692
Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%

Database : Listing first 1500 summaries
1: Geneseq_16Dec04:*

2: Geneseqp1980s:*
3: Geneseqp2000s:*
4: Geneseqp2001s:*
5: Geneseqp2002s:*
6: Geneseqp2003as:*
7: Geneseqp2003bs:*
8: Geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Description

RESULT 1 No. Score Match Length DB ID
ID AA41733 standard; protein; 323 AA.
DE Human PRO195 protein sequence.

PN WO9946281-A2.
PD 16-SEP-1999.

PA (GETH) GENENTECH INC.

Query Match 100.0%; Score 1694; DB 2; Length 323;
Best Local Similarity 100.0%; Pred. No. 8.4e-167;

RESULT 2 ID AA57939 standard; protein; 323 AA.
DE Human transmembrane protein HTMPN-63.

PN WO9961471-A2.
PD 02-DEC-1999.

PA (INCY-) INCYTE PHARM INC.

Query Match 100.0%; Score 1694; DB 3; Length 323;
Best Local Similarity 100.0%; Pred. No. 8.4e-167;

RESULT 3 ID AAB44289 standard; protein; 323 AA.
DE Human PRO195 (UNQ169) protein sequence SEQ ID NO:330.

PN WO200053756-A2.
PD 14-SEP-2000.

PA (GETH) GENENTECH INC.

Query Match 100.0%; Score 1694; DB 3; Length 323;
Best Local Similarity 100.0%; Pred. No. 8.4e-167;

RESULT 4 ID AAB24394 standard; protein; 323 AA.
DE Human PRO195 protein sequence SEQ ID NO:31.

PN WO200032221-A2.
PD 08-JUN-2000.

PA (GETH) GENENTECH INC.

Query Match 100.0%; Score 1694; DB 3; Length 323;
Best Local Similarity 100.0%; Pred. No. 8.4e-167;

RESULT 5 ID AA778804 standard; protein; 323 AA.
DE Hydrophobic domain containing protein clone HPI0349 protein sequence.

PN WO200005056-A2.
PD 06-JAN-2000.

PA (SAGA) SAGAMI CHEM RES CENT.
PA (PROT-) PROTESENE INC.

Query Match 100.0%; Score 1694; DB 3; Length 323;
Best Local Similarity 100.0%; Pred. No. 8.4e-167;

RESULT 6 ID ABO25235 standard; protein; 323 AA.
DE Novel human secreted and transmembrane protein PRO195.

ID AAM93600 standard; protein; 323 AA.
DE Human polypeptide, SEQ ID NO: 3412.

PN EPI13094-A2.
PD 05-SEP-2001.

PA (HELI-) HELIX RES INST.

Query Match 100.0%; Score 1694; DB 4; Length 323;
Best Local Similarity 100.0%; Pred. No. 8.4e-167;

RESULT 7 ID AAU12307 standard; protein; 323 AA.
DE Human PRO195 polypeptide sequence.

PN WO200140466-A2.
PD 07-JUN-2001.

PA (GETH) GENENTECH INC.

Query Match 100.0%; Score 1694; DB 4; Length 323;
Best Local Similarity 100.0%; Pred. No. 8.4e-167;

RESULT 8 ID AAB53073 standard; protein; 323 AA.
DE Human angio genesis-associated protein PRO195, SEQ ID NO:46.

PN WO200053753-A2.
PD 14-SEP-2000.

PA (GETH) GENENTECH INC.

Query Match 100.0%; Score 1694; DB 4; Length 323;
Best Local Similarity 100.0%; Pred. No. 8.4e-167;

RESULT 9 ID AAB88428 standard; protein; 323 AA.
DE Human membrane or secretory protein clone PSEC0203.

PN EPI067182-A2.
PD 10-JAN-2001.

PA (HELI-) HELIX RES INST.

Query Match 100.0%; Score 1694; DB 4; Length 323;
Best Local Similarity 100.0%; Pred. No. 8.4e-167;

RESULT 10 ID AAB84820 standard; protein; 323 AA.
DE Human PRO195 protein sequence SEQ ID NO:8.

PN WO200200690-A2.
PD 03-JAN-2002.

PA (GETH) GENENTECH INC.

Query Match 100.0%; Score 1694; DB 5; Length 323;
Best Local Similarity 100.0%; Pred. No. 8.4e-167;

RESULT 11 ID ABB95426 standard; protein; 323 AA.
DE Human angio genesis related protein PRO195 SEQ ID NO: 8.

PN WO200208284-A2.
PD 31-JAN-2002.

PA (GETH) GENENTECH INC.

PA (BACE/) BAKER K P.

PA (FERF/) FERRARA N.

PA (GERB/) GERBER H.

PA (GERR/) GERRITSEN M E.

PA (GODD/) GODDARD A.

PA (GODO/) GODOMSKI P J.

PA (GURN/) GURNEY A L.

PA (HILL/) HILLAN K J.

PA (MARS/) MARSTERS S A.

PA (PANU/) PAN J.

PA (PAON/) PAONI N F.

PA (STEP/) STEPHAN J F.

PA (WATA/) WATANABE C K.

PA (WILL/) WILLIAMS P M.

PA (WOOD/) WOOD W I.

Query Match 100.0%; Score 1694; DB 5; Length 323;
Best Local Similarity 100.0%; Pred. No. 8.4e-167;

RESULT 12 ID ABO17751 standard; protein; 323 AA.
DE Novel human secreted and transmembrane protein PRO195.

PN US2003032156-A1.
PD 13-FEB-2003.

PA (GETH) GENENTECH INC.

Query Match 100.0%; Score 1694; DB 6; Length 323;
Best Local Similarity 100.0%; Pred. No. 8.4e-167;

RESULT 13 ID ABO25235 standard; protein; 323 AA.
DE Novel human secreted and transmembrane protein PRO195.

PN WO200200690-A2.
PD 03-JAN-2002.

PA (GETH) GENENTECH INC.

Query Match 100.0%; Score 1694; DB 6; Length 323;
Best Local Similarity 100.0%; Pred. No. 8.4e-167;

PN US2003050239-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1694; DB 6; Length 323;
Best Local Similarity 100.0%; Pred. No. 8.4e-167;
RESULT 14
ID ABU81005 standard; protein; 323 AA.
DE Human PRO polypeptide #136.
PN US2003004311-A1.
PD 02-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1694; DB 6; Length 323;
Best Local Similarity 100.0%; Pred. No. 8.4e-167;
RESULT 15
ID ABU72241 standard; protein; 323 AA.
DE Novel human secreted and transmembrane protein PRO195.
PN US2002192706-A1.
PD 19-DEC-2002.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1694; DB 6; Length 323;
Best Local Similarity 100.0%; Pred. No. 8.4e-167;
RESULT 16
ID ABU66705 standard; protein; 323 AA.
DE Human PRO polypeptide #136.
PN US2003036180-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1694; DB 6; Length 323;
Best Local Similarity 100.0%; Pred. No. 8.4e-167;
RESULT 17
ID ABU84921 standard; protein; 323 AA.
DE Human secreted and transmembrane polypeptide PRO195.
PN US2002177553-A1.
PD 28-NOV-2002.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1694; DB 6; Length 323;
Best Local Similarity 100.0%; Pred. No. 8.4e-167;
RESULT 18
ID ABU59786 standard; protein; 323 AA.
DE Novel secreted and transmembrane protein PRO195.
PN US2003017563-A1.
PD 23-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1694; DB 6; Length 323;
Best Local Similarity 100.0%; Pred. No. 8.4e-167;
RESULT 19
ID ABU61119 standard; protein; 323 AA.
DE Human PRO195 polypeptide.
PN US2002169284-A1.
PD 14-NOV-2002.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1694; DB 6; Length 323;
Best Local Similarity 100.0%; Pred. No. 8.4e-167;
RESULT 20
ID ABO24976 standard; protein; 323 AA.
DE Human secreted/transmembrane protein (PRO) #136.
PN US2003036179-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1694; DB 6; Length 323;
Best Local Similarity 100.0%; Pred. No. 8.4e-167;
RESULT 21
ID ABU80388 standard; protein; 323 AA.
DE Human secreted/transmembrane protein PRO195.
PN US2003004102-A1.
PD 02-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1694; DB 6; Length 323;
Best Local Similarity 100.0%; Pred. No. 8.4e-167;
RESULT 22
ID ABU66981 standard; protein; 323 AA.
DE Human secreted/transmembrane, PRO, protein SEQ ID 272.
PN US2003032155-A1.

PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1694; DB 6; Length 323;
Best Local Similarity 100.0%; Pred. No. 8.4e-167;
RESULT 23
ID ADA45791 standard; protein; 323 AA.
DE Novel human secreted and transmembrane protein PRO195.
PN US2003022328-A1.
PD 30-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1694; DB 6; Length 323;
Best Local Similarity 100.0%; Pred. No. 8.4e-167;
RESULT 24
ID ADA76222 standard; protein; 323 AA.
DE Human PRO polypeptide #136.
PN US2003073212-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1694; DB 6; Length 323;
Best Local Similarity 100.0%; Pred. No. 8.4e-167;
RESULT 25
ID ADA18872 standard; protein; 323 AA.
DE Human PRO polypeptide #136.
PN US2003054517-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1694; DB 6; Length 323;
Best Local Similarity 100.0%; Pred. No. 8.4e-167;
RESULT 26
ID ADA61495 standard; protein; 323 AA.
DE Homo sapiens.
PN US2003049816-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1694; DB 6; Length 323;
Best Local Similarity 100.0%; Pred. No. 8.4e-167;
RESULT 27
ID ADB19280 standard; protein; 323 AA.
DE Novel human secreted and transmembrane protein PRO195.
PN US2003068796-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1694; DB 6; Length 323;
Best Local Similarity 100.0%; Pred. No. 8.4e-167;
RESULT 28
ID ADB27821 standard; protein; 323 AA.
DE Human PRO polypeptide #136.
PN US2003082704-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1694; DB 6; Length 323;
Best Local Similarity 100.0%; Pred. No. 8.4e-167;
RESULT 29
ID ADA86300 standard; protein; 323 AA.
DE Novel human secreted and transmembrane protein PRO195.
PN US2003082711-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1694; DB 6; Length 323;
Best Local Similarity 100.0%; Pred. No. 8.4e-167;
RESULT 30
ID ADB15864 standard; protein; 323 AA.
DE Human PRO polypeptide #136.
PN US2003087350-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1694; DB 6; Length 323;
Best Local Similarity 100.0%; Pred. No. 8.4e-167;
RESULT 31
ID ADA47650 standard; protein; 323 AA.
DE Human PRO polypeptide #136.
PN US2003073215-A1.
PD 17-APR-2003.

PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1694; DB 6; Length 323;
Best Local Similarity 100.0%; Pred. No. 8.4e-167;
RESULT 32
ID ADA67445 standard; protein; 323 AA.
DE Human PRO polypeptide #136.
PN US2003068795-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1694; DB 6; Length 323;
Best Local Similarity 100.0%; Pred. No. 8.4e-167;
RESULT 33
ID ADA30452 standard; protein; 323 AA.
DE Human PRO polypeptide #136.
PN US2003068794-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1694; DB 6; Length 323;
Best Local Similarity 100.0%; Pred. No. 8.4e-167;
RESULT 34
ID ADA85748 standard; protein; 323 AA.
DE Novel human secreted and transmembrane protein PRO195.
PN US2003082693-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1694; DB 6; Length 323;
Best Local Similarity 100.0%; Pred. No. 8.4e-167;
RESULT 35
ID ADA69690 standard; protein; 323 AA.
DE Human PRO polypeptide #136.
PN US2003082705-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1694; DB 6; Length 323;
Best Local Similarity 100.0%; Pred. No. 8.4e-167;
RESULT 36
ID ADA79264 standard; protein; 323 AA.
DE Human PRO polypeptide #136.
PN US2003082763-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1694; DB 6; Length 323;
Best Local Similarity 100.0%; Pred. No. 8.4e-167;
RESULT 37
ID ADA87403 standard; protein; 323 AA.
DE Novel human secreted and transmembrane protein PRO195.
PN US2003087345-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1694; DB 6; Length 323;
Best Local Similarity 100.0%; Pred. No. 8.4e-167;
RESULT 38
ID ADB16605 standard; protein; 323 AA.
DE Human PRO polypeptide #136.
PN US2003087349-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1694; DB 6; Length 323;
Best Local Similarity 100.0%; Pred. No. 8.4e-167;
RESULT 39
ID ADA91697 standard; protein; 323 AA.
DE Novel human secreted and transmembrane protein PRO195.
PN US2003082694-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1694; DB 6; Length 323;
Best Local Similarity 100.0%; Pred. No. 8.4e-167;
RESULT 40
ID ADB14760 standard; protein; 323 AA.
DE Human PRO polypeptide #136.
PN US2003087351-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1694; DB 6; Length 323;
Best Local Similarity 100.0%; Pred. No. 8.4e-167;
RESULT 41
ID ADA24669 standard; protein; 323 AA.
DE Novel human secreted and transmembrane protein PRO195.
PN US2003050241-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1694; DB 6; Length 323;
Best Local Similarity 100.0%; Pred. No. 8.4e-167;
RESULT 42
ID ADB18721 standard; protein; 323 AA.
DE Novel human secreted and transmembrane protein PRO195.
PN US2003073211-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1694; DB 6; Length 323;
Best Local Similarity 100.0%; Pred. No. 8.4e-167;
RESULT 43
ID ADA93936 standard; protein; 323 AA.
DE Human PRO polypeptide #136.
PN US2003077722-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1694; DB 6; Length 323;
Best Local Similarity 100.0%; Pred. No. 8.4e-167;
RESULT 44
ID ADB19832 standard; protein; 323 AA.
DE Novel human secreted and transmembrane protein PRO195.
PN US2003082691-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1694; DB 6; Length 323;
Best Local Similarity 100.0%; Pred. No. 8.4e-167;
RESULT 45
ID ADB13144 standard; protein; 323 AA.
DE Human PRO polypeptide #136.
PN US2003082710-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1694; DB 6; Length 323;
Best Local Similarity 100.0%; Pred. No. 8.4e-167;
RESULT 46
ID ABO43284 standard; protein; 323 AA.
DE Novel human secreted and transmembrane protein PRO195.
PN US2003044945-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1694; DB 6; Length 323;
Best Local Similarity 100.0%; Pred. No. 8.4e-167;
RESULT 47
ID ABO19690 standard; protein; 323 AA.
DE Novel human secreted and transmembrane protein PRO195.
PN US2003050240-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1694; DB 6; Length 323;
Best Local Similarity 100.0%; Pred. No. 8.4e-167;
RESULT 48
ID ADA12530 standard; protein; 323 AA.
DE Human secreted/transmembrane polypeptide PRO195.
PN US2003055216-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1694; DB 6; Length 323;
Best Local Similarity 100.0%; Pred. No. 8.4e-167;
RESULT 49
ID ADA74398 standard; protein; 323 AA.
DE Human PRO polypeptide #136.
PN US2003068798-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1694; DB 6; Length 323;
Best Local Similarity 100.0%; Pred. No. 8.4e-167;

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Best Local Similarity 100.0%; Pred. No. 8.4e-167;
RESULT 50
ID ADB24631 standard; protein; 323 AA.
DE Human PRO polypeptide SEQ ID NO 272.
FN US200307713-A1.
PD 24-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1694; DB 6; Length 323;
Best Local Similarity 100.0%; Pred. No. 8.4e-167;
RESULT 51
ID ADA82155 standard; protein; 323 AA.
DE Human PRO polypeptide #136.
FN US2003082701-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1694; DB 6; Length 323;
Best Local Similarity 100.0%; Pred. No. 8.4e-167;
RESULT 52
ID ADA75118 standard; protein; 323 AA.
DE Human PRO polypeptide #136.
FN US2003073216-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1694; DB 6; Length 323;
Best Local Similarity 100.0%; Pred. No. 8.4e-167;
RESULT 53
ID ADA85196 standard; protein; 323 AA.
DE Novel human secreted and transmembrane protein PRO195.
FN US2003082695-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1694; DB 6; Length 323;
Best Local Similarity 100.0%; Pred. No. 8.4e-167;
RESULT 54
ID ADA84644 standard; protein; 323 AA.
DE Novel human secreted and transmembrane protein PRO195.
FN US2003082708-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1694; DB 6; Length 323;
Best Local Similarity 100.0%; Pred. No. 8.4e-167;
RESULT 55
ID ADB29900 standard; protein; 323 AA.
DE Human PRO polypeptide #136.
FN US2003073214-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1694; DB 6; Length 323;
Best Local Similarity 100.0%; Pred. No. 8.4e-167;
RESULT 56
ID ADA80428 standard; protein; 323 AA.
DE Human PRO polypeptide #136.
FN US2003082761-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1694; DB 6; Length 323;
Best Local Similarity 100.0%; Pred. No. 8.4e-167;
RESULT 57
ID ADA75670 standard; protein; 323 AA.
DE Human PRO polypeptide #136.
FN US2003082703-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1694; DB 6; Length 323;
Best Local Similarity 100.0%; Pred. No. 8.4e-167;
RESULT 58
ID ADA46895 standard; protein; 323 AA.
DE Human PRO polypeptide #136.
FN US2003073210-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1694; DB 6; Length 323;
Best Local Similarity 100.0%; Pred. No. 8.4e-167;
RESULT 59
ID ADB25191 standard; protein; 323 AA.
DE Human PRO polypeptide SEQ ID NO 272.
FN US200307715-A1.
PD 24-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1694; DB 6; Length 323;
Best Local Similarity 100.0%; Pred. No. 8.4e-167;
RESULT 60
ID ADA93367 standard; protein; 323 AA.
DE Human PRO polypeptide #136.
FN US200307721-A1.
PD 24-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1694; DB 6; Length 323;
Best Local Similarity 100.0%; Pred. No. 8.4e-167;
RESULT 61
ID ADB26717 standard; protein; 323 AA.
DE Human PRO polypeptide #136.
FN US2003092147-A1.
PD 15-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1694; DB 6; Length 323;
Best Local Similarity 100.0%; Pred. No. 8.4e-167;
RESULT 62
ID AD31004 standard; protein; 323 AA.
DE Human PRO polypeptide #136.
FN US2003096386-A1.
PD 22-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1694; DB 6; Length 323;
Best Local Similarity 100.0%; Pred. No. 8.4e-167;
RESULT 63
ID ADA60932 standard; protein; 323 AA.
DE Homo sapiens.
FN US2003049817-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1694; DB 6; Length 323;
Best Local Similarity 100.0%; Pred. No. 8.4e-167;
RESULT 64
ID ADB24079 standard; protein; 323 AA.
DE Human PRO polypeptide SEQ ID NO 272.
FN US200307714-A1.
PD 24-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1694; DB 6; Length 323;
Best Local Similarity 100.0%; Pred. No. 8.4e-167;
RESULT 65
ID ADA96408 standard; protein; 323 AA.
DE Human PRO polypeptide #136.
FN US2003082650-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1694; DB 6; Length 323;
Best Local Similarity 100.0%; Pred. No. 8.4e-167;
RESULT 66
ID ADA80980 standard; protein; 323 AA.
DE Human PRO polypeptide #136.
FN US2003082702-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1694; DB 6; Length 323;
Best Local Similarity 100.0%; Pred. No. 8.4e-167;
RESULT 67
ID ADA95856 standard; protein; 323 AA.
DE Human PRO polypeptide #136.
FN US2003082759-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1694; DB 6; Length 323;
Best Local Similarity 100.0%; Pred. No. 8.4e-167;
RESULT 68
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ID ADB26165 standard; protein; 323 AA.
DE Human PRO polypeptide #136.
PN US2003082760-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1694; DB 6; Length 323;
Best Local Similarity 100.0%; Pred. No. 8.4e-167;
RESULT 69
ID ADB21650 standard; protein; 323 AA.
DE Novel human secreted and transmembrane protein PRO195.
PN US2003082765-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1694; DB 6; Length 323;
Best Local Similarity 100.0%; Pred. No. 8.4e-167;
RESULT 70
ID ABO19581 standard; protein; 323 AA.
DE Novel human secreted and transmembrane polypeptide #49.
PN US2003049633-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1694; DB 6; Length 323;
Best Local Similarity 100.0%; Pred. No. 8.4e-167;
RESULT 71
ID ADA77429 standard; protein; 323 AA.
DE Human PRO polypeptide #136.
PN US2003068797-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1694; DB 7; Length 323;
Best Local Similarity 100.0%; Pred. No. 8.4e-167;
RESULT 72
ID ADB18169 standard; protein; 323 AA.
DE Human PRO polypeptide #136.
PN US2003077710-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1694; DB 7; Length 323;
Best Local Similarity 100.0%; Pred. No. 8.4e-167;
RESULT 73
ID ADA86652 standard; protein; 323 AA.
DE Novel human secreted and transmembrane protein PRO195.
PN US2003082709-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1694; DB 7; Length 323;
Best Local Similarity 100.0%; Pred. No. 8.4e-167;
RESULT 74
ID ADA87955 standard; protein; 323 AA.
DE Novel human secreted and transmembrane protein PRO195.
PN US2003082700-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1694; DB 7; Length 323;
Best Local Similarity 100.0%; Pred. No. 8.4e-167;
RESULT 75
ID ADA46343 standard; protein; 323 AA.
DE Novel human secreted and transmembrane protein PRO195.
PN US2003054516-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1694; DB 7; Length 323;
Best Local Similarity 100.0%; Pred. No. 8.4e-167;
RESULT 76
ID ADB28373 standard; protein; 323 AA.
DE Human PRO polypeptide #136.
PN US2003082699-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1694; DB 7; Length 323;
Best Local Similarity 100.0%; Pred. No. 8.4e-167;
RESULT 77
ID ADB28925 standard; protein; 323 AA.
DE Human PRO polypeptide #136.
PA (GETH) GENENTECH INC.

PN US2003082706-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1694; DB 7; Length 323;
Best Local Similarity 100.0%; Pred. No. 8.4e-167;
RESULT 78
ID ADA76877 standard; protein; 323 AA.
DE Human PRO polypeptide #136.
PN US2003059909-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1694; DB 7; Length 323;
Best Local Similarity 100.0%; Pred. No. 8.4e-167;
RESULT 79
ID ADB8507 standard; protein; 323 AA.
DE Novel human secreted and transmembrane protein PRO195.
PN US2003073213-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1694; DB 7; Length 323;
Best Local Similarity 100.0%; Pred. No. 8.4e-167;
RESULT 80
ID ADA97512 standard; protein; 323 AA.
DE Human PRO polypeptide #136.
PN US2003082686-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1694; DB 7; Length 323;
Best Local Similarity 100.0%; Pred. No. 8.4e-167;
RESULT 81
ID ADB27269 standard; protein; 323 AA.
DE Human PRO polypeptide #136.
PN US2003022239-A1.
PD 30-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1694; DB 7; Length 323;
Best Local Similarity 100.0%; Pred. No. 8.4e-167;
RESULT 82
ID ADB22202 standard; protein; 323 AA.
DE Novel human secreted and transmembrane protein PRO195.
PN US2003087344-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1694; DB 7; Length 323;
Best Local Similarity 100.0%; Pred. No. 8.4e-167;
RESULT 83
ID ADA66893 standard; protein; 323 AA.
DE Human PRO polypeptide #136.
PN US2003068793-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1694; DB 7; Length 323;
Best Local Similarity 100.0%; Pred. No. 8.4e-167;
RESULT 84
ID ADB22754 standard; protein; 323 AA.
DE Human PRO polypeptide #136.
PN US2003077711-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1694; DB 7; Length 323;
Best Local Similarity 100.0%; Pred. No. 8.4e-167;
RESULT 85
ID ADB23527 standard; protein; 323 AA.
DE Human PRO polypeptide SEQ ID NO 272.
PN US2003077712-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1694; DB 7; Length 323;
Best Local Similarity 100.0%; Pred. No. 8.4e-167;
RESULT 86
ID ADA92249 standard; protein; 323 AA.
DE Novel human secreted and transmembrane protein PRO195.
PN US2003082712-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.

Query Match 100.0%; Score 1694; DB 7; Length 323;
Best Local Similarity 100.0%; Pred. No. 8.4e-167;
RESULT 87
ID ADB15312 standard; protein; 323 AA.
DE Human PRO polypeptide #136.
PN US2003087352-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1694; DB 7; Length 323;
Best Local Similarity 100.0%; Pred. No. 8.4e-167;
RESULT 88
ID ADB38564 standard; protein; 323 AA.
DE Novel human secreted and transmembrane protein PRO195.
PN US2003082766-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1694; DB 7; Length 323;
Best Local Similarity 100.0%; Pred. No. 8.4e-167;
RESULT 89
ID ADB38012 standard; protein; 323 AA.
DE Novel human secreted and transmembrane protein PRO195.
PN US2003087347-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1694; DB 7; Length 323;
Best Local Similarity 100.0%; Pred. No. 8.4e-167;
RESULT 90
ID ADB66484 standard; protein; 323 AA.
DE Novel human secreted and transmembrane protein PRO195.
PN US2003082689-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1694; DB 7; Length 323;
Best Local Similarity 100.0%; Pred. No. 8.4e-167;
RESULT 91
ID ADB89564 standard; protein; 323 AA.
DE Human PRO polypeptide #136.
PN US2003082698-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1694; DB 7; Length 323;
Best Local Similarity 100.0%; Pred. No. 8.4e-167;
RESULT 92
ID ADB90296 standard; protein; 323 AA.
DE Human PRO polypeptide #136.
PN US2003082762-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1694; DB 7; Length 323;
Best Local Similarity 100.0%; Pred. No. 8.4e-167;
RESULT 93
ID ADB39397 standard; protein; 323 AA.
DE Novel human secreted and transmembrane protein PRO195.
PN US2003082764-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1694; DB 7; Length 323;
Best Local Similarity 100.0%; Pred. No. 8.4e-167;
RESULT 94
ID ADB73836 standard; protein; 323 AA.
DE Human PRO polypeptide #49.
PN US2003045462-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1694; DB 7; Length 323;
Best Local Similarity 100.0%; Pred. No. 8.4e-167;
RESULT 95
ID ADB7020 standard; protein; 323 AA.
DE Novel human secreted and transmembrane protein PRO195.
PN US2003082687-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1694; DB 7; Length 323;
Best Local Similarity 100.0%; Pred. No. 8.4e-167;

Best Local Similarity 100.0%; Pred. No. 8.4e-167;
RESULT 96
ID ADB86627 standard; protein; 323 AA.
DE Human PRO polypeptide #136.
PN US2003082697-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1694; DB 7; Length 323;
Best Local Similarity 100.0%; Pred. No. 8.4e-167;
RESULT 97
ID ADB76552 standard; protein; 323 AA.
DE Human PRO polypeptide #49.
PN US2003083248-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1694; DB 7; Length 323;
Best Local Similarity 100.0%; Pred. No. 8.4e-167;
RESULT 98
ID ADB77232 standard; protein; 323 AA.
DE Novel human secreted and transmembrane protein PRO195.
PN US2003082696-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1694; DB 7; Length 323;
Best Local Similarity 100.0%; Pred. No. 8.4e-167;
RESULT 99
ID ADB34389 standard; protein; 323 AA.
DE Human PRO polypeptide SEQ ID NO 272.
PN US2003077717-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1694; DB 7; Length 323;
Best Local Similarity 100.0%; Pred. No. 8.4e-167;
RESULT 100
ID ADB35493 standard; protein; 323 AA.
DE Human PRO polypeptide SEQ ID NO 272.
PN US2003077719-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1694; DB 7; Length 323;
Best Local Similarity 100.0%; Pred. No. 8.4e-167;
RESULT 101
ID ADB33837 standard; protein; 323 AA.
DE Human PRO polypeptide SEQ ID NO 272.
PN US2003077716-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1694; DB 7; Length 323;
Best Local Similarity 100.0%; Pred. No. 8.4e-167;
RESULT 102
ID ADB34941 standard; protein; 323 AA.
DE Human PRO polypeptide SEQ ID NO 272.
PN US2003077718-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1694; DB 7; Length 323;
Best Local Similarity 100.0%; Pred. No. 8.4e-167;
RESULT 103
ID ADB36045 standard; protein; 323 AA.
DE Human PRO polypeptide SEQ ID NO 272.
PN US2003077720-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1694; DB 7; Length 323;
Best Local Similarity 100.0%; Pred. No. 8.4e-167;
RESULT 104
ID ADB46440 standard; protein; 323 AA.
DE Novel human secreted and transmembrane protein PRO195.
PN US2003082692-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1694; DB 7; Length 323;
Best Local Similarity 100.0%; Pred. No. 8.4e-167;

RESULT 105
ID ADC37345 standard; protein; 323 AA.
DE Nuclear factor kappa B (NF-kappaB) activating protein, SEQ ID 178.
PN WO2003048202-A2.
PD 12-JUN-2003.
PA (ASAH) ASAH KASEI KK.
Query Match 100.0%; Score 1694; DB 7; Length 323;
Best Local Similarity 100.0%; Pred. No. 8.4e-167;
RESULT 106
ID ADC3978 standard; protein; 323 AA.
DE Human secreted/transmembrane protein, PRO195.
PN US2003054986-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1694; DB 7; Length 323;
Best Local Similarity 100.0%; Pred. No. 8.4e-167;
RESULT 107
ID ADC61738 standard; protein; 323 AA.
DE Human secreted/transmembrane protein, PRO195.
PN US2003049684-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1694; DB 7; Length 323;
Best Local Similarity 100.0%; Pred. No. 8.4e-167;
RESULT 108
ID ADC63702 standard; protein; 323 AA.
DE Human secreted/transmembrane protein, PRO195.
PN US2003054405-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1694; DB 7; Length 323;
Best Local Similarity 100.0%; Pred. No. 8.4e-167;
RESULT 109
ID ADC66802 standard; protein; 323 AA.
DE Human secreted/transmembrane protein, PRO195.
PN US2003060406-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1694; DB 7; Length 323;
Best Local Similarity 100.0%; Pred. No. 8.4e-167;
RESULT 110
ID ADC68926 standard; protein; 323 AA.
DE Human secreted/transmembrane protein, PRO195.
PN US2003064407-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1694; DB 7; Length 323;
Best Local Similarity 100.0%; Pred. No. 8.4e-167;
RESULT 111
ID ADC62986 standard; protein; 323 AA.
DE Human secreted/transmembrane protein, PRO195.
PN US2003068648-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1694; DB 7; Length 323;
Best Local Similarity 100.0%; Pred. No. 8.4e-167;
RESULT 112
ID ADC68051 standard; protein; 323 AA.
DE Human secreted/transmembrane protein, PRO195.
PN US2003069178-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1694; DB 7; Length 323;
Best Local Similarity 100.0%; Pred. No. 8.4e-167;
RESULT 113
ID ADC41371 standard; protein; 323 AA.
DE Human secreted/transmembrane protein, PRO195.
PN US2003072745-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1694; DB 7; Length 323;
Best Local Similarity 100.0%; Pred. No. 8.4e-167;
RESULT 114
ID ADC50866 standard; protein; 323 AA.
DE Human secreted/transmembrane protein, PRO195.
PN US2003073624-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1694; DB 7; Length 323;
Best Local Similarity 100.0%; Pred. No. 8.4e-167;
RESULT 115
ID ADC62362 standard; protein; 323 AA.
DE Human secreted/transmembrane protein, PRO195.
PN US2003073624-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1694; DB 7; Length 323;
Best Local Similarity 100.0%; Pred. No. 8.4e-167;
RESULT 116
ID ADC41995 standard; protein; 323 AA.
DE Human secreted/transmembrane protein, PRO195.
PN US2003104998-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1694; DB 7; Length 323;
Best Local Similarity 100.0%; Pred. No. 8.4e-167;
RESULT 117
ID ADC50313 standard; protein; 323 AA.
DE Novel human secreted and transmembrane protein PRO195.
PN US2003092106-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1694; DB 7; Length 323;
Best Local Similarity 100.0%; Pred. No. 8.4e-167;
RESULT 118
ID ADC71860 standard; protein; 323 AA.
DE Novel human secreted and transmembrane protein PRO195.
PN US2003092107-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1694; DB 7; Length 323;
Best Local Similarity 100.0%; Pred. No. 8.4e-167;
RESULT 119
ID ADC59839 standard; protein; 323 AA.
DE Novel human secreted and transmembrane protein PRO195.
PN US2003092105-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1694; DB 7; Length 323;
Best Local Similarity 100.0%; Pred. No. 8.4e-167;
RESULT 120
ID ADC52846 standard; protein; 323 AA.
DE Novel human secreted and transmembrane protein Seq ID272.
PN US2003087365-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1694; DB 7; Length 323;
Best Local Similarity 100.0%; Pred. No. 8.4e-167;
RESULT 121
ID ADC57200 standard; protein; 323 AA.
DE Novel human secreted and transmembrane protein Seq ID272.
PN US2003087366-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1694; DB 7; Length 323;
Best Local Similarity 100.0%; Pred. No. 8.4e-167;
RESULT 122
ID ADC60391 standard; protein; 323 AA.
DE Novel human secreted and transmembrane protein PRO195.
PN US2003087367-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1694; DB 7; Length 323;
Best Local Similarity 100.0%; Pred. No. 8.4e-167;
RESULT 123
ID ADC50866 standard; protein; 323 AA.

DE Novel human secreted and transmembrane protein PRO195.
PN US2003087361-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1694; DB 7; Length 323;
Best Local Similarity 100.0%; Pred. No. 8.4e-167;
RESULT 124
ID ADC65393 standard; protein; 323 AA.
DE Human PRO polypeptide #136.
PN US2003087362-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1694; DB 7; Length 323;
Best Local Similarity 100.0%; Pred. No. 8.4e-167;
RESULT 125
ID ADC54491 standard; protein; 323 AA.
DE Novel human secreted and transmembrane protein Seq ID272.
PN US2003087363-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1694; DB 7; Length 323;
Best Local Similarity 100.0%; Pred. No. 8.4e-167;
RESULT 126
ID ADC53452 standard; protein; 323 AA.
DE Novel human secreted and transmembrane protein Seq ID272.
PN US2003087364-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1694; DB 7; Length 323;
Best Local Similarity 100.0%; Pred. No. 8.4e-167;
RESULT 127
ID ADC8975 standard; protein; 323 AA.
DE Novel human secreted and transmembrane protein Seq ID272.
PN US2003087359-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1694; DB 7; Length 323;
Best Local Similarity 100.0%; Pred. No. 8.4e-167;
RESULT 128
ID ADC5853 standard; protein; 323 AA.
DE Novel human secreted and transmembrane protein Seq ID272.
PN US2003087360-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1694; DB 7; Length 323;
Best Local Similarity 100.0%; Pred. No. 8.4e-167;
RESULT 129
ID ADC58423 standard; protein; 323 AA.
DE Novel human secreted and transmembrane protein Seq ID272.
PN US2003087346-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1694; DB 7; Length 323;
Best Local Similarity 100.0%; Pred. No. 8.4e-167;
RESULT 130
ID ADD03097 standard; protein; 323 AA.
DE Novel human secreted and transmembrane protein PRO195.
PN US2003092104-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1694; DB 7; Length 323;
Best Local Similarity 100.0%; Pred. No. 8.4e-167;
RESULT 131
ID ADC90089 standard; protein; 323 AA.
DE Novel human secreted and transmembrane protein PRO195.
PN US2003087348-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1694; DB 7; Length 323;
Best Local Similarity 100.0%; Pred. No. 8.4e-167;
RESULT 132
ID ADC69508 standard; protein; 323 AA.
DE Human PRO polypeptide #136.

PN US2003194770-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1694; DB 7; Length 323;
Best Local Similarity 100.0%; Pred. No. 8.4e-167;
RESULT 133
ID ADC48397 standard; protein; 323 AA.
DE Human PRO polypeptide #136.
PN US2003194773-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1694; DB 7; Length 323;
Best Local Similarity 100.0%; Pred. No. 8.4e-167;
RESULT 134
ID ADD09926 standard; protein; 323 AA.
DE Human PRO polypeptide #136.
PN US2003194776-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1694; DB 7; Length 323;
Best Local Similarity 100.0%; Pred. No. 8.4e-167;
RESULT 135
ID ADD04501 standard; protein; 323 AA.
DE Novel human secreted and transmembrane protein PRO195.
PN US2003087354-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1694; DB 7; Length 323;
Best Local Similarity 100.0%; Pred. No. 8.4e-167;
RESULT 136
ID ADC80457 standard; protein; 323 AA.
DE Novel human secreted and transmembrane protein PRO195.
PN US2003092103-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1694; DB 7; Length 323;
Best Local Similarity 100.0%; Pred. No. 8.4e-167;
RESULT 137
ID ADD10964 standard; protein; 323 AA.
DE Human PRO polypeptide #136.
PN US2003194774-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1694; DB 7; Length 323;
Best Local Similarity 100.0%; Pred. No. 8.4e-167;
RESULT 138
ID ADP10297 standard; protein; 323 AA.
DE Human secreted/transmembrane PRO polypeptide #4.
PN US2003105011-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1694; DB 7; Length 323;
Best Local Similarity 100.0%; Pred. No. 8.4e-167;
RESULT 139
ID ADC47845 standard; protein; 323 AA.
DE Human PRO polypeptide #136.
PN US2003194771-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1694; DB 7; Length 323;
Best Local Similarity 100.0%; Pred. No. 8.4e-167;
RESULT 140
ID ADC79905 standard; protein; 323 AA.
DE Novel human secreted and transmembrane protein PRO195.
PN US2003087358-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1694; DB 7; Length 323;
Best Local Similarity 100.0%; Pred. No. 8.4e-167;
RESULT 141
ID ADP11257 standard; protein; 323 AA.
DE Human secreted/transmembrane PRO polypeptide #4.
PN US2003105013-A1.

PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1694; DB 7; Length 323;
Pred. No. 8.4e-167;
RESULT 142
ID ADD09374 standard; protein; 323 AA.
DE Human PRO polypeptide #136.
PN US2003194775-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1694; DB 7; Length 323;
Pred. No. 8.4e-167;
RESULT 143
ID ADD41087 standard; protein; 323 AA.
DE Novel human secreted and transmembrane protein PRO195.
PN US2003203438-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1694; DB 7; Length 323;
Pred. No. 8.4e-167;
RESULT 144
ID ADD52226 standard; protein; 323 AA.
DE Human PRO polypeptide #136.
PN US2003194769-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1694; DB 7; Length 323;
Pred. No. 8.4e-167;
RESULT 145
ID ADD52966 standard; protein; 323 AA.
DE Human PRO polypeptide #136.
PN US2003194792-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1694; DB 7; Length 323;
Pred. No. 8.4e-167;
RESULT 146
ID ADD53518 standard; protein; 323 AA.
DE Novel human secreted and transmembrane protein PRO195.
PN US2003203437-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1694; DB 7; Length 323;
Pred. No. 8.4e-167;
RESULT 147
ID ADD37050 standard; protein; 323 AA.
DE Human secreted/transmembrane PRO polypeptide #4.
PN US2003105012-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1694; DB 7; Length 323;
Pred. No. 8.4e-167;
RESULT 148
ID ADD51674 standard; protein; 323 AA.
DE Human PRO polypeptide #136.
PN US2003194779-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1694; DB 7; Length 323;
Pred. No. 8.4e-167;
RESULT 149
ID ADD02473 standard; protein; 323 AA.
DE Human PRO polypeptide #136.
PN US2003203431-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1694; DB 7; Length 323;
Pred. No. 8.4e-167;
RESULT 150
ID ADD01907 standard; protein; 323 AA.
DE Human PRO polypeptide #136.
PN US2003203430-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1694; DB 7; Length 323;
Pred. No. 8.4e-167;
RESULT 151
ID ADD54089 standard; protein; 323 AA.
DE Novel human secreted and transmembrane protein PRO195.
PN US2003203432-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1694; DB 7; Length 323;
Pred. No. 8.4e-167;
RESULT 152
ID ADD49364 standard; protein; 323 AA.
DE Human secreted/transmembrane protein, PRO195.
PN US2003096744-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1694; DB 7; Length 323;
Pred. No. 8.4e-167;
RESULT 153
ID ADD92406 standard; protein; 323 AA.
DE Human PRO polypeptide #136.
PN US200319030-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1694; DB 7; Length 323;
Pred. No. 8.4e-167;
RESULT 154
ID ADD91302 standard; protein; 323 AA.
DE Human PRO polypeptide #136.
PN US2003190505-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1694; DB 7; Length 323;
Pred. No. 8.4e-167;
RESULT 155
ID ADE03916 standard; protein; 323 AA.
DE Human PRO polypeptide #136.
PN US200319057-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1694; DB 7; Length 323;
Pred. No. 8.4e-167;
RESULT 156
ID ADE32223 standard; protein; 323 AA.
DE Novel human secreted and transmembrane protein PRO195.
PN US2003194765-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1694; DB 7; Length 323;
Pred. No. 8.4e-167;
RESULT 157
ID ADE22145 standard; protein; 323 AA.
DE Human PRO polypeptide #136.
PN US200319056-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1694; DB 7; Length 323;
Pred. No. 8.4e-167;
RESULT 158
ID ADD79369 standard; protein; 323 AA.
DE Human PRO polypeptide #136.
PN US2003203428-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1694; DB 7; Length 323;
Pred. No. 8.4e-167;
RESULT 159
ID ADE35418 standard; protein; 323 AA.
DE Human secreted/transmembrane protein, PRO195.
PN US2003203434-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.

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| Query Match | 100.0%; | Score 1694; | DB 7; | Length 323; |
| Best Local Similarity | 100.0%; | Pred. No. 8.4e-167; | | |
| RESULT 160 | | | | |
| ID ADP16532 standard; protein; 323 AA. | | | | |
| DE Human secreted/transmembrane protein, PRO195. | | | | |
| FN US2003203435-A1. | | | | |
| PD 30-OCT-2003. | | | | |
| PA (GETH) GENENTECH INC. | | | | |
| Query Match | 100.0%; | Score 1694; | DB 7; | Length 323 |
| Best Local Similarity | 100.0%; | Pred. No. 8.4e-167; | | |
| RESULT 161 | | | | |
| ID ADD73147 standard; protein; 323 AA. | | | | |
| DE Human secreted/transmembrane protein, PRO195. | | | | |
| FN US2003203436-A1. | | | | |
| PD 30-OCT-2003. | | | | |
| PA (GETH) GENENTECH INC. | | | | |
| Query Match | 100.0%; | Score 1694; | DB 7; | Length 323 |
| Best Local Similarity | 100.0%; | Pred. No. 8.4e-167; | | |
| RESULT 162 | | | | |
| ID ADP41905 standard; protein; 323 AA. | | | | |
| DE Human PRO polypeptide #136. | | | | |
| FN US2003194772-A1. | | | | |
| PD 16-OCT-2003. | | | | |
| PA (GETH) GENENTECH INC. | | | | |
| Query Match | 100.0%; | Score 1694; | DB 7; | Length 323 |
| Best Local Similarity | 100.0%; | Pred. No. 8.4e-167; | | |
| RESULT 163 | | | | |
| ID ADP17722 standard; protein; 323 AA. | | | | |
| DE Human PRO polypeptide #136. | | | | |
| FN US2003199023-A1. | | | | |
| PD 23-OCT-2003. | | | | |
| PA (GETH) GENENTECH INC. | | | | |
| Query Match | 100.0%; | Score 1694; | DB 7; | Length 323; |
| Best Local Similarity | 100.0%; | Pred. No. 8.4e-167; | | |
| RESULT 164 | | | | |
| ID ADP1854 standard; protein; 323 AA. | | | | |
| DE Human PRO polypeptide #136. | | | | |
| FN US2003199053-A1. | | | | |
| PD 23-OCT-2003. | | | | |
| PA (GETH) GENENTECH INC. | | | | |
| Query Match | 100.0%; | Score 1694; | DB 7; | Length 323; |
| Best Local Similarity | 100.0%; | Pred. No. 8.4e-167; | | |
| RESULT 165 | | | | |
| ID ADP33317 standard; protein; 323 AA. | | | | |
| DE Novel human secreted and transmembrane protein PRO195. | | | | |
| FN US2003194767-A1. | | | | |
| PD 16-OCT-2003. | | | | |
| PA (GETH) GENENTECH INC. | | | | |
| Query Match | 100.0%; | Score 1694; | DB 7; | Length 323 |
| Best Local Similarity | 100.0%; | Pred. No. 8.4e-167; | | |
| RESULT 166 | | | | |
| ID ADP33869 standard; protein; 323 AA. | | | | |
| DE Novel human secreted and transmembrane protein PRO195. | | | | |
| FN US2003194791-A1. | | | | |
| PD 16-OCT-2003. | | | | |
| PA (GETH) GENENTECH INC. | | | | |
| Query Match | 100.0%; | Score 1694; | DB 7; | Length 323 |
| Best Local Similarity | 100.0%; | Pred. No. 8.4e-167; | | |
| RESULT 167 | | | | |
| ID ADD79921 standard; protein; 323 AA. | | | | |
| DE Human PRO polypeptide #136. | | | | |
| FN US2003207417-A1. | | | | |
| PD 06-NOV-2003. | | | | |
| PA (GETH) GENENTECH INC. | | | | |
| Query Match | 100.0%; | Score 1694; | DB 7; | Length 323; |
| Best Local Similarity | 100.0%; | Pred. No. 8.4e-167; | | |
| RESULT 168 | | | | |
| ID ADP2958 standard; protein; 323 AA. | | | | |
| DE Human PRO polypeptide #136. | | | | |
| FN US2003194768-A1. | | | | |
| PD 16-OCT-2003. | | | | |
| PA (GETH) GENENTECH INC. | | | | |
| Query Match | 100.0%; | Score 1694; | DB 7; | Length 323; |
| Best Local Similarity | 100.0%; | Pred. No. 8.4e-167; | | |
| RESULT 169 | | | | |
| ID ADP2958 standard; protein; 323 AA. | | | | |
| DE Human PRO polypeptide #136. | | | | |
| FN US2003194768-A1. | | | | |
| PD 16-OCT-2003. | | | | |
| PA (GETH) GENENTECH INC. | | | | |
| Query Match | 100.0%; | Score 1694; | DB 7; | Length 323; |
| Best Local Similarity | 100.0%; | Pred. No. 8.4e-167; | | |
| RESULT 170 | | | | |
| ID ADP2958 standard; protein; 323 AA. | | | | |
| DE Human PRO polypeptide #136. | | | | |
| FN US2003194768-A1. | | | | |
| PD 16-OCT-2003. | | | | |
| PA (GETH) GENENTECH INC. | | | | |
| Query Match | 100.0%; | Score 1694; | DB 7; | Length 323; |
| Best Local Similarity | 100.0%; | Pred. No. 8.4e-167; | | |
| RESULT 171 | | | | |
| ID ADP2958 standard; protein; 323 AA. | | | | |
| DE Human PRO polypeptide #136. | | | | |
| FN US2003194768-A1. | | | | |
| PD 16-OCT-2003. | | | | |
| PA (GETH) GENENTECH INC. | | | | |
| Query Match | 100.0%; | Score 1694; | DB 7; | Length 323; |
| Best Local Similarity | 100.0%; | Pred. No. 8.4e-167; | | |
| RESULT 172 | | | | |
| ID ADP2958 standard; protein; 323 AA. | | | | |
| DE Human PRO polypeptide #136. | | | | |
| FN US2003194768-A1. | | | | |
| PD 16-OCT-2003. | | | | |
| PA (GETH) GENENTECH INC | | | | |

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| Best Local Similarity | 100.0%; | Pred. No. 8.4e-167; |
| RESULT 169 | | |
| ID | ADD72505 standard; protein; 323 AA. | |
| DE | Human secreted/transmembrane protein, PRO195. | |
| PN | US2003194781-A1. | |
| PD | 16-OCT-2003. | |
| PA | (GETH) GENENTECH INC. | |
| Query Match | 100.0%; | Score 1694; DB 7; Length 323; |
| Best Local Similarity | 100.0%; | Pred. No. 8.4e-167; |
| RESULT 170 | | |
| ID | ADBI9378 standard; protein; 323 AA. | |
| DE | Human PRO polypeptide #136. | |
| PN | US2003199025-A1. | |
| PD | 23-OCT-2003. | |
| PA | (GETH) GENENTECH INC. | |
| Query Match | 100.0%; | Score 1694; DB 7; Length 323; |
| Best Local Similarity | 100.0%; | Pred. No. 8.4e-167; |
| RESULT 171 | | |
| ID | ADBI8826 standard; protein; 323 AA. | |
| DE | Human PRO polypeptide #136. | |
| PN | US2003199026-A1. | |
| PD | 23-OCT-2003. | |
| PA | (GETH) GENENTECH INC. | |
| Query Match | 100.0%; | Score 1694; DB 7; Length 323; |
| Best Local Similarity | 100.0%; | Pred. No. 8.4e-167; |
| RESULT 172 | | |
| ID | ADBI43022 standard; protein; 323 AA. | |
| DE | Human PRO polypeptide #136. | |
| PN | US2003199033-A1. | |
| PD | 23-OCT-2003. | |
| PA | (GETH) GENENTECH INC. | |
| Query Match | 100.0%; | Score 1694; DB 7; Length 323; |
| Best Local Similarity | 100.0%; | Pred. No. 8.4e-167; |
| RESULT 173 | | |
| ID | ADBI5811 standard; protein; 323 AA. | |
| DE | Human PRO polypeptide #136. | |
| PN | US2003199059-A1. | |
| PD | 23-OCT-2003. | |
| PA | (GETH) GENENTECH INC. | |
| Query Match | 100.0%; | Score 1694; DB 7; Length 323; |
| Best Local Similarity | 100.0%; | Pred. No. 8.4e-167; |
| RESULT 174 | | |
| ID | ADBI2697 standard; protein; 323 AA. | |
| DE | Human PRO polypeptide #136. | |
| PN | US2003199064-A1. | |
| PD | 23-OCT-2003. | |
| PA | (GETH) GENENTECH INC. | |
| Query Match | 100.0%; | Score 1694; DB 7; Length 323; |
| Best Local Similarity | 100.0%; | Pred. No. 8.4e-167; |
| RESULT 175 | | |
| ID | ADBI7815 standard; protein; 323 AA. | |
| DE | Human PRO polypeptide #136. | |
| PN | US2003203429-A1. | |
| PD | 30-OCT-2003. | |
| PA | (GETH) GENENTECH INC. | |
| Query Match | 100.0%; | Score 1694; DB 7; Length 323; |
| Best Local Similarity | 100.0%; | Pred. No. 8.4e-167; |
| RESULT 176 | | |
| ID | ADBI32765 standard; protein; 323 AA. | |
| DE | Novel human secreted and transmembrane protein PRO195. | |
| PN | US2003194766-A1. | |
| PD | 16-OCT-2003. | |
| PA | (GETH) GENENTECH INC. | |
| Query Match | 100.0%; | Score 1694; DB 7; Length 323; |
| Best Local Similarity | 100.0%; | Pred. No. 8.4e-167; |
| RESULT 177 | | |
| ID | ADBI42457 standard; protein; 323 AA. | |
| DE | Human PRO polypeptide #136. | |
| PN | US2003199032-A1. | |
| PD | 23-OCT-2003. | |
| PA | (GETH) GENENTECH INC. | |
| Query Match | 100.0%; | Score 1694; DB 7; Length 323; |
| Best Local Similarity | 100.0%; | Pred. No. 8.4e-167; |
| RESULT 178 | | |
| ID | ADBI42457 standard; protein; 323 AA. | |
| DE | Human PRO polypeptide #136. | |
| PN | US2003199032-A1. | |
| PD | 23-OCT-2003. | |
| PA | (GETH) GENENTECH INC. | |
| Query Match | 100.0%; | Score 1694; DB 7; Length 323; |
| Best Local Similarity | 100.0%; | Pred. No. 8.4e-167; |

RESULT 178
ID ADE17156 standard; protein; 323 AA.
DE Human secreted/transmembrane protein, PRO195.
PN US2003203433-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1694; DB 7; Length 323;
Best Local Similarity 100.0%; Pred. No. 8.4e-167;
RESULT 179
ID ADD80473 standard; protein; 323 AA.
DE Human PRO polypeptide #136.
PN US2003207418-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1694; DB 7; Length 323;
Best Local Similarity 100.0%; Pred. No. 8.4e-167;
RESULT 180
ID ADD89501 standard; protein; 323 AA.
DE Human PRO polypeptide #136.
PN US2003199028-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1694; DB 7; Length 323;
Best Local Similarity 100.0%; Pred. No. 8.4e-167;
RESULT 181
ID ADE40785 standard; protein; 323 AA.
DE Human PRO polypeptide #136.
PN US2003199031-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1694; DB 7; Length 323;
Best Local Similarity 100.0%; Pred. No. 8.4e-167;
RESULT 182
ID ADE04584 standard; protein; 323 AA.
DE Human PRO polypeptide #136.
PN US2003199034-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1694; DB 7; Length 323;
Best Local Similarity 100.0%; Pred. No. 8.4e-167;
RESULT 183
ID ADE92713 standard; protein; 323 AA.
DE Human PRO polypeptide #136.
PN US2003194777-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1694; DB 7; Length 323;
Best Local Similarity 100.0%; Pred. No. 8.4e-167;
RESULT 184
ID ADF47170 standard; protein; 323 AA.
DE Human secreted/transmembrane protein, PRO195.
PN US2003195333-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1694; DB 7; Length 323;
Best Local Similarity 100.0%; Pred. No. 8.4e-167;
RESULT 185
ID ADE21422 standard; protein; 323 AA.
DE Novel human secreted and transmembrane protein PRO195.
PN US2003207355-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1694; DB 7; Length 323;
Best Local Similarity 100.0%; Pred. No. 8.4e-167;
RESULT 186
ID ADE23063 standard; protein; 323 AA.
DE Novel human secreted and transmembrane protein PRO195.
PN US2003207384-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1694; DB 7; Length 323;
Best Local Similarity 100.0%; Pred. No. 8.4e-167;
RESULT 187

ID ADF97398 standard; protein; 323 AA.
DE Human PRO polypeptide #136.
PN US2003207370-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1694; DB 7; Length 323;
Best Local Similarity 100.0%; Pred. No. 8.4e-167;
RESULT 188
ID ADE80462 standard; protein; 323 AA.
DE Human PRO polypeptide #136.
PN US2003207373-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1694; DB 7; Length 323;
Best Local Similarity 100.0%; Pred. No. 8.4e-167;
RESULT 189
ID ADE52927 standard; protein; 323 AA.
DE Human secreted/transmembrane protein, PRO195.
PN US2003216561-A1.
PD 20-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1694; DB 7; Length 323;
Best Local Similarity 100.0%; Pred. No. 8.4e-167;
RESULT 190
ID ADE60247 standard; protein; 323 AA.
DE Human secreted/transmembrane protein, PRO195.
PN US2003206915-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1694; DB 7; Length 323;
Best Local Similarity 100.0%; Pred. No. 8.4e-167;
RESULT 191
ID ADE79910 standard; protein; 323 AA.
DE Human PRO polypeptide #136.
PN US2003207372-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1694; DB 7; Length 323;
Best Local Similarity 100.0%; Pred. No. 8.4e-167;
RESULT 192
ID ADH55202 standard; protein; 323 AA.
DE Novel human secreted and transmembrane protein PRO195.
PN US2003207381-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1694; DB 7; Length 323;
Best Local Similarity 100.0%; Pred. No. 8.4e-167;
RESULT 193
ID ADH55754 standard; protein; 323 AA.
DE Novel human secreted and transmembrane protein PRO195.
PN US2003207379-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1694; DB 7; Length 323;
Best Local Similarity 100.0%; Pred. No. 8.4e-167;
RESULT 194
ID ADI61007 standard; protein; 323 AA.
DE Human secreted/transmembrane protein, PRO195.
PN US2003077700-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1694; DB 7; Length 323;
Best Local Similarity 100.0%; Pred. No. 8.4e-167;
RESULT 195
ID ADI63973 standard; protein; 323 AA.
DE Novel human secreted and transmembrane protein PRO195.
PN US2003207385-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1694; DB 7; Length 323;
Best Local Similarity 100.0%; Pred. No. 8.4e-167;
RESULT 196
ID ADI64922 standard; protein; 323 AA.

DE Novel human secreted and transmembrane protein PRO195.
PN US2003207386-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1694; DB 7; Length 323;
Best Local Similarity 100.0%; Pred. No. 8.4e-167;
RESULT 197
ID ADI63421 standard; protein; 323 AA.
DE Novel human secreted and transmembrane protein PRO195.
PN US2003207387-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1694; DB 7; Length 323;
Best Local Similarity 100.0%; Pred. No. 8.4e-167;
RESULT 198
ID ADH81835 standard; protein; 323 AA.
DE Novel human secreted and transmembrane protein PRO195.
PN US2003207388-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1694; DB 7; Length 323;
Best Local Similarity 100.0%; Pred. No. 8.4e-167;
RESULT 199
ID ADH81283 standard; protein; 323 AA.
DE Novel human secreted and transmembrane protein PRO195.
PN US2003207377-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1694; DB 7; Length 323;
Best Local Similarity 100.0%; Pred. No. 8.4e-167;
RESULT 200
ID ADM82452 standard; protein; 323 AA.
DE Novel human secreted and transmembrane protein PRO195.
PN US2003087355-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1694; DB 7; Length 323;
Best Local Similarity 100.0%; Pred. No. 8.4e-167;
RESULT 201
ID ADN15851 standard; protein; 323 AA.
DE Novel human secreted and transmembrane protein PRO195.
PN US2003087353-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1694; DB 7; Length 323;
Best Local Similarity 100.0%; Pred. No. 8.4e-167;
RESULT 202
ID ADN16480 standard; protein; 323 AA.
DE Novel human secreted and transmembrane protein PRO195.
PN US2003087385-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1694; DB 7; Length 323;
Best Local Similarity 100.0%; Pred. No. 8.4e-167;
RESULT 203
ID ADN15299 standard; protein; 323 AA.
DE Novel human secreted and transmembrane protein PRO195.
PN US2003087356-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1694; DB 7; Length 323;
Best Local Similarity 100.0%; Pred. No. 8.4e-167;
RESULT 204
ID ADN14747 standard; protein; 323 AA.
DE Novel human secreted and transmembrane protein PRO195.
PN US2003087357-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1694; DB 7; Length 323;
Best Local Similarity 100.0%; Pred. No. 8.4e-167;
RESULT 205
ID ADG81009 standard; protein; 323 AA.
DE Novel human secreted and transmembrane protein PRO195.

PN US2003092115-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1694; DB 8; Length 323;
Best Local Similarity 100.0%; Pred. No. 8.4e-167;
RESULT 206
ID ADD76457 standard; protein; 323 AA.
DE Human PRO polypeptide #136.
PN US200310087-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1694; DB 8; Length 323;
Best Local Similarity 100.0%; Pred. No. 8.4e-167;
RESULT 207
ID ADH87821 standard; protein; 323 AA.
DE Human PRO polypeptide #136.
PN US2003092113-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1694; DB 8; Length 323;
Best Local Similarity 100.0%; Pred. No. 8.4e-167;
RESULT 208
ID ADB66225 standard; protein; 323 AA.
DE Human PRO polypeptide #136.
PN US2003203440-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1694; DB 8; Length 323;
Best Local Similarity 100.0%; Pred. No. 8.4e-167;
RESULT 209
ID ADE75673 standard; protein; 323 AA.
DE Human PRO polypeptide #136.
PN US2003211571-A1.
PD 13-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1694; DB 8; Length 323;
Best Local Similarity 100.0%; Pred. No. 8.4e-167;
RESULT 210
ID ADB48664 standard; protein; 323 AA.
DE Human secreted/transmembrane protein, PRO195.
PN US2003104536-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1694; DB 8; Length 323;
Best Local Similarity 100.0%; Pred. No. 8.4e-167;
RESULT 211
ID ADA41258 standard; protein; 323 AA.
DE Human secreted/transmembrane PRO polypeptide #4.
PN US2003100497-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1694; DB 8; Length 323;
Best Local Similarity 100.0%; Pred. No. 8.4e-167;
RESULT 212
ID ADE23249 standard; protein; 323 AA.
DE Human PRO polypeptide #136.
PN US2003092108-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1694; DB 8; Length 323;
Best Local Similarity 100.0%; Pred. No. 8.4e-167;
RESULT 213
ID ADE23801 standard; protein; 323 AA.
DE Human PRO polypeptide #136.
PN US2003092110-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1694; DB 8; Length 323;
Best Local Similarity 100.0%; Pred. No. 8.4e-167;
RESULT 214
ID ADE24444 standard; protein; 323 AA.
DE Human PRO polypeptide #136.
PN US2003092111-A1.

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PD 15-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1694; DB 8; Length 323;
Best Local Similarity 100.0%; Pred. No. 8.4e-167;
RESULT 215
ID ADD87269 standard; protein; 323 AA.
DE Human PRO polypeptide #136.
PN US2003203439-A1.
PD 30-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1694; DB 8; Length 323;
Best Local Similarity 100.0%; Pred. No. 8.4e-167;
RESULT 216
ID ADE89135 standard; protein; 323 AA.
DE Human PRO polypeptide #136.
PN US2003199062-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1694; DB 8; Length 323;
Best Local Similarity 100.0%; Pred. No. 8.4e-167;
RESULT 217
ID ADE18274 standard; protein; 323 AA.
DE Human PRO polypeptide #136.
PN US2003194794-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1694; DB 8; Length 323;
Best Local Similarity 100.0%; Pred. No. 8.4e-167;
RESULT 218
ID ADE88583 standard; protein; 323 AA.
DE Human PRO polypeptide #136.
PN US2003199054-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1694; DB 8; Length 323;
Best Local Similarity 100.0%; Pred. No. 8.4e-167;
RESULT 219
ID ADE89765 standard; protein; 323 AA.
DE Human secreted/transmembrane protein, PRO195.
PN US2003130181-A1.
PD 10-JUL-2003.
PA (ASHK/) ASHKENAZI A J.
PA (BAKE/) BAKER K P.
PA (BOTS/) BOTSTEIN D.
PA (DESN/) DESNOYERS L.
PA (EATO/) EATON D L.
PA (FERR/) FERRARA N.
PA (FILV/) FILVAROFF E.
PA (FONG/) FONG S.
PA (GAOW/) GAO W.
PA (GERB/) GERBER H.
PA (GERR/) GERRITSEN M E.
PA (GODO/) GODDARD A.
PA (GODO/) GODOWSKI P J.
PA (GIRM/) GIRMALDI J C.
PA (GURN/) GURNEY A L.
PA (HILL/) HILLMAN K J.
PA (KLAJ/) KLAJAVIN I J.
PA (KUOS/) KUO S S.
PA (KUAN/) KUAN J.
PA (NAPI/) NAPIER M A.
PA (PANJ/) PAN J.
PA (PAON/) PAONI N F.
PA (ROYM/) ROY M A.
PA (SHEL/) SHELTON D L.
PA (STEW/) STEWART T A.
PA (TUMA/) TUMAS D.
PA (WILL/) WILLIAMS P M.
PA (WOOD/) WOOD W I.
Query Match 100.0%; Score 1694; DB 8; Length 323;
Best Local Similarity 100.0%; Pred. No. 8.4e-167;
RESULT 220
ID ADF61405 standard; protein; 323 AA.
DE Human secreted/transmembrane protein, PRO195.
PN US2003195345-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1694; DB 8; Length 323;
Best Local Similarity 100.0%; Pred. No. 8.4e-167;
RESULT 221
ID ADF40097 standard; protein; 323 AA.
DE Human secreted/transmembrane protein, PRO195.
PN US2003198994-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1694; DB 8; Length 323;
Best Local Similarity 100.0%; Pred. No. 8.4e-167;
RESULT 222
ID ADF45893 standard; protein; 323 AA.
DE Human secreted/transmembrane protein, PRO195.
PN US2003195148-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1694; DB 8; Length 323;
Best Local Similarity 100.0%; Pred. No. 8.4e-167;
RESULT 223
ID ADE94603 standard; protein; 323 AA.
DE Human PRO polypeptide #136.
PN US2003199027-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1694; DB 8; Length 323;
Best Local Similarity 100.0%; Pred. No. 8.4e-167;
RESULT 224
ID ADE91014 standard; protein; 323 AA.
DE Human PRO polypeptide #136.
PN US2003199051-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1694; DB 8; Length 323;
Best Local Similarity 100.0%; Pred. No. 8.4e-167;
RESULT 225
ID ADE95155 standard; protein; 323 AA.
DE Human PRO polypeptide #136.
PN US2003199052-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1694; DB 8; Length 323;
Best Local Similarity 100.0%; Pred. No. 8.4e-167;
RESULT 226
ID ADE93265 standard; protein; 323 AA.
DE Human PRO polypeptide #136.
PN US2003199060-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1694; DB 8; Length 323;
Best Local Similarity 100.0%; Pred. No. 8.4e-167;
RESULT 227
ID ADF4289 standard; protein; 323 AA.
DE Human secreted/transmembrane protein, PRO195.
PN US2003204055-A1.
PD 30-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1694; DB 8; Length 323;
Best Local Similarity 100.0%; Pred. No. 8.4e-167;
RESULT 228
ID ADF40721 standard; protein; 323 AA.
DE Human secreted/transmembrane protein, PRO195.
PN US2003199021-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1694; DB 8; Length 323;
Best Local Similarity 100.0%; Pred. No. 8.4e-167;
RESULT 229
ID ADF23665 standard; protein; 323 AA.
DE Human secreted/transmembrane protein, PRO195.
PN US2003203402-A1.
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PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1694; DB 8; Length 323;
Best Local Similarity 100.0%; Pred. No. 8.4e-167;
RESULT 230
ID ADF3648 standard; protein; 323 AA.
DE Human secreted/transmembrane protein, PRO195.
PN US2003194780-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1694; DB 8; Length 323;
Best Local Similarity 100.0%; Pred. No. 8.4e-167;
RESULT 231
ID ADF34846 standard; protein; 323 AA.
DE Human PRO polypeptide #136.
PN US2003199029-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1694; DB 8; Length 323;
Best Local Similarity 100.0%; Pred. No. 8.4e-167;
RESULT 232
ID ADF27115 standard; protein; 323 AA.
DE Human secreted/transmembrane protein, PRO195.
PN US2003199436-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1694; DB 8; Length 323;
Best Local Similarity 100.0%; Pred. No. 8.4e-167;
RESULT 233
ID ADF27751 standard; protein; 323 AA.
DE Human secreted/transmembrane protein, PRO195.
PN US2003199437-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1694; DB 8; Length 323;
Best Local Similarity 100.0%; Pred. No. 8.4e-167;
RESULT 234
ID ADF27161 standard; protein; 323 AA.
DE Novel human secreted and transmembrane protein PRO195.
PN US2003199051-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1694; DB 8; Length 323;
Best Local Similarity 100.0%; Pred. No. 8.4e-167;
RESULT 235
ID ADF30462 standard; protein; 323 AA.
DE Human PRO polypeptide #136.
PN US2003199063-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1694; DB 8; Length 323;
Best Local Similarity 100.0%; Pred. No. 8.4e-167;
RESULT 236
ID ADF41345 standard; protein; 323 AA.
DE Human secreted/transmembrane protein, PRO195.
PN US2003199435-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1694; DB 8; Length 323;
Best Local Similarity 100.0%; Pred. No. 8.4e-167;
RESULT 237
ID ADF33024 standard; protein; 323 AA.
DE Human secreted/transmembrane protein, PRO195.
PN US2003211091-A1.
PD 13-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1694; DB 8; Length 323;
Best Local Similarity 100.0%; Pred. No. 8.4e-167;
RESULT 238
ID ADF25390 standard; protein; 323 AA.
DE Human secreted/transmembrane protein, PRO195.
PN US2003211092-A1.
PD 13-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1694; DB 8; Length 323;
Best Local Similarity 100.0%; Pred. No. 8.4e-167;
RESULT 239
ID ADF26491 standard; protein; 323 AA.
DE Human secreted/transmembrane protein, PRO195.
PN US2003199674-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1694; DB 8; Length 323;
Best Local Similarity 100.0%; Pred. No. 8.4e-167;
RESULT 240
ID ADF34280 standard; protein; 323 AA.
DE Human secreted/transmembrane protein, PRO195.
PN US2003194410-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1694; DB 8; Length 323;
Best Local Similarity 100.0%; Pred. No. 8.4e-167;
RESULT 241
ID ADF46517 standard; protein; 323 AA.
DE Human secreted/transmembrane protein, PRO195.
PN US2003195344-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1694; DB 8; Length 323;
Best Local Similarity 100.0%; Pred. No. 8.4e-167;
RESULT 242
ID ADF31609 standard; protein; 323 AA.
DE Novel human secreted and transmembrane protein PRO195.
PN US2003199058-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1694; DB 8; Length 323;
Best Local Similarity 100.0%; Pred. No. 8.4e-167;
RESULT 243
ID ADF302188 standard; protein; 323 AA.
DE Human PRO polypeptide #136.
PN US2003207352-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1694; DB 8; Length 323;
Best Local Similarity 100.0%; Pred. No. 8.4e-167;
RESULT 244
ID ADF31974 standard; protein; 323 AA.
DE Novel human secreted and transmembrane protein PRO195.
PN US2003207360-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1694; DB 8; Length 323;
Best Local Similarity 100.0%; Pred. No. 8.4e-167;
RESULT 245
ID ADF20044 standard; protein; 323 AA.
DE Human PRO polypeptide #136.
PN US2003207376-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1694; DB 8; Length 323;
Best Local Similarity 100.0%; Pred. No. 8.4e-167;
RESULT 246
ID ADF37950 standard; protein; 323 AA.
DE Human PRO polypeptide #136.
PN US2003207422-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1694; DB 8; Length 323;
Best Local Similarity 100.0%; Pred. No. 8.4e-167;
RESULT 247
ID ADF24167 standard; protein; 323 AA.
DE Novel human secreted and transmembrane protein PRO195.
PN US2003207426-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.

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Query Match          100.0%; Score 1694; DB 8; Length 323;
Best Local Similarity 100.0%; Pred. No. 8.4e-167;
RESULT 248
ID ADP98521 standard; protein; 323 AA.
DE Human PRO polypeptide #136.
PN US2003208055-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match          100.0%; Score 1694; DB 8; Length 323;
Best Local Similarity 100.0%; Pred. No. 8.4e-167;
RESULT 249
ID ADG03352 standard; protein; 323 AA.
DE Human PRO polypeptide #136.
PN US2003207351-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match          100.0%; Score 1694; DB 8; Length 323;
Best Local Similarity 100.0%; Pred. No. 8.4e-167;
RESULT 250
ID ADP99073 standard; protein; 323 AA.
DE Human PRO polypeptide #136.
PN US2003207353-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match          100.0%; Score 1694; DB 8; Length 323;
Best Local Similarity 100.0%; Pred. No. 8.4e-167;
RESULT 251
ID ADG16658 standard; protein; 323 AA.
DE Human PRO polypeptide #136.
PN US2003207359-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match          100.0%; Score 1694; DB 8; Length 323;
Best Local Similarity 100.0%; Pred. No. 8.4e-167;
RESULT 252
ID ADG05117 standard; protein; 323 AA.
DE Human PRO polypeptide #136.
PN US2003207375-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match          100.0%; Score 1694; DB 8; Length 323;
Best Local Similarity 100.0%; Pred. No. 8.4e-167;
RESULT 253
ID ADG19384 standard; protein; 323 AA.
DE Human PRO polypeptide #136.
PN US2003207425-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match          100.0%; Score 1694; DB 8; Length 323;
Best Local Similarity 100.0%; Pred. No. 8.4e-167;
RESULT 254
ID ADG13221 standard; protein; 323 AA.
DE Human PRO polypeptide #136.
PN US2003207357-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match          100.0%; Score 1694; DB 8; Length 323;
Best Local Similarity 100.0%; Pred. No. 8.4e-167;
RESULT 255
ID ADG08278 standard; protein; 323 AA.
DE Novel human secreted and transmembrane protein PRO195.
PN US2003207424-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match          100.0%; Score 1694; DB 8; Length 323;
Best Local Similarity 100.0%; Pred. No. 8.4e-167;
RESULT 256
ID ADG15448 standard; protein; 323 AA.
DE Human PRO polypeptide #136.
PN US2003219885-A1.
PD 27-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match          100.0%; Score 1694; DB 8; Length 323;
Best Local Similarity 100.0%; Pred. No. 8.4e-167;
RESULT 257
ID ADP96846 standard; protein; 323 AA.
DE Human PRO polypeptide #136.
PN US2003207371-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match          100.0%; Score 1694; DB 8; Length 323;
Best Local Similarity 100.0%; Pred. No. 8.4e-167;
RESULT 258
ID ADG06031 standard; protein; 323 AA.
DE Human PRO polypeptide #136.
PN US2003207374-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match          100.0%; Score 1694; DB 8; Length 323;
Best Local Similarity 100.0%; Pred. No. 8.4e-167;
RESULT 259
ID ADG33615 standard; protein; 323 AA.
DE Novel human secreted and transmembrane protein PRO195.
PN US2003207389-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match          100.0%; Score 1694; DB 8; Length 323;
Best Local Similarity 100.0%; Pred. No. 8.4e-167;
RESULT 260
ID ADG03904 standard; protein; 323 AA.
DE Human PRO polypeptide #136.
PN US2003207423-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match          100.0%; Score 1694; DB 8; Length 323;
Best Local Similarity 100.0%; Pred. No. 8.4e-167;
RESULT 261
ID ADG24805 standard; protein; 323 AA.
DE Novel human secreted and transmembrane protein PRO195.
PN US2003207427-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match          100.0%; Score 1694; DB 8; Length 323;
Best Local Similarity 100.0%; Pred. No. 8.4e-167;
RESULT 262
ID ADG07102 standard; protein; 323 AA.
DE Novel human secreted and transmembrane protein PRO195.
PN US2003207350-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match          100.0%; Score 1694; DB 8; Length 323;
Best Local Similarity 100.0%; Pred. No. 8.4e-167;
RESULT 263
ID ADG07654 standard; protein; 323 AA.
DE Novel human secreted and transmembrane protein PRO195.
PN US2003207356-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match          100.0%; Score 1694; DB 8; Length 323;
Best Local Similarity 100.0%; Pred. No. 8.4e-167;
RESULT 264
ID ADG55149 standard; protein; 323 AA.
DE Novel human secreted and transmembrane protein PRO195.
PN US2003194778-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match          100.0%; Score 1694; DB 8; Length 323;
Best Local Similarity 100.0%; Pred. No. 8.4e-167;
RESULT 265
ID ADG60813 standard; protein; 323 AA.
DE Novel human secreted and transmembrane protein PRO195.
PN US2003207390-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match          100.0%; Score 1694; DB 8; Length 323;
Best Local Similarity 100.0%; Pred. No. 8.4e-167;
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RESULT 266
ID ADG61917 standard; protein; 323 AA.
DE Novel human secreted and transmembrane protein PRO195.
PN US2003207428-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1694; DB 8; Length 323;
Best Local Similarity 100.0%; Pred. No. 8.4e-167;
RESULT 267
ID ADG82118 standard; protein; 323 AA.
DE Human PRO polypeptide #136.
PN US2003207358-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1694; DB 8; Length 323;
Best Local Similarity 100.0%; Pred. No. 8.4e-167;
RESULT 268
ID ADG57357 standard; protein; 323 AA.
DE Novel human secreted and transmembrane protein PRO195.
PN US2003207362-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1694; DB 8; Length 323;
Best Local Similarity 100.0%; Pred. No. 8.4e-167;
RESULT 269
ID ADG56805 standard; protein; 323 AA.
DE Novel human secreted and transmembrane protein PRO195.
PN US2003207364-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1694; DB 8; Length 323;
Best Local Similarity 100.0%; Pred. No. 8.4e-167;
RESULT 270
ID ADG55701 standard; protein; 323 AA.
DE Novel human secreted and transmembrane protein PRO195.
PN US2003207365-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1694; DB 8; Length 323;
Best Local Similarity 100.0%; Pred. No. 8.4e-167;
RESULT 271
ID ADG58461 standard; protein; 323 AA.
DE Novel human secreted and transmembrane protein PRO195.
PN US2003207368-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1694; DB 8; Length 323;
Best Local Similarity 100.0%; Pred. No. 8.4e-167;
RESULT 272
ID ADG70827 standard; protein; 323 AA.
DE Novel human secreted and transmembrane protein PRO195.
PN US2003207420-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1694; DB 8; Length 323;
Best Local Similarity 100.0%; Pred. No. 8.4e-167;
RESULT 273
ID ADG57909 standard; protein; 323 AA.
DE Novel human secreted and transmembrane protein PRO195.
PN US2003207363-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1694; DB 8; Length 323;
Best Local Similarity 100.0%; Pred. No. 8.4e-167;
RESULT 274
ID ADG53493 standard; protein; 323 AA.
DE Novel human secreted and transmembrane protein PRO195.
PN US2003207415-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1694; DB 8; Length 323;
Best Local Similarity 100.0%; Pred. No. 8.4e-167;
RESULT 275

ID ADG71379 standard; protein; 323 AA.
DE Novel human secreted and transmembrane protein PRO195.
PN US2003207421-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1694; DB 8; Length 323;
Best Local Similarity 100.0%; Pred. No. 8.4e-167;
RESULT 276
ID ADG50503 standard; protein; 323 AA.
DE Human secreted/transmembrane protein, PRO195.
PN US2003207803-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1694; DB 8; Length 323;
Best Local Similarity 100.0%; Pred. No. 8.4e-167;
RESULT 277
ID ADG81566 standard; protein; 323 AA.
DE Human PRO polypeptide #136.
PN US2003207805-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1694; DB 8; Length 323;
Best Local Similarity 100.0%; Pred. No. 8.4e-167;
RESULT 278
ID ADH30528 standard; protein; 323 AA.
DE Human PRO polypeptide #136.
PN US2003077723-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1694; DB 8; Length 323;
Best Local Similarity 100.0%; Pred. No. 8.4e-167;
RESULT 279
ID ADH11895 standard; protein; 323 AA.
DE Novel human secreted and transmembrane protein PRO195.
PN US2003207419-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1694; DB 8; Length 323;
Best Local Similarity 100.0%; Pred. No. 8.4e-167;
RESULT 280
ID ADG49879 standard; protein; 323 AA.
DE Human secreted/transmembrane protein, PRO195.
PN US2003215905-A1.
PD 20-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1694; DB 8; Length 323;
Best Local Similarity 100.0%; Pred. No. 8.4e-167;
RESULT 281
ID ADG51751 standard; protein; 323 AA.
DE Human secreted/transmembrane protein, PRO195.
PN US2003215908-A1.
PD 20-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1694; DB 8; Length 323;
Best Local Similarity 100.0%; Pred. No. 8.4e-167;
RESULT 282
ID ADG52317 standard; protein; 323 AA.
DE Novel human secreted and transmembrane protein PRO195.
PN US2003207414-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1694; DB 8; Length 323;
Best Local Similarity 100.0%; Pred. No. 8.4e-167;
RESULT 283
ID ADG54045 standard; protein; 323 AA.
DE Novel human secreted and transmembrane protein PRO195.
PN US2003207416-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1694; DB 8; Length 323;
Best Local Similarity 100.0%; Pred. No. 8.4e-167;
RESULT 284
ID ADG49255 standard; protein; 323 AA.
DE Human secreted/transmembrane protein, PRO195.

PN US2003216305-A1.
PD 20-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1694; DB 8; Length 323;
Best Local Similarity 100.0%; Pred. No. 8.4e-167;
RESULT 285
ID ADG81014 standard; protein; 323 AA.
DE Human PRO polypeptide #136.
PN US2003194793-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1694; DB 8; Length 323;
Best Local Similarity 100.0%; Pred. No. 8.4e-167;
RESULT 286
ID ADG56253 standard; protein; 323 AA.
DE Novel human secreted and transmembrane protein PRO195.
PN US2003207366-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1694; DB 8; Length 323;
Best Local Similarity 100.0%; Pred. No. 8.4e-167;
RESULT 287
ID ADH12519 standard; protein; 323 AA.
DE Novel human secreted and transmembrane protein PRO195.
PN US2003207378-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1694; DB 8; Length 323;
Best Local Similarity 100.0%; Pred. No. 8.4e-167;
RESULT 288
ID ADG48631 standard; protein; 323 AA.
DE Human secreted/transmembrane protein, PRO195.
PN US2003216560-A1.
PD 20-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1694; DB 8; Length 323;
Best Local Similarity 100.0%; Pred. No. 8.4e-167;
RESULT 289
ID ADG61365 standard; protein; 323 AA.
DE Novel human secreted and transmembrane protein PRO195.
PN US2003207429-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1694; DB 8; Length 323;
Best Local Similarity 100.0%; Pred. No. 8.4e-167;
RESULT 290
ID ADH28452 standard; protein; 323 AA.
DE Human PRO polypeptide #136.
PN US2003022331-A1.
PD 30-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1694; DB 8; Length 323;
Best Local Similarity 100.0%; Pred. No. 8.4e-167;
RESULT 291
ID ADG54597 standard; protein; 323 AA.
DE Novel human secreted and transmembrane protein PRO195.
PN US2003207367-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1694; DB 8; Length 323;
Best Local Similarity 100.0%; Pred. No. 8.4e-167;
RESULT 292
ID ADG559637 standard; protein; 323 AA.
DE Novel human secreted and transmembrane protein PRO195.
PN US2003207369-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1694; DB 8; Length 323;
Best Local Similarity 100.0%; Pred. No. 8.4e-167;
RESULT 293
ID ADG51127 standard; protein; 323 AA.
DE Human secreted/transmembrane protein, PRO195.
PN US2004005312-A1.

PD 08-JAN-2004.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1694; DB 8; Length 323;
Best Local Similarity 100.0%; Pred. No. 8.4e-167;
RESULT 294
ID ADH43441 standard; protein; 323 AA.
DE Human PRO polypeptide #4.
PN US2003224984-A1.
PD 04-DEC-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1694; DB 8; Length 323;
Best Local Similarity 100.0%; Pred. No. 8.4e-167;
RESULT 295
ID ADG59071 standard; protein; 323 AA.
DE Human secreted/transmembrane protein, PRO195.
PN US2004005557-A1.
PD 08-JAN-2004.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1694; DB 8; Length 323;
Best Local Similarity 100.0%; Pred. No. 8.4e-167;
RESULT 296
ID ADG62527 standard; protein; 323 AA.
DE Human secreted/transmembrane protein, PRO195.
PN US2004006219-A1.
PD 08-JAN-2004.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1694; DB 8; Length 323;
Best Local Similarity 100.0%; Pred. No. 8.4e-167;
RESULT 297
ID ADH1061 standard; protein; 323 AA.
DE Human PRO polypeptide #136.
PN US2003207361-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1694; DB 8; Length 323;
Best Local Similarity 100.0%; Pred. No. 8.4e-167;
RESULT 298
ID ADH25552 standard; protein; 323 AA.
DE Human neurotrophin homologue related protein sequence SEQ ID NO:330.
PN EP1386931-A1.
PD 04-FEB-2004.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1694; DB 8; Length 323;
Best Local Similarity 100.0%; Pred. No. 8.4e-167;
RESULT 299
ID ADG09804 standard; protein; 323 AA.
DE Novel human secreted and transmembrane protein PRO195.
PN US2004009548-A1.
PD 15-JAN-2004.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1694; DB 8; Length 323;
Best Local Similarity 100.0%; Pred. No. 8.4e-167;
RESULT 300
ID ADH15275 standard; protein; 323 AA.
DE Novel human secreted and transmembrane protein PRO195.
PN US2003207382-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1694; DB 8; Length 323;
Best Local Similarity 100.0%; Pred. No. 8.4e-167;
RESULT 301
ID ADG09152 standard; protein; 323 AA.
DE Novel human secreted and transmembrane protein PRO195.
PN US2004009547-A1.
PD 15-JAN-2004.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1694; DB 8; Length 323;
Best Local Similarity 100.0%; Pred. No. 8.4e-167;
RESULT 302
ID ADH14607 standard; protein; 323 AA.
DE Novel human secreted and transmembrane protein PRO195.
PN US2003207383-A1.
PD 06-NOV-2003.

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PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1694; DB 8; Length 323;
Best Local Similarity 100.0%; Pred. No. 8.4e-167;
RESULT 303
ID AD118202 standard; protein; 323 AA.
DE Novel human secreted and transmembrane protein PRO195.
PN US2003207349-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1694; DB 8; Length 323;
Best Local Similarity 100.0%; Pred. No. 8.4e-167;
RESULT 304
ID AD113089 standard; protein; 323 AA.
DE Human steroid-induced C3A liver cell protein #128.
PN US6673549-B1.
PD 06-JAN-2004.
PA (INCY-) INCYTE CORP.
Query Match 100.0%; Score 1694; DB 8; Length 323;
Best Local Similarity 100.0%; Pred. No. 8.4e-167;
RESULT 305
ID AD163483 standard; protein; 323 AA.
DE Novel human secreted and transmembrane protein PRO195.
PN US2004039164-A1.
PD 26-FEB-2004.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1694; DB 8; Length 323;
Best Local Similarity 100.0%; Pred. No. 8.4e-167;
RESULT 306
ID ADU77378 standard; protein; 323 AA.
DE Human PRO polypeptide #136.
PN US2004038336-A1.
PD 26-FEB-2004.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1694; DB 8; Length 323;
Best Local Similarity 100.0%; Pred. No. 8.4e-167;
RESULT 307
ID ADK82786 standard; protein; 323 AA.
DE Human PRO polypeptide #.
PN US2004043927-A1.
PD 04-MAR-2004.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1694; DB 8; Length 323;
Best Local Similarity 100.0%; Pred. No. 8.4e-167;
RESULT 308
ID AD165500 standard; protein; 323 AA.
DE Human PRO polypeptide #136.
PN US2004038335-A1.
PD 26-FEB-2004.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1694; DB 8; Length 323;
Best Local Similarity 100.0%; Pred. No. 8.4e-167;
RESULT 309
ID ADJ13179 standard; protein; 323 AA.
DE Human protein encoded by a full length cDNA clone seqid 3412.
PN EP1396543-A2.
PD 10-MAR-2004.
PA (REAS-) REB ASSOC BIOTECHNOLOGY.
Query Match 100.0%; Score 1694; DB 8; Length 323;
Best Local Similarity 100.0%; Pred. No. 8.4e-167;
RESULT 310
ID ADM27636 standard; protein; 323 AA.
DE Human PRO polypeptide #136.
PN US2004048333-A1.
PD 11-MAR-2004.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1694; DB 8; Length 323;
Best Local Similarity 100.0%; Pred. No. 8.4e-167;
RESULT 311
ID ADM17329 standard; protein; 323 AA.
DE Human secreted/transmembrane protein, PRO195.
PN US2004048332-A1.
PD 11-MAR-2004.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1694; DB 8; Length 323;
Best Local Similarity 100.0%; Pred. No. 8.4e-167;

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Query Match 100.0%; Score 1694; DB 8; Length 323;
Best Local Similarity 100.0%; Pred. No. 8.4e-167;
RESULT 312
ID ADU07163 standard; protein; 323 AA.
DE Human secreted/transmembrane protein, PRO195.
PN US2004063921-A1.
PD 01-APR-2004.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1694; DB 8; Length 323;
Best Local Similarity 100.0%; Pred. No. 8.4e-167;
RESULT 313
ID ADM42360 standard; protein; 323 AA.
DE Human PRO polypeptide #136.
PN US2004058424-A1.
PD 25-MAR-2004.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1694; DB 8; Length 323;
Best Local Similarity 100.0%; Pred. No. 8.4e-167;
RESULT 314
ID ADM28222 standard; protein; 323 AA.
DE Human PRO polypeptide #136.
PN US2004077064-A1.
PD 22-APR-2004.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1694; DB 8; Length 323;
Best Local Similarity 100.0%; Pred. No. 8.4e-167;
RESULT 315
ID AD195704 standard; protein; 323 AA.
DE Human PRO polypeptide #136.
PN US200307659-A1.
PD 24-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1694; DB 8; Length 323;
Best Local Similarity 100.0%; Pred. No. 8.4e-167;
RESULT 316
ID AD196256 standard; protein; 323 AA.
DE Novel human secreted and transmembrane protein PRO195.
PN US2003207354-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1694; DB 8; Length 323;
Best Local Similarity 100.0%; Pred. No. 8.4e-167;
RESULT 317
ID ADT94201 standard; protein; 323 AA.
DE Human PRO195 protein.
PN AU2003259607-A1.
PD 27-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1694; DB 8; Length 323;
Best Local Similarity 100.0%; Pred. No. 8.4e-167;
RESULT 318
ID AAY02282 standard; protein; 324 AA.
DE Secreted protein clone bm41_7 polypeptide sequence.
PN WO9918127-A1.
PD 15-APR-1999.
PA (GENY ) GENETICS INST INC.
Query Match 98.8%; Score 1674.5; DB 2; Length 324;
Best Local Similarity 99.4%; Pred. No. 8.9e-165;
RESULT 319
ID ADA45143 standard; protein; 324 AA.
DE Human polypeptide #63.
PN US2003044935-A1.
PD 06-MAR-2003.
PA (JACO/) JACOBS K.
PA (MCCO/) MCCOY J M.
PA (LVAL/) LA VALLE E R.
PA (COLL/) COLLINS-RACIE L A.
PA (EVAN/) EVANS C.
PA (MERB/) MERBERG D.
PA (TREA/) TREACY M.
PA (SPAU/) SPAULDING V.
Query Match 98.8%; Score 1674.5; DB 7; Length 324;
Best Local Similarity 99.4%; Pred. No. 8.9e-165;

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RESULT 320
 ID ADC37347 standard; protein: 324 AA.
 DE Nuclear factor kappa B (NF-kappaB) activating protein, SEQ ID 180.
 PN WO2003048202-A2.
 PD 12-JUN-2003.
 PA (ASAH) ASAH KASEI KK.
 Query Match
 Best Local Similarity 98.8%; Score 1674.5; DB 7; Length 324;
 RESULT 321
 ID AD162986 standard; protein: 324 AA.
 DE Human apoptosis-associated protein SEQ ID 429.
 PN WO2003058021-A2.
 PD 17-JUL-2003.
 PA (XANT-) XANTOS BIOMEDICINE AG.
 Query Match
 Best Local Similarity 98.8%; Score 1674.5; DB 7; Length 324;
 RESULT 322
 ID ADC37343 standard; protein: 323 AA.
 DE Nuclear factor kappa B (NF-kappaB) activating protein, SEQ ID 176.
 PN WO2003048202-A2.
 PD 12-JUN-2003.
 PA (ASAH) ASAH KASEI KK.
 Query Match
 Best Local Similarity 95.1%; Score 1611; DB 7; Length 323;
 RESULT 323
 ID AA17299 standard; protein: 300 AA.
 DE Human CBGAD807 polypeptide.
 PN WO9936522-A1.
 PD 22-JUL-1999.
 PA (UYSH-) UNIV SHANGHAI SECOND MEDICAL.
 Query Match
 Best Local Similarity 93.0%; Score 1576; DB 2; Length 300;
 RESULT 324
 ID ABP71501 standard; protein: 300 AA.
 DE Amino acid sequence of protein AAC39890.
 PN WO2003006687-A2.
 PD 23-JAN-2003.
 PA (MED1-) MEDIGENE AG.
 Query Match
 Best Local Similarity 93.0%; Score 1576; DB 6; Length 300;
 RESULT 325
 ID ABR43173 standard; protein: 256 AA.
 DE Human REMAP-5 protein SEQ ID NO:5.
 PN WO2003025130-A2.
 PD 27-MAR-2003.
 PA (INCY-) INCYTE GENOMICS INC.
 Query Match
 Best Local Similarity 75.8%; Score 1283.5; DB 6; Length 256;
 RESULT 326
 ID AAW74884 standard; protein: 273 AA.
 DE Human secreted protein encoded by gene 157 clone HLTED27.
 PN WO9839448-A2.
 PD 11-SEP-1998.
 PA (HUMA-) HUMAN GENOME SCL INC.
 Query Match
 Best Local Similarity 74.5%; Score 1262.5; DB 2; Length 273;
 RESULT 327
 ID ABG95336 standard; protein: 273 AA.
 DE Human novel secreted protein #157.
 PN US6420526-B1.
 PD 16-JUL-2002.
 PA (HUMA-) HUMAN GENOME SCL INC.
 Query Match
 Best Local Similarity 74.5%; Score 1262.5; DB 5; Length 273;
 RESULT 328
 ID AB034530 standard; protein: 273 AA.
 DE Region of human secreted protein encoded by cDNA sequence #157.
 PN US2003049618-A1.
 PD 13-MAR-2003.
 PA (RUBE/) RUBEN S M.
 PA (ROSE/) ROSEN C A.
 PA (SOPP/) SOPP D R.
 PA (CART/) CARTER K C.

PA (BEDN/) BEDNARIK D P.
 PA (ENDR/) ENDRESS G A.
 PA (YUGG/) YU G.
 PA (NTJ/) NI J.
 PA (FENG/) FENG P E.
 PA (YOUN/) YOUNG P E.
 PA (GREE/) GREENE J M.
 PA (FERR/) FERRIE A M.
 PA (DUAN/) DUAN D R.
 PA (HUJ/) HU J.
 PA (FLO/) FLORENCE K A.
 PA (OLSE/) OLSEN H S.
 PA (FISC/) FISCHER C L.
 PA (BENR/) BRENNER R.
 PA (BREM/) BREMER L A.
 PA (MOOR/) MOORE P A.
 PA (SHIY/) SHI Y.
 PA (LAF/) LAFLEUR D W.
 PA (LIY/) LI Y.
 PA (ZENG/) ZENG Z.
 PA (KYAW/) KYAW H.
 Query Match
 Best Local Similarity 74.5%; Score 1262.5; DB 6; Length 273;
 RESULT 329
 ID AD123191 standard; protein: 273 AA.
 DE Novel human secreted protein seq id 476.
 PN US2003175858-A1.
 PD 18-SEP-2003.
 PA (RUBE/) RUBEN S M.
 PA (ROSE/) ROSEN C A.
 PA (SOPP/) SOPP D R.
 PA (CART/) CARTER K C.
 PA (BEDN/) BEDNARIK D P.
 PA (ENDR/) ENDRESS G A.
 PA (YUGG/) YU G.
 PA (NIJ/) NI J.
 PA (FENG/) FENG P E.
 PA (YOUN/) YOUNG P E.
 PA (GREE/) GREENE J M.
 PA (FERR/) FERRIE A M.
 PA (DUAN/) DUAN D R.
 PA (HUJ/) HU J.
 PA (FLO/) FLORENCE K A.
 PA (OLSE/) OLSEN H S.
 PA (FISC/) FISCHER C L.
 PA (BENR/) BRENNER R.
 PA (BREM/) BREMER L A.
 PA (MOOR/) MOORE P A.
 PA (SHIY/) SHI Y.
 PA (LAF/) LAFLEUR D W.
 PA (LIY/) LI Y.
 PA (ZENG/) ZENG Z.
 PA (KYAW/) KYAW H.
 Query Match
 Best Local Similarity 74.5%; Score 1262.5; DB 7; Length 273;
 RESULT 330
 ID ADH74193 standard; protein: 273 AA.
 DE Human secreted protein #157.
 PN US200325248-A1.
 PD 04-DEC-2003.
 PA (HUMA-) HUMAN GENOME SCL INC.
 Query Match
 Best Local Similarity 74.5%; Score 1262.5; DB 8; Length 273;
 RESULT 331
 ID AAU30578 standard; protein: 345 AA.
 DE Novel human secreted protein #1069.
 PN WO200179449-A2.
 PD 25-OCT-2001.
 PA (HYSE-) HYSEQ INC.
 Query Match
 Best Local Similarity 67.4%; Score 1142; DB 4; Length 345;
 RESULT 332
 ID AD065587 standard; protein: 193 AA.

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DE Novel human protein sequence #560.
PN EP1440981-A2.
PD 28-JUL-2004.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
Query Match 57.4%; Score 972.5; DB 8; Length 193;
Best Local Similarity 99.0%; Pred. No. 3.4e-92;
RESULT 333
ID ABB04513 standard; protein; 183 AA.
DE Murine apoptosis related protein #1.
PN DE10126344-A1.
PD 24-JAN-2002.
PA (PLAC) MAX PLANCK GRS FOERDERUNG WISSENSCHAFTEN.
Query Match 55.5%; Score 941; DB 5; Length 183;
Best Local Similarity 95.6%; Pred. No. 5.9e-89;
RESULT 334
ID AAG00091 standard; protein; 132 AA.
DE Human secreted protein, SEQ ID NO: 4172.
PN EP1033401-A2.
PD 06-SEP-2000.
PA (GSEST) GENSEST.
Query Match 41.7%; Score 707; DB 3; Length 132;
Best Local Similarity 100.0%; Pred. No. 7.3e-65;
RESULT 335
ID AAY11918 standard; protein; 113 AA.
DE Human 5' EST secreted protein SEQ ID No: 518.
PN WO9906550-A2.
PD 11-FEB-1999.
PA (GSEST) GENSEST.
Query Match 30.2%; Score 512; DB 2; Length 113;
Best Local Similarity 94.2%; Pred. No. 1e-44;
RESULT 336
ID AAY12407 standard; protein; 88 AA.
DE Human 5' EST secreted protein SEQ ID NO:438.
PN WO9906548-A2.
PD 11-FEB-1999.
PA (GSEST) GENSEST.
Query Match 26.9%; Score 456; DB 2; Length 88;
Best Local Similarity 100.0%; Pred. No. 4.8e-39;
RESULT 337
ID AAY16785 standard; protein; 342 AA.
DE Human secreted protein (clone ct489_14).
PN WO9924469-A1.
PD 20-MAY-1999.
PA (GENY) GENETICS INST INC.
Query Match 25.0%; Score 423.5; DB 2; Length 342;
Best Local Similarity 33.5%; Pred. No. 8e-35;
RESULT 338
ID AAB00163 standard; protein; 342 AA.
DE Brain specific membrane anchored protein (BSMAP).
PN WO200055317-A1.
PD 21-SEP-2000.
PA (FABR) FABRE MEDICAMENT SA PIERRE.
Query Match 25.0%; Score 423.5; DB 3; Length 342;
Best Local Similarity 33.5%; Pred. No. 8e-35;
RESULT 339
ID AAM25762 standard; protein; 353 AA.
DE Human protein sequence SEQ ID NO:1297.
PN WO200153455-A2.
PD 26-JUL-2001.
PA (HYSE-) HYSEQ INC.
Query Match 25.0%; Score 423.5; DB 4; Length 353;
Best Local Similarity 33.5%; Pred. No. 8.3e-35;
RESULT 340
ID ADA45175 standard; protein; 342 AA.
DE Human polypeptide #75.
PN US200304435-A1.
PD 06-MAR-2003.
PA (JACO/) JACOBS K.
PA (MCCO/) MCCOY J M.
PA (LVAL/) LA VALLIE E R.
PA (COLL/) COLLINS-RACIE L A.
PA (EVAN/) EVANS C.
PA (MERB/) MERBERG D.

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PA (TREA/) TREACY M.
PA (SPAU/) SPAULDING V.
Query Match 24.6%; Score 416.5; DB 7; Length 342;
Best Local Similarity 33.0%; Pred. No. 4.2e-34;
RESULT 341
ID ABP69819 standard; protein; 93 AA.
DE Human polypeptide SEQ ID NO 1866.
PN WO200270539-A2.
PD 12-SEP-2002.
PA (HYSE-) HYSEQ INC.
Query Match 19.6%; Score 331.5; DB 5; Length 93;
Best Local Similarity 80.7%; Pred. No. 4.4e-26;
RESULT 342
ID AAU30577 standard; protein; 96 AA.
DE Novel human secreted protein #1068.
PN WO200179449-A2.
PD 25-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match 19.6%; Score 331.5; DB 4; Length 96;
Best Local Similarity 80.7%; Pred. No. 4.6e-26;
RESULT 343
ID ADG14985 standard; protein; 286 AA.
DE Human SECP-18 protein.
PN WO2003087300-A2.
PD 23-OCT-2003.
PA (INCY-) INCYTE CORP.
Query Match 19.2%; Score 324.5; DB 7; Length 286;
Best Local Similarity 32.1%; Pred. No. 1.2e-24;
RESULT 344
ID ADU66975 standard; protein; 309 AA.
DE Human secreted protein (SECP) #1.
PN WO2004007527-A2.
PD 22-JAN-2004.
PA (INCY-) INCYTE CORP.
Query Match 18.7%; Score 317.5; DB 8; Length 309;
Best Local Similarity 38.1%; Pred. No. 7e-24;
RESULT 345
ID AAB00167 standard; protein; 251 AA.
DE Brain specific membrane anchored protein (BSMAP) fragment.
PN WO200055317-A1.
PD 21-SEP-2000.
PA (FABR) FABRE MEDICAMENT SA PIERRE.
Query Match 18.6%; Score 314.5; DB 3; Length 251;
Best Local Similarity 33.3%; Pred. No. 1.1e-23;
RESULT 346
ID AAB00166 standard; protein; 114 AA.
DE Brain specific membrane anchored protein (BSMAP) fragment.
PN WO200055317-A1.
PD 21-SEP-2000.
PA (FABR) FABRE MEDICAMENT SA PIERRE.
Query Match 9.9%; Score 168; DB 3; Length 114;
Best Local Similarity 38.7%; Pred. No. 5.6e-09;
RESULT 347
ID AAB00168 standard; protein; 80 AA.
DE Brain specific membrane anchored protein (BSMAP) fragment.
PN WO200055317-A1.
PD 21-SEP-2000.
PA (FABR) FABRE MEDICAMENT SA PIERRE.
Query Match 5.9%; Score 100; DB 3; Length 80;
Best Local Similarity 51.9%; Pred. No. 0.039;
RESULT 348
ID ADH17466 standard; protein; 914 AA.
DE Human NOV13f protein - SEQ ID 156.
PN WO2003093432-A2.
PD 13-NOV-2003.
PA (CORA-) CURAGEN CORP.
Query Match 5.8%; Score 99; DB 8; Length 914;
Best Local Similarity 19.7%; Pred. No. 1.6;
RESULT 349
ID ABP62957 standard; protein; 811 AA.
DE Human polypeptide SEQ ID NO 394.
PN WO200218424-A2.
PD 07-MAR-2002.

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PA (HYSE-) HYSEQ INC.
 Query Match 5.7%; Score 96; DB 5; Length 811;
 Best Local Similarity 19.4%; Pred. NO. 2.8;
 RESULT 350
 ID ABU10550 standard; protein; 896 AA.
 DE Human NOVab protein.
 PN WO200246408-A2.
 PD 13-JUN-2002.
 PA (CURA-) CURAGEN CORP.
 Query Match 5.7%; Score 96; DB 5; Length 896;
 Best Local Similarity 19.4%; Pred. NO. 3.3;
 RESULT 351
 ID ADH17468 standard; protein; 896 AA.
 DE Human NOV13g protein - SEQ ID 158.
 PN WO2003093432-A2.
 PD 13-NOV-2003.
 PA (CURA-) CURAGEN CORP.
 Query Match 5.7%; Score 96; DB 8; Length 896;
 Best Local Similarity 19.4%; Pred. NO. 3.3;
 RESULT 352
 ID ADH17468 standard; protein; 920 AA.
 DE Human NOV14i protein - SEQ ID 178.
 PN WO2003093432-A2.
 PD 13-NOV-2003.
 PA (CURA-) CURAGEN CORP.
 Query Match 5.7%; Score 96; DB 8; Length 920;
 Best Local Similarity 19.4%; Pred. NO. 3.4;
 RESULT 353
 ID AD059436 standard; protein; 922 AA.
 DE Human cancer-associated (CA) protein sequence SEQ ID NO:72.
 PN WO2004058288-A1.
 PD 15-JUN-2004.
 PA (SAGRES-) SAGRES DISCOVERY INC.
 Query Match 5.7%; Score 96; DB 8; Length 922;
 Best Local Similarity 19.4%; Pred. NO. 3.4;
 RESULT 354
 ID ADH17464 standard; protein; 945 AA.
 DE Human NOV13g protein - SEQ ID 154.
 PN WO2003093432-A2.
 PD 13-NOV-2003.
 PA (CURA-) CURAGEN CORP.
 Query Match 5.7%; Score 96; DB 8; Length 945;
 Best Local Similarity 19.4%; Pred. NO. 3.5;
 RESULT 355
 ID AAB38627 standard; protein; 471 AA.
 DE Human secreted protein sequence encoded by gene 38 SEQ ID NO:164.
 PN WO2000056882-A1.
 PD 28-SEP-2000.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match 5.6%; Score 95.5; DB 3; Length 471;
 Best Local Similarity 18.0%; Pred. NO. 1.5;
 RESULT 356
 ID ADH1504 standard; protein; 486 AA.
 DE Human CD-like molecule HBBF81, SEQ ID NO:303.
 PN WO200226930-A2.
 PD 04-APR-2002.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match 5.6%; Score 95.5; DB 5; Length 486;
 Best Local Similarity 18.0%; Pred. NO. 1.5;
 RESULT 357
 ID AAB95417 standard; protein; 537 AA.
 DE Human protein sequence SEQ ID NO:17814.
 PN EP1074617-A2.
 PD 07-FEB-2001.
 PA (HELI-) HELIX RES INST.
 Query Match 5.6%; Score 95.5; DB 4; Length 537;
 Best Local Similarity 18.0%; Pred. NO. 1.8;
 RESULT 358
 ID AD69381 standard; protein; 741 AA.
 DE Human heat mitochondrial protein as a therapeutic target SeqID1187.
 PN WO2003087768-A2.
 PD 23-OCT-2003.
 PA (MITO-) MITOKOR.

PA (BUCK-) BUCK INST AGE RES.
 Query Match 5.6%; Score 95.5; DB 7; Length 741;
 Best Local Similarity 18.0%; Pred. NO. 2.8;
 RESULT 359
 ID ADQ21134 standard; protein; 741 AA.
 DE Human soft tissue sarcoma-upregulated protein - SEQ ID 3954.
 PN WO2004048938-A2.
 PD 10-JUN-2004.
 PA (PROT-) PROTEIN DESIGN LABS INC.
 Query Match 5.6%; Score 95.5; DB 8; Length 741;
 Best Local Similarity 18.0%; Pred. NO. 2.8;
 RESULT 360
 ID ABP62956 standard; protein; 830 AA.
 DE Human polypeptide SEQ ID NO 393.
 PN WO200218424-A2.
 PD 07-MAR-2002.
 PA (HYSE-) HYSEQ INC.
 Query Match 5.6%; Score 95.5; DB 5; Length 830;
 Best Local Similarity 18.0%; Pred. NO. 3.3;
 RESULT 361
 ID AAY13350 standard; protein; 915 AA.
 DE Amino acid sequence of protein PRO219.
 PN WO9914328-A2.
 PD 25-MAR-1999.
 PA (GETH-) GENENTECH INC.
 Query Match 5.6%; Score 95.5; DB 2; Length 915;
 Best Local Similarity 18.0%; Pred. NO. 3.8;
 RESULT 362
 ID AAY95340 standard; protein; 915 AA.
 DE Human PRO219 antitumour protein.
 PN WO20037638-A2.
 PD 29-JUN-2000.
 PA (GETH-) GENENTECH INC.
 Query Match 5.6%; Score 95.5; DB 3; Length 915;
 Best Local Similarity 18.0%; Pred. NO. 3.8;
 RESULT 363
 ID ADC78354 standard; protein; 915 AA.
 DE Human PRO219 protein.
 PN WO200015796-A2.
 PD 23-MAR-2000.
 PA (GETH-) GENENTECH INC.
 Query Match 5.6%; Score 95.5; DB 3; Length 915;
 Best Local Similarity 18.0%; Pred. NO. 3.8;
 RESULT 364
 ID AAB80218 standard; protein; 915 AA.
 DE Human PRO219 protein.
 PN WO200104311-A1.
 PD 18-JAN-2001.
 PA (GETH-) GENENTECH INC.
 Query Match 5.6%; Score 95.5; DB 4; Length 915;
 Best Local Similarity 18.0%; Pred. NO. 3.8;
 RESULT 365
 ID AAU12318 standard; protein; 915 AA.
 DE Human PRO219 polypeptide sequence.
 PN WO200140466-A2.
 PD 07-JUN-2001.
 PA (GETH-) GENENTECH INC.
 Query Match 5.6%; Score 95.5; DB 4; Length 915;
 Best Local Similarity 18.0%; Pred. NO. 3.8;
 RESULT 366
 ID AAB53077 standard; protein; 915 AA.
 DE Human angiogenesis-associated protein PRO219, SEQ ID NO:67.
 PN WO200053753-A2.
 PD 14-SEP-2000.
 PA (GETH-) GENENTECH INC.
 Query Match 5.6%; Score 95.5; DB 4; Length 915;
 Best Local Similarity 18.0%; Pred. NO. 3.8;
 RESULT 367
 ID ABU71596 standard; protein; 915 AA.
 DE Human PRO polypeptide #7.
 PN US2002146709-A1.
 PD 10-OCT-2002.
 PA (GETH-) GENENTECH INC.

Query Match 5.6%; Score 95.5; DB 6; Length 915;
Best Local Similarity 18.0%; Pred. No. 3.8;
RESULT 368
ID ABO17762 standard; protein; 915 AA.
DE Novel human secreted and transmembrane protein PRO219.
PN US2003032156-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 5.6%; Score 95.5; DB 6; Length 915;
Best Local Similarity 18.0%; Pred. No. 3.8;
RESULT 359
ID ABO171451 standard; protein; 915 AA.
DE Human PRO polypeptide #7.
PN US2002192659-A1.
PD 19-DEC-2002.
PA (GETH) GENENTECH INC.
Query Match 5.6%; Score 95.5; DB 6; Length 915;
Best Local Similarity 18.0%; Pred. No. 3.8;
RESULT 370
ID ABO181016 standard; protein; 915 AA.
DE Human PRO polypeptide #147.
PN US2003004311-A1.
PD 02-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 5.6%; Score 95.5; DB 6; Length 915;
Best Local Similarity 18.0%; Pred. No. 3.8;
RESULT 371
ID ABO17897 standard; protein; 915 AA.
DE Human secreted/transmembrane protein PRO219.
PN US2003003530-A1.
PD 02-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 5.6%; Score 95.5; DB 6; Length 915;
Best Local Similarity 18.0%; Pred. No. 3.8;
RESULT 372
ID ABO1780 standard; protein; 915 AA.
DE Novel human secreted and transmembrane protein PRO219.
PN US2002197671-A1.
PD 26-DEC-2002.
PA (GETH) GENENTECH INC.
Query Match 5.6%; Score 95.5; DB 6; Length 915;
Best Local Similarity 18.0%; Pred. No. 3.8;
RESULT 373
ID ABO66716 standard; protein; 915 AA.
DE Human PRO polypeptide #147.
PN US2003036180-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 5.6%; Score 95.5; DB 6; Length 915;
Best Local Similarity 18.0%; Pred. No. 3.8;
RESULT 374
ID ABO14353 standard; protein; 915 AA.
DE Human secreted/transmembrane protein PRO219.
PN US2002132240-A1.
PD 19-SEP-2002.
PA (GETH) GENENTECH INC.
Query Match 5.6%; Score 95.5; DB 6; Length 915;
Best Local Similarity 18.0%; Pred. No. 3.8;
RESULT 375
ID ABO47368 standard; protein; 915 AA.
DE Human secreted/transmembrane polypeptide PRO219.
PN US2003044839-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 5.6%; Score 95.5; DB 6; Length 915;
Best Local Similarity 18.0%; Pred. No. 3.8;
RESULT 376
ID ABO59797 standard; protein; 915 AA.
DE Novel secreted and transmembrane protein PRO219.
PN US2003017563-A1.
PD 23-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 5.6%; Score 95.5; DB 6; Length 915;

Best Local Similarity 18.0%; Pred. No. 3.8;
RESULT 377
ID ABO24987 standard; protein; 915 AA.
DE Human secreted/transmembrane protein (PRO) #147.
PN US2003036179-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 5.6%; Score 95.5; DB 6; Length 915;
Best Local Similarity 18.0%; Pred. No. 3.8;
RESULT 378
ID ABO64505 standard; protein; 915 AA.
DE Human secreted/transmembrane protein, #8.
PN US2002160374-A1.
PD 31-OCT-2002.
PA (GETH) GENENTECH INC.
Query Match 5.6%; Score 95.5; DB 6; Length 915;
Best Local Similarity 18.0%; Pred. No. 3.8;
RESULT 379
ID ABO67351 standard; protein; 915 AA.
DE Human secreted protein PRO219.
PN US2003032054-A1.
PD 30-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 5.6%; Score 95.5; DB 6; Length 915;
Best Local Similarity 18.0%; Pred. No. 3.8;
RESULT 380
ID ABO14871 standard; protein; 915 AA.
DE Human secreted / transmembrane polypeptide PRO219.
PN US2003036060-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 5.6%; Score 95.5; DB 6; Length 915;
Best Local Similarity 18.0%; Pred. No. 3.8;
RESULT 381
ID ABO66992 standard; protein; 915 AA.
DE Human secreted/transmembrane, PRO, protein SEQ ID 294.
PN US2003032155-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 5.6%; Score 95.5; DB 6; Length 915;
Best Local Similarity 18.0%; Pred. No. 3.8;
RESULT 382
ID ABO69628 standard; protein; 915 AA.
DE Novel human secreted and transmembrane protein PRO219.
PN US2003017463-A1.
PD 23-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 5.6%; Score 95.5; DB 6; Length 915;
Best Local Similarity 18.0%; Pred. No. 3.8;
RESULT 383
ID ABO14810 standard; protein; 915 AA.
DE Human secreted / transmembrane polypeptide PRO219.
PN US2003027143-A1.
PD 06-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 5.6%; Score 95.5; DB 6; Length 915;
Best Local Similarity 18.0%; Pred. No. 3.8;
RESULT 384
ID ADA45813 standard; protein; 915 AA.
DE Novel human secreted and transmembrane protein PRO219.
PN US2003022328-A1.
PD 30-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 5.6%; Score 95.5; DB 6; Length 915;
Best Local Similarity 18.0%; Pred. No. 3.8;
RESULT 385
ID ADA76244 standard; protein; 915 AA.
DE Human PRO polypeptide #147.
PN US2003073212-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 5.6%; Score 95.5; DB 6; Length 915;
Best Local Similarity 18.0%; Pred. No. 3.8;

RESULT 386
ID ADB29239 standard; protein; 915 AA.
DE Human secreted/transmembrane protein, #8.
PN US2003092002-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 5.6%; Score 95.5; DB 6; Length 915;
Best Local Similarity 18.0%; Pred. No. 3.8;
RESULT 387
ID ADA18694 standard; protein; 915 AA.
DE Human PRO polypeptide #147.
PN US2003054517-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 5.6%; Score 95.5; DB 6; Length 915;
Best Local Similarity 18.0%; Pred. No. 3.8;
RESULT 388
ID ADA61517 standard; protein; 915 AA.
DE Homo sapiens.
PN US2003049816-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 5.6%; Score 95.5; DB 6; Length 915;
Best Local Similarity 18.0%; Pred. No. 3.8;
RESULT 389
ID ADH19302 standard; protein; 915 AA.
DE Novel human secreted and transmembrane protein PRO219.
PN US2003068796-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 5.6%; Score 95.5; DB 6; Length 915;
Best Local Similarity 18.0%; Pred. No. 3.8;
RESULT 390
ID ADB27843 standard; protein; 915 AA.
DE Human PRO polypeptide #147.
PN US2003082704-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 5.6%; Score 95.5; DB 6; Length 915;
Best Local Similarity 18.0%; Pred. No. 3.8;
RESULT 391
ID ADA86322 standard; protein; 915 AA.
DE Novel human secreted and transmembrane protein PRO219.
PN US2003082711-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 5.6%; Score 95.5; DB 6; Length 915;
Best Local Similarity 18.0%; Pred. No. 3.8;
RESULT 392
ID ADB15686 standard; protein; 915 AA.
DE Human PRO polypeptide #147.
PN US2003087350-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 5.6%; Score 95.5; DB 6; Length 915;
Best Local Similarity 18.0%; Pred. No. 3.8;
RESULT 393
ID ADA47672 standard; protein; 915 AA.
DE Human PRO polypeptide #147.
PN US2003073215-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 5.6%; Score 95.5; DB 6; Length 915;
Best Local Similarity 18.0%; Pred. No. 3.8;
RESULT 394
ID ADA18095 standard; protein; 915 AA.
DE Human secreted/transmembrane protein, #8.
PN US2003039971-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 5.6%; Score 95.5; DB 6; Length 915;
Best Local Similarity 18.0%; Pred. No. 3.8;
RESULT 395
ID ABO32762 standard; protein; 915 AA.
DE Human secreted/transmembrane protein PRO219.
PN US2003045693-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 5.6%; Score 95.5; DB 6; Length 915;
Best Local Similarity 18.0%; Pred. No. 3.8;
RESULT 396
ID ADA67467 standard; protein; 915 AA.
DE Human PRO polypeptide #147.
PN US2003068795-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 5.6%; Score 95.5; DB 6; Length 915;
Best Local Similarity 18.0%; Pred. No. 3.8;
RESULT 397
ID ADB30474 standard; protein; 915 AA.
DE Human PRO polypeptide #147.
PN US2003068794-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 5.6%; Score 95.5; DB 6; Length 915;
Best Local Similarity 18.0%; Pred. No. 3.8;
RESULT 398
ID ADA85770 standard; protein; 915 AA.
DE Novel human secreted and transmembrane protein PRO219.
PN US2003082693-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 5.6%; Score 95.5; DB 6; Length 915;
Best Local Similarity 18.0%; Pred. No. 3.8;
RESULT 399
ID ADA96982 standard; protein; 915 AA.
DE Human PRO polypeptide #147.
PN US2003082705-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 5.6%; Score 95.5; DB 6; Length 915;
Best Local Similarity 18.0%; Pred. No. 3.8;
RESULT 400
ID ADA79286 standard; protein; 915 AA.
DE Human PRO polypeptide #147.
PN US2003082763-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 5.6%; Score 95.5; DB 6; Length 915;
Best Local Similarity 18.0%; Pred. No. 3.8;
RESULT 401
ID ADA87425 standard; protein; 915 AA.
DE Novel human secreted and transmembrane protein PRO219.
PN US2003087345-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 5.6%; Score 95.5; DB 6; Length 915;
Best Local Similarity 18.0%; Pred. No. 3.8;
RESULT 402
ID ADB16627 standard; protein; 915 AA.
DE Human PRO polypeptide #147.
PN US2003087349-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 5.6%; Score 95.5; DB 6; Length 915;
Best Local Similarity 18.0%; Pred. No. 3.8;
RESULT 403
ID ABO34822 standard; protein; 915 AA.
DE Human PRO polypeptide #7.
PN US2003044793-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 5.6%; Score 95.5; DB 6; Length 915;
Best Local Similarity 18.0%; Pred. No. 3.8;
RESULT 404
ID ADA16070 standard; protein; 915 AA.

DE Human secreted/transmembrane protein, #8.
PN US2003049621-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 5.6%; Score 95.5; DB 6; Length 915;
Best Local Similarity 18.0%; Pred. No. 3.8;
RESULT 405
ID ADA91719 standard; protein; 915 AA.
DE Novel human secreted and transmembrane protein PRO219.
PN US2003082694-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 5.6%; Score 95.5; DB 6; Length 915;
Best Local Similarity 18.0%; Pred. No. 3.8;
RESULT 406
ID ADH14782 standard; protein; 915 AA.
DE Human PRO polypeptide #147.
PN US2003087351-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 5.6%; Score 95.5; DB 6; Length 915;
Best Local Similarity 18.0%; Pred. No. 3.8;
RESULT 407
ID ADB18743 standard; protein; 915 AA.
DE Novel human secreted and transmembrane protein PRO219.
PN US2003073211-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 5.6%; Score 95.5; DB 6; Length 915;
Best Local Similarity 18.0%; Pred. No. 3.8;
RESULT 408
ID ADA93958 standard; protein; 915 AA.
DE Human PRO polypeptide #147.
PN US2003077722-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 5.6%; Score 95.5; DB 6; Length 915;
Best Local Similarity 18.0%; Pred. No. 3.8;
RESULT 409
ID ADB19854 standard; protein; 915 AA.
DE Novel human secreted and transmembrane protein PRO219.
PN US2003082691-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 5.6%; Score 95.5; DB 6; Length 915;
Best Local Similarity 18.0%; Pred. No. 3.8;
RESULT 410
ID ADB13166 standard; protein; 915 AA.
DE Human PRO polypeptide #147.
PN US2003082710-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 5.6%; Score 95.5; DB 6; Length 915;
Best Local Similarity 18.0%; Pred. No. 3.8;
RESULT 411
ID ABO43295 standard; protein; 915 AA.
DE Novel human secreted and transmembrane protein PRO219.
PN US2003044945-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 5.6%; Score 95.5; DB 6; Length 915;
Best Local Similarity 18.0%; Pred. No. 3.8;
RESULT 412
ID ADA74420 standard; protein; 915 AA.
DE Human PRO polypeptide #147.
PN US2003068798-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 5.6%; Score 95.5; DB 6; Length 915;
Best Local Similarity 18.0%; Pred. No. 3.8;
RESULT 413
ID ADA42215 standard; protein; 915 AA.
DE Human secreted/transmembrane protein, #8.
PN US2003054401-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 5.6%; Score 95.5; DB 6; Length 915;
Best Local Similarity 18.0%; Pred. No. 3.8;
RESULT 414
ID ADB24653 standard; protein; 915 AA.
DE Human PRO polypeptide SEQ ID NO 294.
PN US2003077713-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 5.6%; Score 95.5; DB 6; Length 915;
Best Local Similarity 18.0%; Pred. No. 3.8;
RESULT 415
ID ADA82177 standard; protein; 915 AA.
DE Human PRO polypeptide #147.
PN US2003082701-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 5.6%; Score 95.5; DB 6; Length 915;
Best Local Similarity 18.0%; Pred. No. 3.8;
RESULT 416
ID ADA75140 standard; protein; 915 AA.
DE Human PRO polypeptide #147.
PN US2003073216-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 5.6%; Score 95.5; DB 6; Length 915;
Best Local Similarity 18.0%; Pred. No. 3.8;
RESULT 417
ID ADA85218 standard; protein; 915 AA.
DE Novel human secreted and transmembrane protein PRO219.
PN US2003082695-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 5.6%; Score 95.5; DB 6; Length 915;
Best Local Similarity 18.0%; Pred. No. 3.8;
RESULT 418
ID ADA84666 standard; protein; 915 AA.
DE Novel human secreted and transmembrane protein PRO219.
PN US2003082708-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 5.6%; Score 95.5; DB 6; Length 915;
Best Local Similarity 18.0%; Pred. No. 3.8;
RESULT 419
ID ABO17500 standard; protein; 915 AA.
DE Human PRO polypeptide #7.
PN US2003064367-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 5.6%; Score 95.5; DB 6; Length 915;
Best Local Similarity 18.0%; Pred. No. 3.8;
RESULT 420
ID ADB29922 standard; protein; 915 AA.
DE Human PRO polypeptide #147.
PN US2003073214-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 5.6%; Score 95.5; DB 6; Length 915;
Best Local Similarity 18.0%; Pred. No. 3.8;
RESULT 421
ID ADA80450 standard; protein; 915 AA.
DE Human PRO polypeptide #147.
PN US2003082761-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 5.6%; Score 95.5; DB 6; Length 915;
Best Local Similarity 18.0%; Pred. No. 3.8;
RESULT 422
ID ADA75692 standard; protein; 915 AA.
DE Human PRO polypeptide #147.
PN US2003082703-A1.

PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 5.6%; Score 95.5; DB 6; Length 915;
Best Local Similarity 18.0%; Pred. No. 3.8;
RESULT 423
ID ADA46917 standard; protein; 915 AA.
DE Human PRO polypeptide #147.
PN US2003073210-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 5.6%; Score 95.5; DB 6; Length 915;
Best Local Similarity 18.0%; Pred. No. 3.8;
RESULT 424
ID ADB25213 standard; protein; 915 AA.
DE Human PRO polypeptide SEQ ID NO 294.
PN US2003077715-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 5.6%; Score 95.5; DB 6; Length 915;
Best Local Similarity 18.0%; Pred. No. 3.8;
RESULT 425
ID ADA93389 standard; protein; 915 AA.
DE Human PRO polypeptide #147.
PN US2003077721-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 5.6%; Score 95.5; DB 6; Length 915;
Best Local Similarity 18.0%; Pred. No. 3.8;
RESULT 426
ID ADB26739 standard; protein; 915 AA.
DE Human PRO polypeptide #147.
PN US2003092147-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 5.6%; Score 95.5; DB 6; Length 915;
Best Local Similarity 18.0%; Pred. No. 3.8;
RESULT 427
ID ADB31026 standard; protein; 915 AA.
DE Human PRO polypeptide #147.
PN US2003096386-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 5.6%; Score 95.5; DB 6; Length 915;
Best Local Similarity 18.0%; Pred. No. 3.8;
RESULT 428
ID ADA60954 standard; protein; 915 AA.
DE Homo sapiens.
PN US2003049817-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 5.6%; Score 95.5; DB 6; Length 915;
Best Local Similarity 18.0%; Pred. No. 3.8;
RESULT 429
ID ADB24101 standard; protein; 915 AA.
DE Human PRO polypeptide SEQ ID NO 294.
PN US2003077714-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 5.6%; Score 95.5; DB 6; Length 915;
Best Local Similarity 18.0%; Pred. No. 3.8;
RESULT 430
ID ADA96430 standard; protein; 915 AA.
DE Human PRO polypeptide #147.
PN US2003082690-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 5.6%; Score 95.5; DB 6; Length 915;
Best Local Similarity 18.0%; Pred. No. 3.8;
RESULT 431
ID ADA81002 standard; protein; 915 AA.
DE Human PRO polypeptide #147.
PN US2003082702-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.

PA (GETH) GENENTECH INC.
Query Match 5.6%; Score 95.5; DB 6; Length 915;
Best Local Similarity 18.0%; Pred. No. 3.8;
RESULT 432
ID ADA95878 standard; protein; 915 AA.
DE Human PRO polypeptide #147.
PN US2003082759-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 5.6%; Score 95.5; DB 6; Length 915;
Best Local Similarity 18.0%; Pred. No. 3.8;
RESULT 433
ID ADB26187 standard; protein; 915 AA.
DE Human PRO polypeptide #147.
PN US2003082760-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 5.6%; Score 95.5; DB 6; Length 915;
Best Local Similarity 18.0%; Pred. No. 3.8;
RESULT 434
ID ADB21672 standard; protein; 915 AA.
DE Novel human secreted and transmembrane protein PRO219.
PN US2003082765-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 5.6%; Score 95.5; DB 6; Length 915;
Best Local Similarity 18.0%; Pred. No. 3.8;
RESULT 435
ID ADA77451 standard; protein; 915 AA.
DE Human PRO polypeptide #147.
PN US2003068797-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 5.6%; Score 95.5; DB 7; Length 915;
Best Local Similarity 18.0%; Pred. No. 3.8;
RESULT 436
ID ADB18191 standard; protein; 915 AA.
DE Human PRO polypeptide #147.
PN US2003077710-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 5.6%; Score 95.5; DB 7; Length 915;
Best Local Similarity 18.0%; Pred. No. 3.8;
RESULT 437
ID ADA86874 standard; protein; 915 AA.
DE Novel human secreted and transmembrane protein PRO219.
PN US2003082709-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 5.6%; Score 95.5; DB 7; Length 915;
Best Local Similarity 18.0%; Pred. No. 3.8;
RESULT 438
ID ADA16494 standard; protein; 915 AA.
DE Human secreted/transmembrane protein, #8.
PN US2003039969-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 5.6%; Score 95.5; DB 7; Length 915;
Best Local Similarity 18.0%; Pred. No. 3.8;
RESULT 439
ID ADA12923 standard; protein; 915 AA.
DE Human secreted/transmembrane protein, #8.
PN US2003049622-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 5.6%; Score 95.5; DB 7; Length 915;
Best Local Similarity 18.0%; Pred. No. 3.8;
RESULT 440
ID ADA41791 standard; protein; 915 AA.
DE Human secreted/transmembrane protein, #8.
PN US2003082540-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.

Query Match 5.6%; Score 95.5; DB 7; Length 915;
Best Local Similarity 18.0%; Pred. No. 3.8;
RESULT 441
ID ADB87977 standard; protein; 915 AA.
DE Novel human secreted and transmembrane protein PRO219.
PN US2003082700-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 5.6%; Score 95.5; DB 7; Length 915;
Best Local Similarity 18.0%; Pred. No. 3.8;
RESULT 442
ID ADA6365 standard; protein; 915 AA.
DE Novel human secreted and transmembrane protein PRO219.
PN US2003054516-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 5.6%; Score 95.5; DB 7; Length 915;
Best Local Similarity 18.0%; Pred. No. 3.8;
RESULT 443
ID ADA17138 standard; protein; 915 AA.
DE Human secreted/transmembrane protein, #8.
PN US2003017498-A1.
PD 23-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 5.6%; Score 95.5; DB 7; Length 915;
Best Local Similarity 18.0%; Pred. No. 3.8;
RESULT 444
ID ADA2641 standard; protein; 915 AA.
DE Human secreted/transmembrane protein, #8.
PN US2003054351-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 5.6%; Score 95.5; DB 7; Length 915;
Best Local Similarity 18.0%; Pred. No. 3.8;
RESULT 445
ID ADB28395 standard; protein; 915 AA.
DE Human PRO polypeptide #147.
PN US2003082699-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 5.6%; Score 95.5; DB 7; Length 915;
Best Local Similarity 18.0%; Pred. No. 3.8;
RESULT 446
ID ADB28947 standard; protein; 915 AA.
DE Human PRO polypeptide #147.
PN US2003082706-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 5.6%; Score 95.5; DB 7; Length 915;
Best Local Similarity 18.0%; Pred. No. 3.8;
RESULT 447
ID ADA76899 standard; protein; 915 AA.
DE Human PRO polypeptide #147.
PN US2003059909-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 5.6%; Score 95.5; DB 7; Length 915;
Best Local Similarity 18.0%; Pred. No. 3.8;
RESULT 448
ID ADA88529 standard; protein; 915 AA.
DE Novel human secreted and transmembrane protein PRO219.
PN US2003073213-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 5.6%; Score 95.5; DB 7; Length 915;
Best Local Similarity 18.0%; Pred. No. 3.8;
RESULT 449
ID ADA97534 standard; protein; 915 AA.
DE Human PRO polypeptide #147.
PN US2003082686-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 5.6%; Score 95.5; DB 7; Length 915;

Best Local Similarity 18.0%; Pred. No. 3.8;
RESULT 450
ID ADB27291 standard; protein; 915 AA.
DE Human PRO polypeptide #147.
PN US2003022239-A1.
PD 30-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 5.6%; Score 95.5; DB 7; Length 915;
Best Local Similarity 18.0%; Pred. No. 3.8;
RESULT 451
ID ADB22224 standard; protein; 915 AA.
DE Novel human secreted and transmembrane protein PRO219.
PN US2003087344-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 5.6%; Score 95.5; DB 7; Length 915;
Best Local Similarity 18.0%; Pred. No. 3.8;
RESULT 452
ID ABO17561 standard; protein; 915 AA.
DE Human PRO polypeptide #7.
PN US2003064923-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 5.6%; Score 95.5; DB 7; Length 915;
Best Local Similarity 18.0%; Pred. No. 3.8;
RESULT 453
ID ADA66915 standard; protein; 915 AA.
DE Human PRO polypeptide #147.
PN US2003068793-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 5.6%; Score 95.5; DB 7; Length 915;
Best Local Similarity 18.0%; Pred. No. 3.8;
RESULT 454
ID ADB22776 standard; protein; 915 AA.
DE Human PRO polypeptide #147.
PN US2003077711-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 5.6%; Score 95.5; DB 7; Length 915;
Best Local Similarity 18.0%; Pred. No. 3.8;
RESULT 455
ID ADB23549 standard; protein; 915 AA.
DE Human PRO polypeptide SEQ ID NO 294.
PN US2003077712-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 5.6%; Score 95.5; DB 7; Length 915;
Best Local Similarity 18.0%; Pred. No. 3.8;
RESULT 456
ID ADA92271 standard; protein; 915 AA.
DE Novel human secreted and transmembrane protein PRO219.
PN US2003082712-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 5.6%; Score 95.5; DB 7; Length 915;
Best Local Similarity 18.0%; Pred. No. 3.8;
RESULT 457
ID ADB15334 standard; protein; 915 AA.
DE Human PRO polypeptide #147.
PN US2003087352-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 5.6%; Score 95.5; DB 7; Length 915;
Best Local Similarity 18.0%; Pred. No. 3.8;
RESULT 458
ID ADB38586 standard; protein; 915 AA.
DE Novel human secreted and transmembrane protein PRO219.
PN US2003082766-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 5.6%; Score 95.5; DB 7; Length 915;
Best Local Similarity 18.0%; Pred. No. 3.8;
RESULT 459
ID ADB38034 standard; protein; 915 AA.

DE Novel human secreted and transmembrane protein PRO219.
PN US2003082747-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 5.6%; Score 95.5; DB 7; Length 915;
Best Local Similarity 18.0%; Pred. No. 3.8;
RESULT 460
ID ADB66506 standard; protein; 915 AA.
DE Novel human secreted and transmembrane protein PRO219.
PN US2003082689-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 5.6%; Score 95.5; DB 7; Length 915;
Best Local Similarity 18.0%; Pred. No. 3.8;
RESULT 461
ID ADB89586 standard; protein; 915 AA.
DE Human PRO polypeptide #147.
PN US2003082698-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 5.6%; Score 95.5; DB 7; Length 915;
Best Local Similarity 18.0%; Pred. No. 3.8;
RESULT 462
ID ADB90318 standard; protein; 915 AA.
DE Human PRO polypeptide #147.
PN US2003082762-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 5.6%; Score 95.5; DB 7; Length 915;
Best Local Similarity 18.0%; Pred. No. 3.8;
RESULT 463
ID ADB77560 standard; protein; 915 AA.
DE Human secreted/transmembrane protein, #8.
PN US2003077654-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 5.6%; Score 95.5; DB 7; Length 915;
Best Local Similarity 18.0%; Pred. No. 3.8;
RESULT 464
ID ADB39419 standard; protein; 915 AA.
DE Novel human secreted and transmembrane protein PRO219.
PN US2003082764-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 5.6%; Score 95.5; DB 7; Length 915;
Best Local Similarity 18.0%; Pred. No. 3.8;
RESULT 465
ID ADB74696 standard; protein; 915 AA.
DE Human secreted/transmembrane protein, #8.
PN US2003082542-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 5.6%; Score 95.5; DB 7; Length 915;
Best Local Similarity 18.0%; Pred. No. 3.8;
RESULT 466
ID ADB37042 standard; protein; 915 AA.
DE Novel human secreted and transmembrane protein PRO219.
PN US2003082687-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 5.6%; Score 95.5; DB 7; Length 915;
Best Local Similarity 18.0%; Pred. No. 3.8;
RESULT 467
ID ADB86649 standard; protein; 915 AA.
DE Human PRO polypeptide #147.
PN US2003082657-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 5.6%; Score 95.5; DB 7; Length 915;
Best Local Similarity 18.0%; Pred. No. 3.8;
RESULT 468
ID ADB77254 standard; protein; 915 AA.
DE Novel human secreted and transmembrane protein PRO219.
PN US2003082696-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 5.6%; Score 95.5; DB 7; Length 915;
Best Local Similarity 18.0%; Pred. No. 3.8;
RESULT 469
ID ADB34411 standard; protein; 915 AA.
DE Human PRO polypeptide SEQ ID NO 294.
PN US200307717-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 5.6%; Score 95.5; DB 7; Length 915;
Best Local Similarity 18.0%; Pred. No. 3.8;
RESULT 470
ID ADB35515 standard; protein; 915 AA.
DE Human PRO polypeptide SEQ ID NO 294.
PN US200307719-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 5.6%; Score 95.5; DB 7; Length 915;
Best Local Similarity 18.0%; Pred. No. 3.8;
RESULT 471
ID ADB33859 standard; protein; 915 AA.
DE Human PRO polypeptide SEQ ID NO 294.
PN US200307716-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 5.6%; Score 95.5; DB 7; Length 915;
Best Local Similarity 18.0%; Pred. No. 3.8;
RESULT 472
ID ADB34963 standard; protein; 915 AA.
DE Human PRO polypeptide SEQ ID NO 294.
PN US200307718-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 5.6%; Score 95.5; DB 7; Length 915;
Best Local Similarity 18.0%; Pred. No. 3.8;
RESULT 473
ID ADB36067 standard; protein; 915 AA.
DE Human PRO polypeptide SEQ ID NO 294.
PN US200307720-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 5.6%; Score 95.5; DB 7; Length 915;
Best Local Similarity 18.0%; Pred. No. 3.8;
RESULT 474
ID ADB46462 standard; protein; 915 AA.
DE Novel human secreted and transmembrane protein PRO219.
PN US2003082692-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 5.6%; Score 95.5; DB 7; Length 915;
Best Local Similarity 18.0%; Pred. No. 3.8;
RESULT 475
ID ADC28342 standard; protein; 915 AA.
DE Human secreted/transmembrane protein, #8.
PN US2003059772-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 5.6%; Score 95.5; DB 7; Length 915;
Best Local Similarity 18.0%; Pred. No. 3.8;
RESULT 476
ID ADC39542 standard; protein; 915 AA.
DE Human secreted/transmembrane protein, #8.
PN US2003059828-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 5.6%; Score 95.5; DB 7; Length 915;
Best Local Similarity 18.0%; Pred. No. 3.8;
RESULT 477
ID ADC40056 standard; protein; 915 AA.
DE Human secreted/transmembrane protein, #8.
PN US2003059829-A1.

PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 5.6%; Score 95.5; DB 7; Length 915;
Best Local Similarity 18.0%; Pred. No. 3.8;
RESULT 478
ID ADC18894 standard; protein; 915 AA.
DE Human secreted/transmembrane protein, #8.
PN US2003036061-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 5.6%; Score 95.5; DB 7; Length 915;
Best Local Similarity 18.0%; Pred. No. 3.8;
RESULT 479
ID ADC34180 standard; protein; 915 AA.
DE Human secreted/transmembrane protein, #8.
PN US2003036094-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 5.6%; Score 95.5; DB 7; Length 915;
Best Local Similarity 18.0%; Pred. No. 3.8;
RESULT 480
ID ADC29235 standard; protein; 915 AA.
DE Human secreted/transmembrane protein, #8.
PN US2003049676-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 5.6%; Score 95.5; DB 7; Length 915;
Best Local Similarity 18.0%; Pred. No. 3.8;
RESULT 481
ID ADC28766 standard; protein; 915 AA.
DE Human secreted/transmembrane protein, #8.
PN US2003049677-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 5.6%; Score 95.5; DB 7; Length 915;
Best Local Similarity 18.0%; Pred. No. 3.8;
RESULT 482
ID ADC40651 standard; protein; 915 AA.
DE Human secreted/transmembrane protein, #8.
PN US2003054400-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 5.6%; Score 95.5; DB 7; Length 915;
Best Local Similarity 18.0%; Pred. No. 3.8;
RESULT 483
ID ADC19308 standard; protein; 915 AA.
DE Human secreted/transmembrane protein, #8.
PN US2003054441-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 5.6%; Score 95.5; DB 7; Length 915;
Best Local Similarity 18.0%; Pred. No. 3.8;
RESULT 484
ID ADC33756 standard; protein; 915 AA.
DE Human secreted/transmembrane protein, #8.
PN US2003073077-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 5.6%; Score 95.5; DB 7; Length 915;
Best Local Similarity 18.0%; Pred. No. 3.8;
RESULT 485
ID ADC12826 standard; protein; 915 AA.
DE Human secreted/transmembrane protein, #8.
PN US2003073079-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 5.6%; Score 95.5; DB 7; Length 915;
Best Local Similarity 18.0%; Pred. No. 3.8;
RESULT 486
ID ADC50335 standard; protein; 915 AA.
DE Novel human secreted and transmembrane protein PRO219.
PN US2003092106-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 5.6%; Score 95.5; DB 7; Length 915;
Best Local Similarity 18.0%; Pred. No. 3.8;
RESULT 487
ID ADC71882 standard; protein; 915 AA.
DE Novel human secreted and transmembrane protein PRO219.
PN US2003092107-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 5.6%; Score 95.5; DB 7; Length 915;
Best Local Similarity 18.0%; Pred. No. 3.8;
RESULT 488
ID ADC59861 standard; protein; 915 AA.
DE Novel human secreted and transmembrane protein PRO219.
PN US2003092105-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 5.6%; Score 95.5; DB 7; Length 915;
Best Local Similarity 18.0%; Pred. No. 3.8;
RESULT 489
ID ADC52868 standard; protein; 915 AA.
DE Novel human secreted and transmembrane protein Seq ID294.
PN US2003087365-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 5.6%; Score 95.5; DB 7; Length 915;
Best Local Similarity 18.0%; Pred. No. 3.8;
RESULT 490
ID ADC57222 standard; protein; 915 AA.
DE Novel human secreted and transmembrane protein Seq ID294.
PN US2003087366-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 5.6%; Score 95.5; DB 7; Length 915;
Best Local Similarity 18.0%; Pred. No. 3.8;
RESULT 491
ID ADC60413 standard; protein; 915 AA.
DE Novel human secreted and transmembrane protein PRO219.
PN US2003087367-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 5.6%; Score 95.5; DB 7; Length 915;
Best Local Similarity 18.0%; Pred. No. 3.8;
RESULT 492
ID ADC50888 standard; protein; 915 AA.
DE Novel human secreted and transmembrane protein PRO219.
PN US2003087361-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 5.6%; Score 95.5; DB 7; Length 915;
Best Local Similarity 18.0%; Pred. No. 3.8;
RESULT 493
ID ADC65415 standard; protein; 915 AA.
DE Human PRO polypeptide #147.
PN US2003087362-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 5.6%; Score 95.5; DB 7; Length 915;
Best Local Similarity 18.0%; Pred. No. 3.8;
RESULT 494
ID ADC54513 standard; protein; 915 AA.
DE Novel human secreted and transmembrane protein Seq ID294.
PN US2003087363-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 5.6%; Score 95.5; DB 7; Length 915;
Best Local Similarity 18.0%; Pred. No. 3.8;
RESULT 495
ID ADC53474 standard; protein; 915 AA.
DE Novel human secreted and transmembrane protein Seq ID294.
PN US2003087364-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.

Query Match 5.6%; Score 95.5; DB 7; Length 915;
Best Local Similarity 18.0%; Pred. No. 3.8;
RESULT 496
ID ADC58997 standard; protein, 915 AA.
DE Novel human secreted and transmembrane protein Seq ID294.
PN US2003087359-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 5.6%; Score 95.5; DB 7; Length 915;
Best Local Similarity 18.0%; Pred. No. 3.8;
RESULT 497
ID ADC55875 standard; protein, 915 AA.
DE Novel human secreted and transmembrane protein Seq ID294.
PN US2003087360-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 5.6%; Score 95.5; DB 7; Length 915;
Best Local Similarity 18.0%; Pred. No. 3.8;
RESULT 498
ID ADC58445 standard; protein, 915 AA.
DE Novel human secreted and transmembrane protein Seq ID294.
PN US2003087346-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 5.6%; Score 95.5; DB 7; Length 915;
Best Local Similarity 18.0%; Pred. No. 3.8;
RESULT 499
ID ADC12278 standard; protein, 915 AA.
DE Human secreted/transmembrane protein, #8.
PN US2003082541-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 5.6%; Score 95.5; DB 7; Length 915;
Best Local Similarity 18.0%; Pred. No. 3.8;
RESULT 500
ID ADD03119 standard; protein, 915 AA.
DE Novel human secreted and transmembrane protein PRO219.
PN US2003082104-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 5.6%; Score 95.5; DB 7; Length 915;
Best Local Similarity 18.0%; Pred. No. 3.8;
RESULT 501
ID ADC90111 standard; protein, 915 AA.
DE Novel human secreted and transmembrane protein PRO219.
PN US2003087348-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 5.6%; Score 95.5; DB 7; Length 915;
Best Local Similarity 18.0%; Pred. No. 3.8;
RESULT 502
ID ADC69530 standard; protein, 915 AA.
DE Human PRO polypeptide #147.
PN US2003194770-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 5.6%; Score 95.5; DB 7; Length 915;
Best Local Similarity 18.0%; Pred. No. 3.8;
RESULT 503
ID ADC48419 standard; protein, 915 AA.
DE Human PRO polypeptide #147.
PN US2003194773-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 5.6%; Score 95.5; DB 7; Length 915;
Best Local Similarity 18.0%; Pred. No. 3.8;
RESULT 504
ID ADD09948 standard; protein, 915 AA.
DE Human PRO polypeptide #147.
PN US2003194776-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 5.6%; Score 95.5; DB 7; Length 915;

Best Local Similarity 18.0%; Pred. No. 3.8;
RESULT 505
ID ADD04523 standard; protein, 915 AA.
DE Novel human secreted and transmembrane protein PRO219.
PN US2003087354-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 5.6%; Score 95.5; DB 7; Length 915;
Best Local Similarity 18.0%; Pred. No. 3.8;
RESULT 506
ID ADC80479 standard; protein, 915 AA.
DE Novel human secreted and transmembrane protein PRO219.
PN US2003092103-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 5.6%; Score 95.5; DB 7; Length 915;
Best Local Similarity 18.0%; Pred. No. 3.8;
RESULT 507
ID ADD10986 standard; protein, 915 AA.
DE Human PRO polypeptide #147.
PN US2003194774-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 5.6%; Score 95.5; DB 7; Length 915;
Best Local Similarity 18.0%; Pred. No. 3.8;
RESULT 508
ID ADC47867 standard; protein, 915 AA.
DE Human PRO polypeptide #147.
PN US2003194771-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 5.6%; Score 95.5; DB 7; Length 915;
Best Local Similarity 18.0%; Pred. No. 3.8;
RESULT 509
ID ADD04833 standard; protein, 915 AA.
DE Human secreted/transmembrane protein, #8.
PN US2003104469-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 5.6%; Score 95.5; DB 7; Length 915;
Best Local Similarity 18.0%; Pred. No. 3.8;
RESULT 510
ID ADC79927 standard; protein, 915 AA.
DE Novel human secreted and transmembrane protein PRO219.
PN US2003087358-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 5.6%; Score 95.5; DB 7; Length 915;
Best Local Similarity 18.0%; Pred. No. 3.8;
RESULT 511
ID ADD09396 standard; protein, 915 AA.
DE Human PRO polypeptide #147.
PN US2003194775-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 5.6%; Score 95.5; DB 7; Length 915;
Best Local Similarity 18.0%; Pred. No. 3.8;
RESULT 512
ID ADD03839 standard; protein, 915 AA.
DE Human secreted/transmembrane protein, #8.
PN US2003104381-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 5.6%; Score 95.5; DB 7; Length 915;
Best Local Similarity 18.0%; Pred. No. 3.8;
RESULT 513
ID ADD03415 standard; protein, 915 AA.
DE Human secreted/transmembrane protein, #8.
PN US2003108983-A1.
PD 12-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 5.6%; Score 95.5; DB 7; Length 915;
Best Local Similarity 18.0%; Pred. No. 3.8;

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RESULT 514
ID ADD1109 standard; protein; 915 AA.
DE Novel human secreted and transmembrane protein PRO219.
PN US2003203438-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 5.6%; Score 95.5; DB 7; Length 915;
Best Local Similarity 18.0%; Pred. No. 3.8;
RESULT 515
ID ADD52248 standard; protein; 915 AA.
DE Human PRO polypeptide #147.
PN US2003194769-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 5.6%; Score 95.5; DB 7; Length 915;
Best Local Similarity 18.0%; Pred. No. 3.8;
RESULT 516
ID ADD52988 standard; protein; 915 AA.
DE Human PRO polypeptide #147.
PN US2003194792-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 5.6%; Score 95.5; DB 7; Length 915;
Best Local Similarity 18.0%; Pred. No. 3.8;
RESULT 517
ID ADD53540 standard; protein; 915 AA.
DE Novel human secreted and transmembrane protein PRO219.
PN US2003203437-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 5.6%; Score 95.5; DB 7; Length 915;
Best Local Similarity 18.0%; Pred. No. 3.8;
RESULT 518
ID ADD51696 standard; protein; 915 AA.
DE Human PRO polypeptide #147.
PN US2003194779-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 5.6%; Score 95.5; DB 7; Length 915;
Best Local Similarity 18.0%; Pred. No. 3.8;
RESULT 519
ID ADD02495 standard; protein; 915 AA.
DE Human PRO polypeptide #147.
PN US2003203431-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 5.6%; Score 95.5; DB 7; Length 915;
Best Local Similarity 18.0%; Pred. No. 3.8;
RESULT 520
ID ADD01929 standard; protein; 915 AA.
DE Human PRO polypeptide #147.
PN US2003203430-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 5.6%; Score 95.5; DB 7; Length 915;
Best Local Similarity 18.0%; Pred. No. 3.8;
RESULT 521
ID ADD54111 standard; protein; 915 AA.
DE Novel human secreted and transmembrane protein PRO219.
PN US2003203432-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 5.6%; Score 95.5; DB 7; Length 915;
Best Local Similarity 18.0%; Pred. No. 3.8;
RESULT 522
ID ADD92428 standard; protein; 915 AA.
DE Human PRO polypeptide #147.
PN US2003199030-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 5.6%; Score 95.5; DB 7; Length 915;
Best Local Similarity 18.0%; Pred. No. 3.8;
RESULT 523
ID ADD91324 standard; protein; 915 AA.
DE Human PRO polypeptide #147.
PN US2003199055-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 5.6%; Score 95.5; DB 7; Length 915;
Best Local Similarity 18.0%; Pred. No. 3.8;
RESULT 524
ID ADD03938 standard; protein; 915 AA.
DE Human PRO polypeptide #147.
PN US2003199057-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 5.6%; Score 95.5; DB 7; Length 915;
Best Local Similarity 18.0%; Pred. No. 3.8;
RESULT 525
ID ADD32235 standard; protein; 915 AA.
DE Novel human secreted and transmembrane protein PRO219.
PN US2003194765-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 5.6%; Score 95.5; DB 7; Length 915;
Best Local Similarity 18.0%; Pred. No. 3.8;
RESULT 526
ID ADD82167 standard; protein; 915 AA.
DE Human PRO polypeptide #147.
PN US2003199056-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 5.6%; Score 95.5; DB 7; Length 915;
Best Local Similarity 18.0%; Pred. No. 3.8;
RESULT 527
ID ADD79391 standard; protein; 915 AA.
DE Human PRO polypeptide #147.
PN US2003203428-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 5.6%; Score 95.5; DB 7; Length 915;
Best Local Similarity 18.0%; Pred. No. 3.8;
RESULT 528
ID ADD84197 standard; protein; 915 AA.
DE Human PRO polypeptide #147.
PN US2003194772-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 5.6%; Score 95.5; DB 7; Length 915;
Best Local Similarity 18.0%; Pred. No. 3.8;
RESULT 529
ID ADD17744 standard; protein; 915 AA.
DE Human PRO polypeptide #147.
PN US2003199023-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 5.6%; Score 95.5; DB 7; Length 915;
Best Local Similarity 18.0%; Pred. No. 3.8;
RESULT 530
ID ADD91876 standard; protein; 915 AA.
DE Human PRO polypeptide #147.
PN US2003199053-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 5.6%; Score 95.5; DB 7; Length 915;
Best Local Similarity 18.0%; Pred. No. 3.8;
RESULT 531
ID ADD33339 standard; protein; 915 AA.
DE Novel human secreted and transmembrane protein PRO219.
PN US2003194767-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 5.6%; Score 95.5; DB 7; Length 915;
Best Local Similarity 18.0%; Pred. No. 3.8;
RESULT 532
ID ADD33891 standard; protein; 915 AA.
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DE Novel human secreted and transmembrane protein PRO219.
PN US2003194791-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 5.6%; Score 95.5; DB 7; Length 915;
Best Local Similarity 18.0%; Pred. No. 3.8;
RESULT 533
ID ADD79943 standard; protein; 915 AA.
DE Human PRO polypeptide #147.
PN US2003207417-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 5.6%; Score 95.5; DB 7; Length 915;
Best Local Similarity 18.0%; Pred. No. 3.8;
RESULT 534
ID ADD92980 standard; protein; 915 AA.
DE Human PRO polypeptide #147.
PN US2003194768-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 5.6%; Score 95.5; DB 7; Length 915;
Best Local Similarity 18.0%; Pred. No. 3.8;
RESULT 535
ID ADE19400 standard; protein; 915 AA.
DE Human PRO polypeptide #147.
PN US2003199025-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 5.6%; Score 95.5; DB 7; Length 915;
Best Local Similarity 18.0%; Pred. No. 3.8;
RESULT 536
ID ADE34667 standard; protein; 915 AA.
DE Human secreted/transmembrane protein, #8.
PN US2003077583-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 5.6%; Score 95.5; DB 7; Length 915;
Best Local Similarity 18.0%; Pred. No. 3.8;
RESULT 537
ID ADE18948 standard; protein; 915 AA.
DE Human PRO polypeptide #147.
PN US2003199026-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 5.6%; Score 95.5; DB 7; Length 915;
Best Local Similarity 18.0%; Pred. No. 3.8;
RESULT 538
ID ADE43044 standard; protein; 915 AA.
DE Human PRO polypeptide #147.
PN US2003199033-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 5.6%; Score 95.5; DB 7; Length 915;
Best Local Similarity 18.0%; Pred. No. 3.8;
RESULT 539
ID ADD95833 standard; protein; 915 AA.
DE Human PRO polypeptide #147.
PN US2003199059-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 5.6%; Score 95.5; DB 7; Length 915;
Best Local Similarity 18.0%; Pred. No. 3.8;
RESULT 540
ID ADE22719 standard; protein; 915 AA.
DE Human PRO polypeptide #147.
PN US2003199064-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 5.6%; Score 95.5; DB 7; Length 915;
Best Local Similarity 18.0%; Pred. No. 3.8;
RESULT 541
ID ADD78837 standard; protein; 915 AA.
DE Human PRO polypeptide #147.
PN US2003207384-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 5.6%; Score 95.5; DB 7; Length 915;
Best Local Similarity 18.0%; Pred. No. 3.8;
RESULT 542
ID ADE32787 standard; protein; 915 AA.
DE Novel human secreted and transmembrane protein PRO219.
PN US2003194766-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 5.6%; Score 95.5; DB 7; Length 915;
Best Local Similarity 18.0%; Pred. No. 3.8;
RESULT 543
ID ADE42479 standard; protein; 915 AA.
DE Human PRO polypeptide #147.
PN US2003199032-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 5.6%; Score 95.5; DB 7; Length 915;
Best Local Similarity 18.0%; Pred. No. 3.8;
RESULT 544
ID ADD80495 standard; protein; 915 AA.
DE Human PRO polypeptide #147.
PN US2003207418-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 5.6%; Score 95.5; DB 7; Length 915;
Best Local Similarity 18.0%; Pred. No. 3.8;
RESULT 545
ID ADD89523 standard; protein; 915 AA.
DE Human PRO polypeptide #147.
PN US2003199028-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 5.6%; Score 95.5; DB 7; Length 915;
Best Local Similarity 18.0%; Pred. No. 3.8;
RESULT 546
ID ADE40807 standard; protein; 915 AA.
DE Human PRO polypeptide #147.
PN US2003199031-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 5.6%; Score 95.5; DB 7; Length 915;
Best Local Similarity 18.0%; Pred. No. 3.8;
RESULT 547
ID ADE04606 standard; protein; 915 AA.
DE Human PRO polypeptide #147.
PN US2003199034-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 5.6%; Score 95.5; DB 7; Length 915;
Best Local Similarity 18.0%; Pred. No. 3.8;
RESULT 548
ID ADE92735 standard; protein; 915 AA.
DE Human PRO polypeptide #147.
PN US2003194777-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 5.6%; Score 95.5; DB 7; Length 915;
Best Local Similarity 18.0%; Pred. No. 3.8;
RESULT 549
ID ADE21444 standard; protein; 915 AA.
DE Novel human secreted and transmembrane protein PRO219.
PN US2003207355-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 5.6%; Score 95.5; DB 7; Length 915;
Best Local Similarity 18.0%; Pred. No. 3.8;
RESULT 550
ID ADE33085 standard; protein; 915 AA.
DE Novel human secreted and transmembrane protein PRO219.
PN US2003207384-A1.

PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 5.6%; Score 95.5; DB 7; Length 915;
Best Local Similarity 18.0%; Pred. No. 3.8;
RESULT 551
ID ADP97420 standard; protein; 915 AA.
DE Human PRO polypeptide #147.
PN US2003207370-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 5.6%; Score 95.5; DB 7; Length 915;
Best Local Similarity 18.0%; Pred. No. 3.8;
RESULT 552
ID ADG80484 standard; protein; 915 AA.
DE Human PRO polypeptide #147.
PN US2003207373-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 5.6%; Score 95.5; DB 7; Length 915;
Best Local Similarity 18.0%; Pred. No. 3.8;
RESULT 553
ID ADG79932 standard; protein; 915 AA.
DE Human PRO polypeptide #147.
PN US2003207372-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 5.6%; Score 95.5; DB 7; Length 915;
Best Local Similarity 18.0%; Pred. No. 3.8;
RESULT 554
ID ADH59150 standard; protein; 915 AA.
DE Human secreted/transmembrane protein, #8.
PN US2003039972-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 5.6%; Score 95.5; DB 7; Length 915;
Best Local Similarity 18.0%; Pred. No. 3.8;
RESULT 555
ID ADH55224 standard; protein; 915 AA.
DE Novel human secreted and transmembrane protein PRO219.
PN US2003207381-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 5.6%; Score 95.5; DB 7; Length 915;
Best Local Similarity 18.0%; Pred. No. 3.8;
RESULT 556
ID ADH55776 standard; protein; 915 AA.
DE Novel human secreted and transmembrane protein PRO219.
PN US2003207379-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 5.6%; Score 95.5; DB 7; Length 915;
Best Local Similarity 18.0%; Pred. No. 3.8;
RESULT 557
ID ADI37929 standard; protein; 915 AA.
DE Human secreted/transmembrane protein, #8.
PN US2003054352-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 5.6%; Score 95.5; DB 7; Length 915;
Best Local Similarity 18.0%; Pred. No. 3.8;
RESULT 558
ID ADI63995 standard; protein; 915 AA.
DE Novel human secreted and transmembrane protein PRO219.
PN US2003207385-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 5.6%; Score 95.5; DB 7; Length 915;
Best Local Similarity 18.0%; Pred. No. 3.8;
RESULT 559
ID ADI64944 standard; protein; 915 AA.
DE Novel human secreted and transmembrane protein PRO219.
PN US2003207386-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 5.6%; Score 95.5; DB 7; Length 915;
Best Local Similarity 18.0%; Pred. No. 3.8;
RESULT 560
ID ADI63443 standard; protein; 915 AA.
DE Novel human secreted and transmembrane protein PRO219.
PN US2003207387-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 5.6%; Score 95.5; DB 7; Length 915;
Best Local Similarity 18.0%; Pred. No. 3.8;
RESULT 561
ID ADH1857 standard; protein; 915 AA.
DE Novel human secreted and transmembrane protein PRO219.
PN US2003207386-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 5.6%; Score 95.5; DB 7; Length 915;
Best Local Similarity 18.0%; Pred. No. 3.8;
RESULT 562
ID ADH81305 standard; protein; 915 AA.
DE Novel human secreted and transmembrane protein PRO219.
PN US2003207377-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 5.6%; Score 95.5; DB 7; Length 915;
Best Local Similarity 18.0%; Pred. No. 3.8;
RESULT 563
ID ADJ26197 standard; protein; 915 AA.
DE Human secreted/transmembrane protein, #8.
PN US2003054349-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 5.6%; Score 95.5; DB 7; Length 915;
Best Local Similarity 18.0%; Pred. No. 3.8;
RESULT 564
ID ADM82474 standard; protein; 915 AA.
DE Novel human secreted and transmembrane protein PRO219.
PN US2003087355-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 5.6%; Score 95.5; DB 7; Length 915;
Best Local Similarity 18.0%; Pred. No. 3.8;
RESULT 565
ID ADN15673 standard; protein; 915 AA.
DE Novel human secreted and transmembrane protein PRO219.
PN US2003087353-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 5.6%; Score 95.5; DB 7; Length 915;
Best Local Similarity 18.0%; Pred. No. 3.8;
RESULT 566
ID ADN16502 standard; protein; 915 AA.
DE Novel human secreted and transmembrane protein PRO219.
PN US2003087385-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 5.6%; Score 95.5; DB 7; Length 915;
Best Local Similarity 18.0%; Pred. No. 3.8;
RESULT 567
ID ADN15321 standard; protein; 915 AA.
DE Novel human secreted and transmembrane protein PRO219.
PN US2003087356-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 5.6%; Score 95.5; DB 7; Length 915;
Best Local Similarity 18.0%; Pred. No. 3.8;
RESULT 568
ID ADN14769 standard; protein; 915 AA.
DE Novel human secreted and transmembrane protein PRO219.
PN US2003087357-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.

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Query Match                    5.6%; Score 95.5; DB 7; Length 915;
Best Local Similarity 18.0%; Pred. No. 3.8;
RESULT 569
ID ADE81031 standard; protein; 915 AA.
DE Novel human secreted and transmembrane protein PRO219.
PN US2003092115-A1.
PD 15-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match                    5.6%; Score 95.5; DB 8; Length 915;
Best Local Similarity 18.0%; Pred. No. 3.8;
RESULT 570
ID ADE79112 standard; protein; 915 AA.
DE Human secreted/transmembrane protein, #8.
PN US2003135025-A1.
PD 17-JUL-2003.
PA (GETH ) GENENTECH INC.
Query Match                    5.6%; Score 95.5; DB 8; Length 915;
Best Local Similarity 18.0%; Pred. No. 3.8;
RESULT 571
ID ADD76479 standard; protein; 915 AA.
DE Human PRO polypeptide #147.
PN US2003100087-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match                    5.6%; Score 95.5; DB 8; Length 915;
Best Local Similarity 18.0%; Pred. No. 3.8;
RESULT 572
ID ADD87843 standard; protein; 915 AA.
DE Human PRO polypeptide #147.
PN US2003092113-A1.
PD 15-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match                    5.6%; Score 95.5; DB 8; Length 915;
Best Local Similarity 18.0%; Pred. No. 3.8;
RESULT 573
ID ADD86247 standard; protein; 915 AA.
DE Human PRO polypeptide #147.
PN US2003203440-A1.
PD 30-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match                    5.6%; Score 95.5; DB 8; Length 915;
Best Local Similarity 18.0%; Pred. No. 3.8;
RESULT 574
ID ADE79536 standard; protein; 915 AA.
DE Human secreted/transmembrane protein, #8.
PN US2003130489-A1.
PD 10-JUL-2003.
PA (GETH ) GENENTECH INC.
Query Match                    5.6%; Score 95.5; DB 8; Length 915;
Best Local Similarity 18.0%; Pred. No. 3.8;
RESULT 575
ID ADE75695 standard; protein; 915 AA.
DE Human PRO polypeptide #147.
PN US2003211571-A1.
PD 13-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match                    5.6%; Score 95.5; DB 8; Length 915;
Best Local Similarity 18.0%; Pred. No. 3.8;
RESULT 576
ID ADE73212 standard; protein; 915 AA.
DE Human secreted/transmembrane protein, #8.
PN US2003129592-A1.
PD 10-JUL-2003.
PA (GETH ) GENENTECH INC.
Query Match                    5.6%; Score 95.5; DB 8; Length 915;
Best Local Similarity 18.0%; Pred. No. 3.8;
RESULT 577
ID ADE23271 standard; protein; 915 AA.
DE Human PRO polypeptide #147.
PN US2003092108-A1.
PD 15-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match                    5.6%; Score 95.5; DB 8; Length 915;
Best Local Similarity 18.0%; Pred. No. 3.8;
RESULT 580
ID ADE89157 standard; protein; 915 AA.
DE Human PRO polypeptide #147.
PN US200319062-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match                    5.6%; Score 95.5; DB 8; Length 915;
Best Local Similarity 18.0%; Pred. No. 3.8;
RESULT 581
ID ADE89157 standard; protein; 915 AA.
DE Human PRO polypeptide #147.
PN US200319062-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match                    5.6%; Score 95.5; DB 8; Length 915;
Best Local Similarity 18.0%; Pred. No. 3.8;
RESULT 582
ID ADE73747 standard; protein; 915 AA.
DE Human secreted/transmembrane protein, #8.
PN US2003148370-A1.
PD 07-AUG-2003.
PA (GETH ) GENENTECH INC.
Query Match                    5.6%; Score 95.5; DB 8; Length 915;
Best Local Similarity 18.0%; Pred. No. 3.8;
RESULT 583
ID ADE818296 standard; protein; 915 AA.
DE Human PRO polypeptide #147.
PN US2003194794-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match                    5.6%; Score 95.5; DB 8; Length 915;
Best Local Similarity 18.0%; Pred. No. 3.8;
RESULT 584
ID ADE88605 standard; protein; 915 AA.
DE Human PRO polypeptide #147.
PN US200319054-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match                    5.6%; Score 95.5; DB 8; Length 915;
Best Local Similarity 18.0%; Pred. No. 3.8;
RESULT 585
ID ADE89301 standard; protein; 915 AA.
DE Human secreted/transmembrane protein, #8.
PN US2003211576-A1.
PD 13-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match                    5.6%; Score 95.5; DB 8; Length 915;
Best Local Similarity 18.0%; Pred. No. 3.8;
RESULT 586
ID ADE94625 standard; protein; 915 AA.
DE Human PRO polypeptide #147.
PN US200319027-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match                    5.6%; Score 95.5; DB 8; Length 915;
Best Local Similarity 18.0%; Pred. No. 3.8;
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RESULT 587
ID ADE91036 standard; protein; 915 AA.
DE Human PRO polypeptide #147.
PN US2003199061-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 5.6%; Score 95.5; DB 8; Length 915;
Best Local Similarity 18.0%; Pred. No. 3.8;
RESULT 588
ID ADE95177 standard; protein; 915 AA.
DE Human PRO polypeptide #147.
PN US2003199052-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 5.6%; Score 95.5; DB 8; Length 915;
Best Local Similarity 18.0%; Pred. No. 3.8;
RESULT 589
ID ADE93287 standard; protein; 915 AA.
DE Human PRO polypeptide #147.
PN US2003199060-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 5.6%; Score 95.5; DB 8; Length 915;
Best Local Similarity 18.0%; Pred. No. 3.8;
RESULT 590
ID ADE94868 standard; protein; 915 AA.
DE Human PRO polypeptide #147.
PN US2003199029-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 5.6%; Score 95.5; DB 8; Length 915;
Best Local Similarity 18.0%; Pred. No. 3.8;
RESULT 591
ID ADE98420 standard; protein; 915 AA.
DE Human secreted/transmembrane protein, #8.
PN US2003211569-A1.
PD 13-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 5.6%; Score 95.5; DB 8; Length 915;
Best Local Similarity 18.0%; Pred. No. 3.8;
RESULT 592
ID ADE92183 standard; protein; 915 AA.
DE Novel human secreted and transmembrane protein PRO219.
PN US2003199051-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 5.6%; Score 95.5; DB 8; Length 915;
Best Local Similarity 18.0%; Pred. No. 3.8;
RESULT 593
ID ADE90484 standard; protein; 915 AA.
DE Human PRO polypeptide #147.
PN US2003199063-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 5.6%; Score 95.5; DB 8; Length 915;
Best Local Similarity 18.0%; Pred. No. 3.8;
RESULT 594
ID ADE91631 standard; protein; 915 AA.
DE Novel human secreted and transmembrane protein PRO219.
PN US2003199058-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 5.6%; Score 95.5; DB 8; Length 915;
Best Local Similarity 18.0%; Pred. No. 3.8;
RESULT 595
ID ADE9847 standard; protein; 915 AA.
DE Human secreted/transmembrane protein, #8.
PN US2003211568-A1.
PD 13-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 5.6%; Score 95.5; DB 8; Length 915;
Best Local Similarity 18.0%; Pred. No. 3.8;
RESULT 596

ID ADG40317 standard; protein; 915 AA.
DE Human secreted/transmembrane protein, #8.
PN US200325253-A1.
PD 04-DEC-2003.
PA (DESN/) DESNOYERS L.
PA (GODD/) GODDARD A.
PA (GODO/) GODOWSKI P J.
PA (GURN/) GURNEY A L.
PA (MATH/) MATHER J P.
PA (WILL/) WILLIAMS P M.
PA (WOOD/) WOOD W I.
Query Match 5.6%; Score 95.5; DB 8; Length 915;
Best Local Similarity 18.0%; Pred. No. 3.8;
RESULT 597
ID ADE97371 standard; protein; 915 AA.
DE Human secreted/transmembrane protein, #8.
PN US2003180312-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 5.6%; Score 95.5; DB 8; Length 915;
Best Local Similarity 18.0%; Pred. No. 3.8;
RESULT 598
ID ADG02210 standard; protein; 915 AA.
DE Human PRO polypeptide #147.
PN US2003207352-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 5.6%; Score 95.5; DB 8; Length 915;
Best Local Similarity 18.0%; Pred. No. 3.8;
RESULT 599
ID ADG21996 standard; protein; 915 AA.
DE Novel human secreted and transmembrane protein PRO219.
PN US2003207360-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 5.6%; Score 95.5; DB 8; Length 915;
Best Local Similarity 18.0%; Pred. No. 3.8;
RESULT 600
ID ADG20066 standard; protein; 915 AA.
DE Human PRO polypeptide #147.
PN US2003207376-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 5.6%; Score 95.5; DB 8; Length 915;
Best Local Similarity 18.0%; Pred. No. 3.8;
RESULT 601
ID ADE97972 standard; protein; 915 AA.
DE Human PRO polypeptide #147.
PN US2003207422-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 5.6%; Score 95.5; DB 8; Length 915;
Best Local Similarity 18.0%; Pred. No. 3.8;
RESULT 602
ID ADG24189 standard; protein; 915 AA.
DE Novel human secreted and transmembrane protein PRO219.
PN US2003207426-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 5.6%; Score 95.5; DB 8; Length 915;
Best Local Similarity 18.0%; Pred. No. 3.8;
RESULT 603
ID ADE98543 standard; protein; 915 AA.
DE Human PRO polypeptide #147.
PN US2003208055-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 5.6%; Score 95.5; DB 8; Length 915;
Best Local Similarity 18.0%; Pred. No. 3.8;
RESULT 604
ID ADG03374 standard; protein; 915 AA.
DE Human PRO polypeptide #147.
PN US2003207351-A1.

PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 5.6%; Score 95.5; DB 8; Length 915;
Best Local Similarity 18.0%; Pred. No. 3.8;
RESULT 605
ID ADF9095 standard; protein; 915 AA.
DE Human PRO polypeptide #147.
PN US2003207353-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 5.6%; Score 95.5; DB 8; Length 915;
Best Local Similarity 18.0%; Pred. No. 3.8;
RESULT 606
ID ADG16680 standard; protein; 915 AA.
DE Human PRO polypeptide #147.
PN US2003207359-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 5.6%; Score 95.5; DB 8; Length 915;
Best Local Similarity 18.0%; Pred. No. 3.8;
RESULT 607
ID ADG05139 standard; protein; 915 AA.
DE Human PRO polypeptide #147.
PN US2003207375-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 5.6%; Score 95.5; DB 8; Length 915;
Best Local Similarity 18.0%; Pred. No. 3.8;
RESULT 608
ID ADG19406 standard; protein; 915 AA.
DE Human PRO polypeptide #147.
PN US2003207425-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 5.6%; Score 95.5; DB 8; Length 915;
Best Local Similarity 18.0%; Pred. No. 3.8;
RESULT 609
ID ADF73287 standard; protein; 915 AA.
DE Human secreted/ transmembrane protein, #8.
PN US2003166051-A1.
PD 04-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 5.6%; Score 95.5; DB 8; Length 915;
Best Local Similarity 18.0%; Pred. No. 3.8;
RESULT 610
ID ADG13243 standard; protein; 915 AA.
DE Human PRO polypeptide #147.
PN US2003207357-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 5.6%; Score 95.5; DB 8; Length 915;
Best Local Similarity 18.0%; Pred. No. 3.8;
RESULT 611
ID ADG08300 standard; protein; 915 AA.
DE Novel human secreted and transmembrane protein PRO219.
PN US2003207424-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 5.6%; Score 95.5; DB 8; Length 915;
Best Local Similarity 18.0%; Pred. No. 3.8;
RESULT 612
ID ADG15470 standard; protein; 915 AA.
DE Human PRO polypeptide #147.
PN US200319885-A1.
PD 27-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 5.6%; Score 95.5; DB 8; Length 915;
Best Local Similarity 18.0%; Pred. No. 3.8;
RESULT 613
ID ADF96868 standard; protein; 915 AA.
DE Human PRO polypeptide #147.
PN US2003207371-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.

PA (GETH) GENENTECH INC.
Query Match 5.6%; Score 95.5; DB 8; Length 915;
Best Local Similarity 18.0%; Pred. No. 3.8;
RESULT 614
ID ADG06053 standard; protein; 915 AA.
DE Human PRO polypeptide #147.
PN US2003207374-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 5.6%; Score 95.5; DB 8; Length 915;
Best Local Similarity 18.0%; Pred. No. 3.8;
RESULT 615
ID ADG3637 standard; protein; 915 AA.
DE Novel human secreted and transmembrane protein PRO219.
PN US2003207389-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 5.6%; Score 95.5; DB 8; Length 915;
Best Local Similarity 18.0%; Pred. No. 3.8;
RESULT 616
ID ADG03926 standard; protein; 915 AA.
DE Human PRO polypeptide #147.
PN US2003207423-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 5.6%; Score 95.5; DB 8; Length 915;
Best Local Similarity 18.0%; Pred. No. 3.8;
RESULT 617
ID ADG24827 standard; protein; 915 AA.
DE Novel human secreted and transmembrane protein PRO219.
PN US2003207427-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 5.6%; Score 95.5; DB 8; Length 915;
Best Local Similarity 18.0%; Pred. No. 3.8;
RESULT 618
ID ADG07124 standard; protein; 915 AA.
DE Novel human secreted and transmembrane protein PRO219.
PN US2003207350-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 5.6%; Score 95.5; DB 8; Length 915;
Best Local Similarity 18.0%; Pred. No. 3.8;
RESULT 619
ID ADG07676 standard; protein; 915 AA.
DE Novel human secreted and transmembrane protein PRO219.
PN US2003207356-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 5.6%; Score 95.5; DB 8; Length 915;
Best Local Similarity 18.0%; Pred. No. 3.8;
RESULT 620
ID ADG55171 standard; protein; 915 AA.
DE Novel human secreted and transmembrane protein PRO219.
PN US2003194778-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 5.6%; Score 95.5; DB 8; Length 915;
Best Local Similarity 18.0%; Pred. No. 3.8;
RESULT 621
ID ADG60835 standard; protein; 915 AA.
DE Novel human secreted and transmembrane protein PRO219.
PN US2003207390-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 5.6%; Score 95.5; DB 8; Length 915;
Best Local Similarity 18.0%; Pred. No. 3.8;
RESULT 622
ID ADG61939 standard; protein; 915 AA.
DE Novel human secreted and transmembrane protein PRO219.
PN US2003207428-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.

Query Match 5.6%; Score 95.5; DB 8; Length 915;
Best Local Similarity 18.0%; Pred. No. 3.8;
RESULT 623
ID ADG92130 standard; protein; 915 AA.
DE Novel human secreted and transmembrane protein, #8.
PN US2003027145-A1.
PD 06-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 5.6%; Score 95.5; DB 8; Length 915;
Best Local Similarity 18.0%; Pred. No. 3.8;
RESULT 624
ID ADG82140 standard; protein; 915 AA.
DE Human PRO polypeptide #147.
PN US2003027358-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 5.6%; Score 95.5; DB 8; Length 915;
Best Local Similarity 18.0%; Pred. No. 3.8;
RESULT 625
ID ADG57379 standard; protein; 915 AA.
DE Novel human secreted and transmembrane protein PRO219.
PN US2003027362-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 5.6%; Score 95.5; DB 8; Length 915;
Best Local Similarity 18.0%; Pred. No. 3.8;
RESULT 626
ID ADG56827 standard; protein; 915 AA.
DE Novel human secreted and transmembrane protein PRO219.
PN US2003027364-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 5.6%; Score 95.5; DB 8; Length 915;
Best Local Similarity 18.0%; Pred. No. 3.8;
RESULT 627
ID ADG55723 standard; protein; 915 AA.
DE Novel human secreted and transmembrane protein PRO219.
PN US2003027365-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 5.6%; Score 95.5; DB 8; Length 915;
Best Local Similarity 18.0%; Pred. No. 3.8;
RESULT 628
ID ADG58483 standard; protein; 915 AA.
DE Novel human secreted and transmembrane protein PRO219.
PN US2003027368-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 5.6%; Score 95.5; DB 8; Length 915;
Best Local Similarity 18.0%; Pred. No. 3.8;
RESULT 629
ID ADG70849 standard; protein; 915 AA.
DE Novel human secreted and transmembrane protein PRO219.
PN US2003027420-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 5.6%; Score 95.5; DB 8; Length 915;
Best Local Similarity 18.0%; Pred. No. 3.8;
RESULT 630
ID ADG92557 standard; protein; 915 AA.
DE Human secreted/transmembrane protein, #8.
PN US2003027146-A1.
PD 06-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 5.6%; Score 95.5; DB 8; Length 915;
Best Local Similarity 18.0%; Pred. No. 3.8;
RESULT 631
ID ADG57931 standard; protein; 915 AA.
DE Novel human secreted and transmembrane protein PRO219.
PN US2003027363-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 5.6%; Score 95.5; DB 8; Length 915;

Best Local Similarity 18.0%; Pred. No. 3.8;
RESULT 632
ID ADG53515 standard; protein; 915 AA.
DE Novel human secreted and transmembrane protein PRO219.
PN US2003027415-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 5.6%; Score 95.5; DB 8; Length 915;
Best Local Similarity 18.0%; Pred. No. 3.8;
RESULT 633
ID ADG71401 standard; protein; 915 AA.
DE Novel human secreted and transmembrane protein PRO219.
PN US2003027421-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 5.6%; Score 95.5; DB 8; Length 915;
Best Local Similarity 18.0%; Pred. No. 3.8;
RESULT 634
ID ADG81588 standard; protein; 915 AA.
DE Human PRO polypeptide #147.
PN US2003027805-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 5.6%; Score 95.5; DB 8; Length 915;
Best Local Similarity 18.0%; Pred. No. 3.8;
RESULT 635
ID ADH30550 standard; protein; 915 AA.
DE Human PRO polypeptide #147.
PN US2003027723-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 5.6%; Score 95.5; DB 8; Length 915;
Best Local Similarity 18.0%; Pred. No. 3.8;
RESULT 636
ID ADH11917 standard; protein; 915 AA.
DE Novel human secreted and transmembrane protein PRO219.
PN US2003027419-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 5.6%; Score 95.5; DB 8; Length 915;
Best Local Similarity 18.0%; Pred. No. 3.8;
RESULT 637
ID ADG52339 standard; protein; 915 AA.
DE Novel human secreted and transmembrane protein PRO219.
PN US2003027414-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 5.6%; Score 95.5; DB 8; Length 915;
Best Local Similarity 18.0%; Pred. No. 3.8;
RESULT 638
ID ADG54067 standard; protein; 915 AA.
DE Novel human secreted and transmembrane protein PRO219.
PN US2003027416-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 5.6%; Score 95.5; DB 8; Length 915;
Best Local Similarity 18.0%; Pred. No. 3.8;
RESULT 639
ID ADG61036 standard; protein; 915 AA.
DE Human PRO polypeptide #147.
PN US2003194793-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 5.6%; Score 95.5; DB 8; Length 915;
Best Local Similarity 18.0%; Pred. No. 3.8;
RESULT 640
ID ADG56275 standard; protein; 915 AA.
DE Novel human secreted and transmembrane protein PRO219.
PN US2003027366-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 5.6%; Score 95.5; DB 8; Length 915;
Best Local Similarity 18.0%; Pred. No. 3.8;
RESULT 641

ID ADH12541 standard; protein; 915 AA.
DE Novel human secreted and transmembrane protein PRO219.
PN US2003207378-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 5.6%; Score 95.5; DB 8; Length 915;
Best Local Similarity 18.0%; Pred. No. 3.8;
RESULT 642
ID ADG61387 standard; protein; 915 AA.
DE Novel human secreted and transmembrane protein PRO219.
PN US2003207429-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 5.6%; Score 95.5; DB 8; Length 915;
Best Local Similarity 18.0%; Pred. No. 3.8;
RESULT 643
ID ADH28474 standard; protein; 915 AA.
DE Human PRO polypeptide #147.
PN US2003022331-A1.
PD 30-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 5.6%; Score 95.5; DB 8; Length 915;
Best Local Similarity 18.0%; Pred. No. 3.8;
RESULT 644
ID ADG54619 standard; protein; 915 AA.
DE Novel human secreted and transmembrane protein PRO219.
PN US2003207367-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 5.6%; Score 95.5; DB 8; Length 915;
Best Local Similarity 18.0%; Pred. No. 3.8;
RESULT 645
ID ADG59659 standard; protein; 915 AA.
DE Novel human secreted and transmembrane protein PRO219.
PN US2003207369-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 5.6%; Score 95.5; DB 8; Length 915;
Best Local Similarity 18.0%; Pred. No. 3.8;
RESULT 646
ID ADH20346 standard; protein; 915 AA.
DE Human secreted/transmembrane protein, #8.
PN US2004005553-A1.
PD 08-JAN-2004.
PA (GETH) GENENTECH INC.
Query Match 5.6%; Score 95.5; DB 8; Length 915;
Best Local Similarity 18.0%; Pred. No. 3.8;
RESULT 647
ID ADH07201 standard; protein; 915 AA.
DE Human secreted/transmembrane protein, #8.
PN US2004006211-A1.
PD 08-JAN-2004.
PA (DESN/) DESNOYERS L.
PA (GODD/) GODDARD A.
PA (GODO/) GODOWSKI P J.
PA (GURN/) GURNEY A L.
PA (MATH/) MATHER J P.
PA (WILL/) WILLIAMS P M.
PA (WOOD/) WOOD W I.
Query Match 5.6%; Score 95.5; DB 8; Length 915;
Best Local Similarity 18.0%; Pred. No. 3.8;
RESULT 648
ID ADH59746 standard; protein; 915 AA.
DE Human secreted/transmembrane protein, #8.
PN US2003215904-A1.
PD 20-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 5.6%; Score 95.5; DB 8; Length 915;
Best Local Similarity 18.0%; Pred. No. 3.8;
RESULT 649
ID ADH06774 standard; protein; 915 AA.
DE Human secreted/transmembrane protein, #8.
PN US2004005665-A1.
PD 08-JAN-2004.
PA (DESN/) DESNOYERS L.
PA (GODD/) GODDARD A.
PA (GODO/) GODOWSKI P J.
PA (GURN/) GURNEY A L.
PA (MATH/) MATHER J P.
PA (WILL/) WILLIAMS P M.
PA (WOOD/) WOOD W I.
Query Match 5.6%; Score 95.5; DB 8; Length 915;
Best Local Similarity 18.0%; Pred. No. 3.8;
RESULT 650
ID ADH1083 standard; protein; 915 AA.
DE Human PRO polypeptide #147.
PN US2003207361-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 5.6%; Score 95.5; DB 8; Length 915;
Best Local Similarity 18.0%; Pred. No. 3.8;
RESULT 651
ID ADH18516 standard; protein; 915 AA.
DE Human secreted/transmembrane protein, #8.
PN US2003152999-A1.
PD 14-AUG-2003.
PA (GETH) GENENTECH INC.
Query Match 5.6%; Score 95.5; DB 8; Length 915;
Best Local Similarity 18.0%; Pred. No. 3.8;
RESULT 652
ID ADH65236 standard; protein; 915 AA.
DE Human secreted/transmembrane protein, #8.
PN US2003148419-A1.
PD 07-AUG-2003.
PA (GETH) GENENTECH INC.
Query Match 5.6%; Score 95.5; DB 8; Length 915;
Best Local Similarity 18.0%; Pred. No. 3.8;
RESULT 653
ID ADH17499 standard; protein; 915 AA.
DE Human secreted/transmembrane protein, #8.
PN US2003096340-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 5.6%; Score 95.5; DB 8; Length 915;
Best Local Similarity 18.0%; Pred. No. 3.8;
RESULT 654
ID ADG09826 standard; protein; 915 AA.
DE Novel human secreted and transmembrane protein PRO219.
PN US2004009548-A1.
PD 15-JAN-2004.
PA (GETH) GENENTECH INC.
Query Match 5.6%; Score 95.5; DB 8; Length 915;
Best Local Similarity 18.0%; Pred. No. 3.8;
RESULT 655
ID ADH97303 standard; protein; 915 AA.
DE Human secreted/transmembrane protein, #8.
PN US2003190610-A1.
PD 09-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 5.6%; Score 95.5; DB 8; Length 915;
Best Local Similarity 18.0%; Pred. No. 3.8;
RESULT 656
ID ADH15297 standard; protein; 915 AA.
DE Novel human secreted and transmembrane protein PRO219.
PN US2003207382-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 5.6%; Score 95.5; DB 8; Length 915;
Best Local Similarity 18.0%; Pred. No. 3.8;
RESULT 657
ID ADG09174 standard; protein; 915 AA.
DE Novel human secreted and transmembrane protein PRO219.
PN US2004009547-A1.
PD 15-JAN-2004.
PA (GETH) GENENTECH INC.
Query Match 5.6%; Score 95.5; DB 8; Length 915;

Best Local Similarity 18.0%; Pred. No. 3.8;
RESULT 658
ID ADI65663 standard; protein; 915 AA.
DE Human secreted/transmembrane protein, #8.
PN US2003148371-A1.
PD 07-AUG-2003.
PA (GETH) GENENTECH INC.
Query Match 5.6%; Score 95.5; DB 8; Length 915;
Best Local Similarity 18.0%; Pred. No. 3.8;
RESULT 659
ID ADI14629 standard; protein; 915 AA.
DE Novel human secreted and transmembrane protein PRO219.
PN US2003207383-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 5.6%; Score 95.5; DB 8; Length 915;
Best Local Similarity 18.0%; Pred. No. 3.8;
RESULT 660
ID ADH60406 standard; protein; 915 AA.
DE Human secreted/transmembrane protein, #8.
PN US2004023331-A1.
PD 05-FEB-2004.
PA (DESN) DESNOYERS L.
PA (GODO) GODDARD A.
PA (GURN) GURNEY A L.
PA (MATH) MATHER J P.
PA (WILL) WILLIAMS P M.
PA (WOOD) WOOD W I.
Query Match 5.6%; Score 95.5; DB 8; Length 915;
Best Local Similarity 18.0%; Pred. No. 3.8;
RESULT 661
ID ADI18224 standard; protein; 915 AA.
DE Novel human secreted and transmembrane protein PRO219.
PN US2003207349-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 5.6%; Score 95.5; DB 8; Length 915;
Best Local Similarity 18.0%; Pred. No. 3.8;
RESULT 662
ID ADJ99463 standard; protein; 915 AA.
DE Human secreted/transmembrane protein, #8.
PN US2003187238-A1.
PD 02-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 5.6%; Score 95.5; DB 8; Length 915;
Best Local Similarity 18.0%; Pred. No. 3.8;
RESULT 663
ID ADL08656 standard; protein; 915 AA.
DE Human secreted/transmembrane protein, #8.
PN US2003186358-A1.
PD 02-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 5.6%; Score 95.5; DB 8; Length 915;
Best Local Similarity 18.0%; Pred. No. 3.8;
RESULT 664
ID ADM25001 standard; protein; 915 AA.
DE Human secreted/transmembrane protein, #8.
PN US2003096233-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 5.6%; Score 95.5; DB 8; Length 915;
Best Local Similarity 18.0%; Pred. No. 3.8;
RESULT 665
ID ADU63505 standard; protein; 915 AA.
DE Novel human secreted and transmembrane protein PRO219.
PN US2004039164-A1.
PD 26-FEB-2004.
PA (GETH) GENENTECH INC.
Query Match 5.6%; Score 95.5; DB 8; Length 915;
Best Local Similarity 18.0%; Pred. No. 3.8;
RESULT 666
ID ADM29747 standard; protein; 915 AA.
DE Human secreted/transmembrane protein, #8.
PN US2003190611-A1.
PD 09-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 5.6%; Score 95.5; DB 8; Length 915;
Best Local Similarity 18.0%; Pred. No. 3.8;
RESULT 667
ID ADJ7400 standard; protein; 915 AA.
DE Human PRO polypeptide #147.
PN US2004038336-A1.
PD 26-FEB-2004.
PA (GETH) GENENTECH INC.
Query Match 5.6%; Score 95.5; DB 8; Length 915;
Best Local Similarity 18.0%; Pred. No. 3.8;
RESULT 668
ID ADU5522 standard; protein; 915 AA.
DE Human PRO polypeptide #147.
PN US2004038335-A1.
PD 26-FEB-2004.
PA (GETH) GENENTECH INC.
Query Match 5.6%; Score 95.5; DB 8; Length 915;
Best Local Similarity 18.0%; Pred. No. 3.8;
RESULT 669
ID ADM27658 standard; protein; 915 AA.
DE Human PRO polypeptide #147.
PN US2004048333-A1.
PD 11-MAR-2004.
PA (GETH) GENENTECH INC.
Query Match 5.6%; Score 95.5; DB 8; Length 915;
Best Local Similarity 18.0%; Pred. No. 3.8;
RESULT 670
ID ADM42382 standard; protein; 915 AA.
DE Human PRO polypeptide #147.
PN US2004058424-A1.
PD 25-MAR-2004.
PA (GETH) GENENTECH INC.
Query Match 5.6%; Score 95.5; DB 8; Length 915;
Best Local Similarity 18.0%; Pred. No. 3.8;
RESULT 671
ID ADO06069 standard; protein; 915 AA.
DE Human PRO polypeptide #7.
PN US6686451-B1.
PD 03-FEB-2004.
PA (GETH) GENENTECH INC.
Query Match 5.6%; Score 95.5; DB 8; Length 915;
Best Local Similarity 18.0%; Pred. No. 3.8;
RESULT 672
ID ADM28244 standard; protein; 915 AA.
DE Human PRO polypeptide #147.
PN US2004077064-A1.
PD 22-APR-2004.
PA (GETH) GENENTECH INC.
Query Match 5.6%; Score 95.5; DB 8; Length 915;
Best Local Similarity 18.0%; Pred. No. 3.8;
RESULT 673
ID ADRI0921 standard; protein; 915 AA.
DE Human secreted/transmembrane protein, #8.
PN US2004137561-A1.
PD 15-JUL-2004.
PA (GETH) GENENTECH INC.
Query Match 5.6%; Score 95.5; DB 8; Length 915;
Best Local Similarity 18.0%; Pred. No. 3.8;
RESULT 674
ID ADRI7830 standard; protein; 915 AA.
DE Human secreted/transmembrane protein, #8.
PN US2004147017-A1.
PD 29-JUL-2004.
PA (ASHK) ASHKENAZI A.
PA (BOTS) BOTSTEIN D.
PA (DESN) DESNOYERS L.
PA (EATO) EATON D L.
PA (FERR) FERRARA N.
PA (FILV) FILVAROFF E.

PA (FONG/) FONG S.
PA (GAOW/) GAO W.
PA (GERB/) GERBER H.
PA (GERR/) GERRITSEN M E.
PA (GODD/) GODDARD A.
PA (GODO/) GODOWSKI P J.
PA (GRIM/) GRIMALDI C J.
PA (GURN/) GURNEY A L.
PA (HILL/) HILLAN K J.
PA (KLJA/) KLJAVIN I J.
PA (MATH/) MATHER J P.
PA (PANU/) PAN J.
PA (PAON/) PAONI N F.
PA (ROYM/) ROY M A.
PA (STEM/) STEWART T A.
PA (TUMA/) TUMAS D.
PA (WILL/) WILLIAMS P M.
PA (WOOD/) WOOD W I.
Query Match
Best Local Similarity 5.6%; Score 95.5; DB 8; Length 915;
Pred. No. 3.8;
RESULT 675
ID ADI95726 standard; protein; 915 AA.
DE Human PRO polypeptide #147.
PN US200307659-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 5.6%; Score 95.5; DB 8; Length 915;
Pred. No. 3.8;
RESULT 676
ID ADI96278 standard; protein; 915 AA.
DE Novel human secreted and transmembrane protein PRO219.
PN US200307354-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 5.6%; Score 95.5; DB 8; Length 915;
Pred. No. 3.8;
RESULT 677
ID ADT03506 standard; protein; 915 AA.
DE Human secreted/transmembrane protein, #8.
PN US200315282-A1.
PD 14-AUG-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 5.6%; Score 95.5; DB 8; Length 915;
Pred. No. 3.8;
RESULT 678
ID ADS74469 standard; protein; 915 AA.
DE Human secreted/transmembrane protein #8.
PN US2004185531-A1.
PD 23-SEP-2004.
PA (ASHK/) ASHKENAZI A.
PA (BOTS/) BOTSTEIN D.
PA (DESN/) DESNOYERS L.
PA (EATO/) EATON D L.
PA (FERR/) FERRARA N.
PA (FILV/) FILVAROFF E.
PA (FONG/) FONG S.
PA (GAOW/) GAO W.
PA (GERB/) GERBER H.
PA (GERR/) GERRITSEN M E.
PA (GODD/) GODDARD A.
PA (GODO/) GODOWSKI P J.
PA (GRIM/) GRIMALDI C J.
PA (GURN/) GURNEY A L.
PA (HILL/) HILLAN K J.
PA (KLJA/) KLJAVIN I J.
PA (MATH/) MATHER J P.
PA (PANU/) PAN J.
PA (PAON/) PAONI N F.
PA (ROYM/) ROY M A.
PA (STEM/) STEWART T A.
PA (TUMA/) TUMAS D.
PA (WILL/) WILLIAMS P M.
PA (WOOD/) WOOD W I.

Query Match
Best Local Similarity 5.6%; Score 95.5; DB 8; Length 915;
Pred. No. 3.8;
RESULT 679
ID AAR03843 standard; protein; 934 AA.
DE Human gene 3 encoded secreted protein HOGDPA6, SEQ ID NO: 89.
PN WO200136440-A1.
PD 25-MAY-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match
Best Local Similarity 5.6%; Score 95.5; DB 4; Length 934;
Pred. No. 3.9;
RESULT 680
ID ABG64542 standard; protein; 934 AA.
DE Human albumin fusion protein #1217.
PN WO200177137-A1.
PD 18-OCT-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match
Best Local Similarity 5.6%; Score 95.5; DB 5; Length 934;
Pred. No. 3.9;
RESULT 681
ID ADL77809 standard; protein; 934 AA.
DE Albumin fusion protein related therapeutic protein X, SEQ ID No 1291.
PN US2004010134-A1.
PD 15-JAN-2004.
PA (ROSE/) ROSEN C A.
PA (HASE/) HASELTINE W A.
Query Match
Best Local Similarity 5.6%; Score 95.5; DB 8; Length 934;
Pred. No. 3.9;
RESULT 682
ID ADH17484 standard; protein; 939 AA.
DE Human NOV13d protein - SEQ ID 174.
PN WO2003093432-A2.
PD 13-NOV-2003.
PA (CURA-) CURAGEN CORP.
Query Match
Best Local Similarity 5.6%; Score 95.5; DB 8; Length 939;
Pred. No. 3.9;
RESULT 683
ID ADH17462 standard; protein; 964 AA.
DE Human NOV13d protein - SEQ ID 152.
PN WO2003093432-A2.
PD 13-NOV-2003.
PA (CURA-) CURAGEN CORP.
Query Match
Best Local Similarity 5.6%; Score 95.5; DB 8; Length 964;
Pred. No. 4.1;
RESULT 684
ID ADH17460 standard; protein; 964 AA.
DE Human NOV13c protein - SEQ ID 150.
PN WO2003093432-A2.
PD 13-NOV-2003.
PA (CURA-) CURAGEN CORP.
Query Match
Best Local Similarity 5.6%; Score 95.5; DB 8; Length 964;
Pred. No. 4.1;
RESULT 685
ID AAE03877 standard; protein; 983 AA.
DE Human gene 3 encoded secreted protein fragment, SEQ ID NO:127.
PN WO200136440-A1.
PD 25-MAY-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match
Best Local Similarity 5.6%; Score 95.5; DB 4; Length 983;
Pred. No. 4.2;
RESULT 686
ID AAY37126 standard; protein; 388 AA.
DE Protein involved in intermediate metabolism of sugars and/or cofactors.
PN WO9928475-A2.
PD 10-JUN-1999.
PA (GEST) GENSET.
Query Match
Best Local Similarity 5.6%; Score 94.5; DB 2; Length 388;
Pred. No. 1.4;
RESULT 687
ID ADJ70087 standard; protein; 956 AA.
DE Human heat mitochondrial protein as a therapeutic target SeqID1893.
PN WO2003087768-A2.
PD 23-OCT-2003.
PA (MITO-) MITOKOR.

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PA (BUCK-) BUCK INST AGE RES.
Query Match 5.5%; Score 93.5; DB 7; Length 956;
Best Local Similarity 18.0%; Pred. No. 6.5;
RESULT 688
ID ADM12924 standard; protein; 956 AA.
DE PRO83470 protein.
PN WO2004024077-A2.
PD 25-MAR-2004.
PA (GETH-) GENENTECH INC.
Query Match 5.5%; Score 93.5; DB 8; Length 956;
Best Local Similarity 18.0%; Pred. No. 6.5;
RESULT 689
ID ADN03855 standard; protein; 956 AA.
DE Antipsoriatic protein sequence #123.
PN WO2004028479-A2.
PD 08-APR-2004.
PA (GETH-) GENENTECH INC.
Query Match 5.5%; Score 93.5; DB 8; Length 956;
Best Local Similarity 18.0%; Pred. No. 6.5;
RESULT 690
ID AAB20159 standard; protein; 959 AA.
DE Human protein SECPS.
PN WO200105971-A2.
PD 25-JAN-2001.
PA (CURA-) CURAGEN CORP.
Query Match 5.4%; Score 92; DB 4; Length 959;
Best Local Similarity 17.9%; Pred. No. 9.4;
RESULT 691
ID ADG38840 standard; protein; 959 AA.
DE Human SECPS.
PN US2003207348-A1.
PD 06-NOV-2003.
PA (SHIM/) SHIMKETS R A.
PA (FERN/) FERNANDES E R.
PA (LILL/) LI L.
PA (GORM/) GORMAN L.
PA (GUSE/) GUSEV V Y.
PA (PADI/) PADIGARU M.
PA (PATT/) PATTURAJAN M.
PA (SHEN/) SHENOY S G.
PA (SPYT/) SPYTEK K A.
Query Match 5.4%; Score 92; DB 7; Length 959;
Best Local Similarity 17.9%; Pred. No. 9.4;
RESULT 692
ID ADH17470 standard; protein; 959 AA.
DE Human NOV13h protein - SEQ ID 160.
PN WO2003093432-A2.
PD 13-NOV-2003.
PA (CURA-) CURAGEN CORP.
Query Match 5.4%; Score 92; DB 8; Length 959;
Best Local Similarity 17.9%; Pred. No. 9.4;
RESULT 693
ID ADH17456 standard; protein; 959 AA.
DE Human NOV13a protein - SEQ ID 146.
PN WO2003093432-A2.
PD 13-NOV-2003.
PA (CURA-) CURAGEN CORP.
Query Match 5.4%; Score 92; DB 8; Length 959;
Best Local Similarity 17.9%; Pred. No. 9.4;
RESULT 694
ID ABO10549 standard; protein; 977 AA.
DE Human NOV4a protein.
PN WO200246408-A2.
PD 13-JUN-2002.
PA (CURA-) CURAGEN CORP.
Query Match 5.4%; Score 92; DB 5; Length 977;
Best Local Similarity 17.9%; Pred. No. 9.6;
RESULT 695
ID ABB94365 standard; protein; 527 AA.
DE Chlamydia trachomatis protein sequence SEQ ID NO:588.
PN WO200208267-A2.
PD 31-JAN-2002.
PA (CORI-) CORIXA CORP.

Query Match 5.2%; Score 88.5; DB 5; Length 527;
Best Local Similarity 19.5%; Pred. No. 9.2;
RESULT 696
ID AAB03820 standard; protein; 794 AA.
DE Human gene 3 encoded secreted protein HOGDP46, SEQ ID NO: 66.
PN WO200136440-A1.
PD 25-MAY-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 5.2%; Score 88.5; DB 4; Length 794;
Best Local Similarity 18.8%; Pred. No. 17;
RESULT 697
ID ABG64543 standard; protein; 794 AA.
DE Human albumin fusion protein #1218.
PN WO200177137-A1.
PD 18-OCT-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 5.2%; Score 88.5; DB 5; Length 794;
Best Local Similarity 18.8%; Pred. No. 17;
RESULT 698
ID ADL77810 standard; protein; 794 AA.
DE Albumin fusion protein related therapeutic protein X, SEQ ID NO 1292.
PN US2004010134-A1.
PD 15-JAN-2004.
PA (ROSE/) ROSEN C A.
PA (HASE/) HASELTINE W A.
Query Match 5.2%; Score 88.5; DB 8; Length 794;
Best Local Similarity 18.8%; Pred. No. 17;
RESULT 699
ID ABB62620 standard; protein; 1349 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 14652.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE-) PE CORP NY.
Query Match 5.2%; Score 88; DB 4; Length 1349;
Best Local Similarity 22.8%; Pred. No. 40;
RESULT 700
ID ADH17486 standard; protein; 782 AA.
DE Human NOV14h protein - SEQ ID 176.
PN WO2003093432-A2.
PD 13-NOV-2003.
PA (CURA-) CURAGEN CORP.
Query Match 5.2%; Score 87.5; DB 8; Length 782;
Best Local Similarity 19.0%; Pred. No. 21;
RESULT 701
ID AAB20158 standard; protein; 776 AA.
DE Human protein SECPS.
PN WO200105971-A2.
PD 25-JAN-2001.
PA (CURA-) CURAGEN CORP.
Query Match 5.1%; Score 87; DB 4; Length 776;
Best Local Similarity 18.6%; Pred. No. 23;
RESULT 702
ID ADG38838 standard; protein; 776 AA.
DE Human SECPS.
PN US2003207348-A1.
PD 06-NOV-2003.
PA (SHIM/) SHIMKETS R A.
PA (FERN/) FERNANDES E R.
PA (LILL/) LI L.
PA (GORM/) GORMAN L.
PA (GUSE/) GUSEV V Y.
PA (PADI/) PADIGARU M.
PA (PATT/) PATTURAJAN M.
PA (SHEN/) SHENOY S G.
PA (SPYT/) SPYTEK K A.
Query Match 5.1%; Score 87; DB 7; Length 776;
Best Local Similarity 18.6%; Pred. No. 23;
RESULT 703
ID ABB37049 standard; protein; 997 AA.
DE Human breast cancer / ovarian cancer related protein #25.
PN WO200300012-A2.
PD 03-JAN-2003.
PA (MILL-) MILLENNIUM PHARM INC.

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Query Match          5.1%; Score 86.5; DB 6; Length 997;
Best Local Similarity 24.6%; Pred. No. 37;
RESULT 704
ID ADS26422 standard; protein; 376 AA.
DE Bacterial polypeptide #15455.
PN US2003233675-A1.
PD 18-DEC-2003.
PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
Query Match          5.1%; Score 86; DB 8; Length 376;
Best Local Similarity 19.5%; Pred. No. 10;
RESULT 705
ID ADS27172 standard; protein; 386 AA.
DE Bacterial polypeptide #16205.
PN US2003233675-A1.
PD 18-DEC-2003.
PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
Query Match          5.1%; Score 86; DB 8; Length 386;
Best Local Similarity 19.5%; Pred. No. 11;
RESULT 706
ID ADS26790 standard; protein; 386 AA.
DE Bacterial polypeptide #15823.
PN US2003233675-A1.
PD 18-DEC-2003.
PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
Query Match          5.1%; Score 86; DB 8; Length 386;
Best Local Similarity 19.5%; Pred. No. 11;
RESULT 707
ID ABM83038 standard; protein; 848 AA.
DE Human diagnostic and therapeutic proteoin SEQ ID NO:3287.
PN WO20040233973-A2.
PD 25-MAR-2004.
PA (INCY-) INCYTE CORP.
Query Match          5.1%; Score 86; DB 8; Length 848;
Best Local Similarity 20.8%; Pred. No. 33;
RESULT 708
ID AAM42001 standard; protein; 376 AA.
DE Human polypeptide SEQ ID NO 6932.
PN WO200153312-A1.
PD 26-JUL-2001.
PA (HYSE-) HYSEQ INC.
Query Match          5.0%; Score 85.5; DB 4; Length 376;
Best Local Similarity 19.8%; Pred. No. 12;
RESULT 709
ID AAO24548 standard; protein; 397 AA.
DE Human BHD mutant truncated protein SEQ ID NO: 6.
PN WO2003102149-A2.
PD 11-DEC-2003.
PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
Query Match          5.0%; Score 85.5; DB 8; Length 397;
Best Local Similarity 19.8%; Pred. No. 12;
RESULT 710
ID ABM67558 standard; protein; 399 AA.
DE Photorhabdus luminescens protein sequence #655.
PN WO200294867-A2.
PD 28-NOV-2002.
PA (INSP) INST PASTEUR.
PA (CNRS) CNRS CENT NAT RECH SCI
Query Match          5.0%; Score 85.5; DB 6; Length 399;
Best Local Similarity 23.0%; Pred. No. 13;
RESULT 711
ID AAO24549 standard; protein; 454 AA.
Query Match          5.0%; Score 85.5; DB 8; Length 466;
Best Local Similarity 19.8%; Pred. No. 16;
RESULT 713
ID AAO24550 standard; protein; 466 AA.
DE Human BHD mutant truncated protein SEQ ID NO: 10.
PN WO2003102149-A2.
PD 11-DEC-2003.
PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
Query Match          5.0%; Score 85.5; DB 8; Length 462;
Best Local Similarity 19.8%; Pred. No. 16;
RESULT 714
ID AAO24546 standard; protein; 579 AA.
DE Human BHD protein, follitropin.
PN WO2003102149-A2.
PD 11-DEC-2003.
PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
Query Match          5.0%; Score 85.5; DB 8; Length 579;
Best Local Similarity 19.8%; Pred. No. 21;
RESULT 715
ID ABP75839 standard; protein; 594 AA.
DE Human secretory polypeptide SPTM SEQ ID NO 1023.
PN WO200283876-A2.
PD 24-OCT-2002.
PA (INCY-) INCYTE GENOMICS INC.
Query Match          5.0%; Score 85.5; DB 6; Length 594;
Best Local Similarity 19.8%; Pred. No. 22;
RESULT 716
ID ADJ68448 standard; protein; 3225 AA.
DE Human heat mitochondrial protein as a therapeutic target SegID254.
PN WO2003087768-A2.
PD 23-OCT-2003.
PA (MITO-) MITOKOR.
PA (BUCK-) BUCK INST AGE RES.
Query Match          5.0%; Score 85.5; DB 7; Length 3225;
Best Local Similarity 22.2%; Pred. No. 2.5e+02;
RESULT 717
ID ADE56037 standard; protein; 3259 AA.
DE Human Protein CAA53052, SEQ ID NO 1876.
PN WO2003016475-A2.
PD 27-FEB-2003.
PA (GERO) GEN HOSPITAL CORP.
PA (FARB) BAYER AG.
Query Match          5.0%; Score 85.5; DB 7; Length 3259;
Best Local Similarity 22.2%; Pred. No. 2.6e+02;
RESULT 718
ID ADE56033 standard; protein; 3259 AA.
DE Human Protein CAA53052, SEQ ID NO 1872.
PN WO2003016475-A2.
PD 27-FEB-2003.
PA (GERO) GEN HOSPITAL CORP.
PA (FARB) BAYER AG.
Query Match          5.0%; Score 85.5; DB 7; Length 3259;
Best Local Similarity 22.2%; Pred. No. 2.6e+02;
RESULT 719
ID ADP29881 standard; protein; 1096 AA.
DE Human secreted protein SEQ ID #648.
PN WO2004035732-A2.
PD 29-APR-2004.
PA (FIVE-) FIVE PRIME THERAPEUTICS INC.
Query Match          5.0%; Score 85; DB 8; Length 1096;
Best Local Similarity 19.7%; Pred. No. 61;
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RESULT 720
ID AAB9304 standard; protein; 890 AA.
DE Human protein sequence SEQ ID NO:17542.
PN EP1074617-A2.
PD 07-FEB-2001.
PA (HELI-) HELIX RES INST.
Query Match 5.0%; Score 84.5; DB 4; Length 890;
Best Local Similarity 18.8%; Pred. No. 51;
RESULT 721
ID ABR8250 standard; protein; 1033 AA.
DE Human nuclear acid-associated protein (NAAP)-Id 1797985CD1.
PN WO2003052048-A2.
PD 26-JUN-2003.
PA (INCY-) INCYTE GENOMICS INC.
Query Match 5.0%; Score 84.5; DB 6; Length 1033;
Best Local Similarity 18.8%; Pred. No. 63;
RESULT 722
ID ABR64202 standard; protein; 1194 AA.
DE Angiogenesis protein BMO381.
PN WO2003027285-A1.
PD 03-APR-2003.
PA (BION-) BIONOMICS LTD.
Query Match 5.0%; Score 84.5; DB 6; Length 1194;
Best Local Similarity 18.8%; Pred. No. 77;
RESULT 723
ID ADO66046 standard; protein; 1375 AA.
DE Novel human protein sequence #1019.
PN EP1440981-A2.
PD 28-JUL-2004.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
Query Match 5.0%; Score 84.5; DB 8; Length 1375;
Best Local Similarity 18.8%; Pred. No. 95;
RESULT 724
ID AAR91296 standard; protein; 1350 AA.
DE Drosophila nitric oxide synthase.
PN WO9611270-A1.
PD 18-APR-1996.
PA (COLD-) COLD SPRING HARBOR LAB.
Query Match 5.0%; Score 84; DB 2; Length 1350;
Best Local Similarity 22.6%; Pred. No. 1e+02;
RESULT 725
ID ADJ95084 standard; protein; 4313 AA.
DE Novel NOVX protein sequence #156.
PN WO2003040325-A2.
PD 15-MAY-2003.
PA (CURA-) CURAGEN CORP.
Query Match 5.0%; Score 84; DB 7; Length 4313;
Best Local Similarity 22.4%; Pred. No. 5.5e+02;
RESULT 726
ID ADA55192 standard; protein; 376 AA.
DE Human protein, SEQ ID 2760.
PN EP1293569-A2.
PD 19-MAR-2003.
PA (HELI-) HELIX RES INST.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
Query Match 4.9%; Score 83.5; DB 6; Length 376;
Best Local Similarity 22.5%; Pred. No. 19;
RESULT 727
ID ADO66652 standard; protein; 623 AA.
DE Novel human protein sequence #1625.
PN EP1440981-A2.
PD 28-JUL-2004.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
Query Match 4.9%; Score 83.5; DB 8; Length 623;
Best Local Similarity 22.5%; Pred. No. 39;
RESULT 728
ID ABR77985 standard; protein; 1318 AA.
DE Amino acid sequence of a human RAD50 homologue.
PN EP1217074-A1.
PD 26-JUN-2002.
PA (UYLE-) RIJCKSUNIV LEIDEN.
PA (BINA-) STICHTING BINAIR VECTOR SYSTEM.
Query Match 4.9%; Score 83.5; DB 5; Length 1318;

Best Local Similarity 23.1%; Pred. No. 1.1e+02;
RESULT 729
ID ADU6860 standard; protein; 1318 AA.
DE Human heat mitochondrial protein as a therapeutic target SeqID666.
PN WO2003087768-A2.
PD 23-OCT-2003.
PA (MITO-) MITOKOR.
PA (BUCK-) BUCK INST AGE RES.
Query Match 4.9%; Score 83.5; DB 7; Length 1318;
Best Local Similarity 23.1%; Pred. No. 1.1e+02;
RESULT 730
ID ADU6509 standard; protein; 1318 AA.
DE RAD50 homolog HSRAD50 for anti-cancer protein complex.
PN WO2004009622-A2.
PD 29-JAN-2004.
PA (CELL-) CELLZOME AG.
Query Match 4.9%; Score 83.5; DB 8; Length 1318;
Best Local Similarity 23.1%; Pred. No. 1.1e+02;
RESULT 731
ID ADS88326 standard; protein; 1318 AA.
DE Human protein of a TNF-alpha signalling pathway protein complex Seq 181.
PN WO2004035783-A2.
PD 29-APR-2004.
PA (CELL-) CELLZOME AG.
Query Match 4.9%; Score 83.5; DB 8; Length 1318;
Best Local Similarity 23.1%; Pred. No. 1.1e+02;
RESULT 732
ID ABR44228 standard; protein; 1664 AA.
DE Novel human diagnostic protein #14219.
PN WO2001175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match 4.9%; Score 83.5; DB 4; Length 1664;
Best Local Similarity 19.7%; Pred. No. 1.6e+02;
RESULT 733
ID AAU29705 standard; protein; 191 AA.
DE Novel human secreted protein #196.
PN WO200119449-A2.
PD 25-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match 4.9%; Score 83; DB 4; Length 191;
Best Local Similarity 29.8%; Pred. No. 7.9;
RESULT 734
ID ABR90643 standard; protein; 500 AA.
DE Chlamydia pneumoniae cp6526 protein, SEQ ID NO:225.
PN WO200202606-A2.
PD 10-JAN-2002.
PA (CHIR-) CHIRON SPA.
Query Match 4.9%; Score 83; DB 5; Length 500;
Best Local Similarity 22.3%; Pred. No. 32;
RESULT 735
ID AA34845 standard; protein; 503 AA.
DE Chlamydia pneumoniae transmembrane protein sequence.
PN WO9927105-A2.
PD 03-JUN-1999.
PA (GEST-) GENSET.
Query Match 4.9%; Score 83; DB 2; Length 503;
Best Local Similarity 22.3%; Pred. No. 32;
RESULT 736
ID ABU26912 standard; protein; 503 AA.
DE Protein encoded by Prokaryotic essential gene #12439.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 4.9%; Score 83; DB 6; Length 503;
Best Local Similarity 22.3%; Pred. No. 32;
RESULT 737
ID AAWS0897 standard; protein; 1607 AA.
DE Mouse laminin G1 chain.
PN WO9815179-A1.
PD 16-APR-1998.
PA (UNITW) UNITV WASHINGTON.
Query Match 4.9%; Score 83; DB 2; Length 1607;

Best Local Similarity 22.8%; Pred. No. 1.7e+02;
 RESULT 738
 ID ABB26371 standard; protein; 415 AA.
 DE Novel human diagnostic protein #26362.
 PN WO200175067-A2.
 PD 11-OCT-2001.
 PA (HYSE-) HYSEQ INC.
 Query Match 4.9%; Score 82.5; DB 4; Length 415;
 Best Local Similarity 19.3%; Pred. No. 27;
 RESULT 739
 ID AAO24552 standard; protein; 579 AA.
 DE Murine BHD protein.
 PN WO2003102149-A2.
 PD 11-DEC-2003.
 PA (USSH-) US DEPT HEALTH & HUMAN SERVICES.
 Query Match 4.9%; Score 82.5; DB 8; Length 579;
 Best Local Similarity 19.4%; Pred. No. 44;
 RESULT 740
 ID ADC96058 standard; protein; 698 AA.
 DE E. faecium protein sequence SEQ ID 5685.
 PN US6583275-B1.
 PD 24-JUN-2003.
 PA (GENO-) GENOME THERAPEUTICS CORP.
 Query Match 4.9%; Score 82.5; DB 7; Length 698;
 Best Local Similarity 20.2%; Pred. No. 58;
 RESULT 741
 ID ABB96081 standard; protein; 769 AA.
 DE Human protein kinase SEQ ID NO:68.
 PN WO2003000501-A2.
 PD 03-JAN-2003.
 PA (DECO-) DECODE GENETICS BHF.
 Query Match 4.9%; Score 82.5; DB 6; Length 769;
 Best Local Similarity 19.9%; Pred. No. 66;
 RESULT 742
 ID ABB57101 standard; protein; 859 AA.
 DE Mouse ischaemic condition related protein sequence SEQ ID NO:228.
 PN WO200188188-A2.
 PD 22-NOV-2001.
 PA (UTNT-) UNIV NIHON SCHOOL JURIDICAL PERSON.
 Query Match 4.9%; Score 82.5; DB 5; Length 859;
 Best Local Similarity 20.2%; Pred. No. 78;
 RESULT 743
 ID ADE54207 standard; protein; 859 AA.
 DE Rat Protein NP 038587, SEQ ID NO 10.
 PN WO2003016475-A2.
 PD 27-FEB-2003.
 PA (GEHO-) GEN HOSPITAL CORP.
 Query Match 4.9%; Score 82.5; DB 7; Length 859;
 Best Local Similarity 20.2%; Pred. No. 78;
 RESULT 744
 ID ADE54203 standard; protein; 859 AA.
 DE Rat Protein NP 038587, SEQ ID NO 6.
 PN WO2003016475-A2.
 PD 27-FEB-2003.
 PA (GEHO-) GEN HOSPITAL CORP.
 Query Match 4.9%; Score 82.5; DB 7; Length 859;
 Best Local Similarity 20.2%; Pred. No. 78;
 RESULT 745
 ID AAP91380 standard; peptide; 119 AA.
 DE Porcine prepro-motilin.
 PN WO9907611-A.
 PD 24-AUG-1999.
 PA (UTOR-) OREGON UNIVERSITY.
 Query Match 4.8%; Score 82; DB 1; Length 119;
 Best Local Similarity 37.5%; Pred. No. 5.1;
 RESULT 746
 ID AAB20102 standard; protein; 119 AA.
 DE Pig motilin.
 PN WO200100830-A1.
 PD 04-JAN-2001.
 PA (ZYMO-) ZYMOGENETICS INC.

Query Match 4.8%; Score 82; DB 4; Length 119;
 Best Local Similarity 37.5%; Pred. No. 5.1;
 RESULT 747
 ID AAB62651 standard; protein; 119 AA.
 DE Motilin receptor, GPR38.
 PN WO200138355-A2.
 PD 31-MAY-2001.
 PA (ZYMO-) ZYMOGENETICS INC.
 Query Match 4.8%; Score 82; DB 4; Length 119;
 Best Local Similarity 37.5%; Pred. No. 5.1;
 RESULT 748
 ID AD13329 standard; protein; 119 AA.
 DE Pig motilin protein homologue to zslg33.
 PN US2003176640-A1.
 PD 18-SEP-2003.
 PA (ZYMO-) ZYMOGENETICS INC.
 Query Match 4.8%; Score 82; DB 7; Length 119;
 Best Local Similarity 37.5%; Pred. No. 5.1;
 RESULT 749
 ID ADN11759 standard; protein; 119 AA.
 DE Porcine motilin protein.
 PN WO2004033645-A2.
 PD 22-APR-2004.
 PA (ZYMO-) ZYMOGENETICS INC.
 Query Match 4.8%; Score 82; DB 8; Length 119;
 Best Local Similarity 37.5%; Pred. No. 5.1;
 RESULT 750
 ID ABB55253 standard; protein; 307 AA.
 DE Lactococcus lactis protein cfa.
 PN FR2807446-A1.
 PD 12-OCT-2001.
 PA (INRG-) INRA INST NAT RECH AGRONOMIQUE.
 Query Match 4.8%; Score 82; DB 5; Length 307;
 Best Local Similarity 19.3%; Pred. No. 20;
 RESULT 751
 ID AAB93590 standard; protein; 520 AA.
 DE Human protein sequence SEQ ID NO:13016.
 PN EP1074617-A2.
 PD 07-FEB-2001.
 PA (HELI-) HELIX RES INST.
 Query Match 4.8%; Score 82; DB 4; Length 520;
 Best Local Similarity 18.0%; Pred. No. 43;
 RESULT 752
 ID AAB94160 standard; protein; 557 AA.
 DE Human protein sequence SEQ ID NO:14452.
 PN EP1074617-A2.
 PD 07-FEB-2001.
 PA (HELI-) HELIX RES INST.
 Query Match 4.8%; Score 82; DB 4; Length 557;
 Best Local Similarity 18.0%; Pred. No. 47;
 RESULT 753
 ID AAB94603 standard; protein; 678 AA.
 DE Human protein sequence SEQ ID NO:15428.
 PN EP1074617-A2.
 PD 07-FEB-2001.
 PA (HELI-) HELIX RES INST.
 Query Match 4.8%; Score 82; DB 4; Length 678;
 Best Local Similarity 18.0%; Pred. No. 62;
 RESULT 754
 ID AAB65969 standard; protein; 754 AA.
 DE Human secreted protein BLAST search protein SEQ ID NO: 109.
 PN WO200077023-A1.
 PD 21-DEC-2000.
 PA (HDMA-) HUMAN GENOME SCT INC.
 Query Match 4.8%; Score 82; DB 4; Length 754;
 Best Local Similarity 20.0%; Pred. No. 73;
 RESULT 755
 ID AAB11665 standard; protein; 1030 AA.
 DE Novel human secreted protein #2156.
 PN WO200179449-A2.
 PD 25-OCT-2001.
 PA (HYSE-) HYSEQ INC.
 Query Match 4.8%; Score 82; DB 4; Length 1030;

Best Local Similarity 20.0%; Pred. No. 1.1e+02;
RESULT 756
ID ADJ70612 standard; protein; 1313 AA.
DE Human heat mitochondrial protein as a therapeutic target SegID2418.
PN WO2003087768-A2.
PD 23-OCT-2003.
PA (MITO-) MITOKOR.
PA (BUCK-) BUCK INST AGE RES.
Query Match 4.8%; Score 82; DB 7; Length 1313;
Best Local Similarity 18.0%; Pred. No. 1.6e+02;
RESULT 757
ID ABW63605 standard; protein; 1538 AA.
DE Human diagnostic and therapeutic protein SEQ ID NO:3854.
PN WO2004023973-A2.
PD 25-MAR-2004.
PA (INCY-) INCYTE CORP.
Query Match 4.8%; Score 82; DB 8; Length 1538;
Best Local Similarity 22.1%; Pred. No. 2e+02;
RESULT 758
ID ADL12580 standard; protein; 1564 AA.
DE Human steroid-induced C3A liver cell protein #44.
PN US673549-B1.
PD 06-JAN-2004.
PA (INCY-) INCYTE CORP.
Query Match 4.8%; Score 82; DB 8; Length 1564;
Best Local Similarity 20.0%; Pred. No. 2.1e+02;
RESULT 759
ID AAB19801 standard; protein; 1609 AA.
DE Human laminin 2 gamma-1 chain.
PN WO200066730-A2.
PD 09-NOV-2000.
PA (UYNE-) UNIV NEW JERSEY MEDICINE & DENTISTRY.
Query Match 4.8%; Score 82; DB 3; Length 1609;
Best Local Similarity 22.1%; Pred. No. 2.2e+02;
RESULT 760
ID AAB48452 standard; protein; 1609 AA.
DE Human laminin 8 polypeptide, SEQ ID NO: 22.
PN WO200066732-A2.
PD 09-NOV-2000.
PA (BIOS-) BIOSTRATUM INC.
Query Match 4.8%; Score 82; DB 3; Length 1609;
Best Local Similarity 22.1%; Pred. No. 2.2e+02;
RESULT 761
ID ABB81594 standard; protein; 1609 AA.
DE Human laminin 10 third chain protein sequence SEQ ID NO:14.
PN WO200250111-A2.
PD 27-JUN-2002.
PA (BIOS-) BIOSTRATUM INC.
Query Match 4.8%; Score 82; DB 5; Length 1609;
Best Local Similarity 22.1%; Pred. No. 2.2e+02;
RESULT 762
ID ADC01887 standard; protein; 1609 AA.
DE Human laminin gamma 1 subunit.
PN US2003103975-A1.
PD 05-JUN-2003.
PA (JONE/) JONES J C R.
PA (GONZ/) GONZALES M.
Query Match 4.8%; Score 82; DB 7; Length 1609;
Best Local Similarity 22.1%; Pred. No. 2.2e+02;
RESULT 763
ID ADG37229 standard; protein; 1609 AA.
DE Human laminin-6 B2 subunit.
PN JP2003212791-A.
PD 30-JUL-2003.
PA (KAGA-) KAGAKU GIUTSU SHINKO JIGYODAN.
Query Match 4.8%; Score 82; DB 7; Length 1609;
Best Local Similarity 22.1%; Pred. No. 2.2e+02;
RESULT 764
ID ADP23021 standard; protein; 1609 AA.
DE PRO polypeptide SEQ ID NO:115.
PN WO2004041170-A2.
PD 21-MAY-2004.
PA (GETH) GENENTECH INC.
Query Match 4.8%; Score 82; DB 8; Length 1609;
Best Local Similarity 22.1%; Pred. No. 2.2e+02;
RESULT 765
ID AAB19803 standard; protein; 1617 AA.
DE Human laminin 2 gamma-1 chain with C-terminal FLAG epitope.
PN WO200066730-A2.
PD 09-NOV-2000.
PA (UYNE-) UNIV NEW JERSEY MEDICINE & DENTISTRY.
Query Match 4.8%; Score 82; DB 3; Length 1617;
Best Local Similarity 22.1%; Pred. No. 2.2e+02;
RESULT 766
ID ADC06797 standard; protein; 2146 AA.
DE Human prostate cancer-related protein NM_015384.
PN WO2003064599-A2.
PD 07-AUG-2003.
PA (ORIG-) ORIGENE TECHNOLOGIES INC.
Query Match 4.8%; Score 82; DB 7; Length 2146;
Best Local Similarity 18.0%; Pred. No. 3.3e+02;
RESULT 767
ID ADC06798 standard; protein; 2265 AA.
DE Human prostate cancer-related protein NM_133433.
PN WO2003064599-A2.
PD 07-AUG-2003.
PA (ORIG-) ORIGENE TECHNOLOGIES INC.
Query Match 4.8%; Score 82; DB 7; Length 2265;
Best Local Similarity 18.0%; Pred. No. 3.5e+02;
RESULT 768
ID ADL68818 standard; protein; 2265 AA.
DE Human heat mitochondrial protein as a therapeutic target SegID624.
PN WO2003087768-A2.
PD 23-OCT-2003.
PA (MITO-) MITOKOR.
PA (BUCK-) BUCK INST AGE RES.
Query Match 4.8%; Score 82; DB 7; Length 2265;
Best Local Similarity 18.0%; Pred. No. 3.5e+02;
RESULT 769
ID ADP24677 standard; protein; 2265 AA.
DE PRO polypeptide SEQ ID NO:1855.
PN WO2004041170-A2.
PD 21-MAY-2004.
PA (GETH) GENENTECH INC.
Query Match 4.8%; Score 82; DB 8; Length 2265;
Best Local Similarity 18.0%; Pred. No. 3.5e+02;
RESULT 770
ID ADC06796 standard; protein; 2685 AA.
DE Human prostate cancer-related protein PCP0623.
PN WO2003064599-A2.
PD 07-AUG-2003.
PA (ORIG-) ORIGENE TECHNOLOGIES INC.
Query Match 4.8%; Score 82; DB 7; Length 2685;
Best Local Similarity 18.0%; Pred. No. 4.5e+02;
RESULT 771
ID ADN04576 standard; protein; 2804 AA.
DE Antipsoriatic protein sequence #477.
PN WO2004028479-A2.
PD 08-APR-2004.
PA (GETH) GENENTECH INC.
Query Match 4.8%; Score 82; DB 8; Length 2804;
Best Local Similarity 18.0%; Pred. No. 4.8e+02;
RESULT 772
ID AAW62831 standard; protein; 525 AA.
DE Theobroma cacao antimicrobial protein.
PN WO9827805-A1.
PD 02-JUL-1998.
PA (RETR-) COOP RES CENT TROPICAL PLANT PATHOLOGY.
Query Match 4.8%; Score 81.5; DB 2; Length 525;
Best Local Similarity 22.6%; Pred. No. 49;
RESULT 773
ID AAR20181 standard; protein; 566 AA.
DE Sequence encoded by 67 kD T. cacao protein cDNA.
PN WO9119801-A.
PD 26-DEC-1991.
PA (MRSC) MARS UK LTD.

Query Match 4.8%; Score 81.5; DB 2; Length 566;
 Best Local Similarity 22.6%; Pred. No. 54;
 RESULT 774
 ID ADI40495 standard; protein; 587 AA.
 DE Human purified secretory polypeptide (SPTM), seq id 188.
 PN WO2003062385-A2.
 PD 31-JUL-2003.
 PA (INCYTE) INCYTE GENOMICS INC.
 PA (JONES) JONES A L.
 PA (DAHL) DAHL C R.
 PA (GIET) GIETZEN D.
 PA (CHIN) CHINN J.
 PA (DUFO) DUFOUR G E.
 PA (JACK) JACKSON J L.
 PA (YUJY) YU J Y.
 PA (TUAS) TUASON O.
 PA (VAPF) VAP P E.
 PA (AMSH) AMSHEY S R.
 PA (DAMT) DAM T C.
 PA (LIUT) LIU T F.
 PA (GERST) GERSTIN E H.
 PA (PERA) PERALTA C H.
 PA (LEWIT) LEWIS S A.
 PA (CHEN) CHEN A J.
 PA (MARW) MARWAHA R.
 PA (LANR) LAN R Y.
 PA (URAS) URASHKA M E.
 PA (KRIS) KRISTNAM S R.
 PA (KOLU) KOLURU V.
 PA (PANE) PANESAR I S.
 Query Match 4.8%; Score 81.5; DB 7; Length 587;
 Best Local Similarity 22.3%; Pred. No. 57;
 RESULT 775
 ID AAG30538 standard; protein; 725 AA.
 DE Arabidopsis thaliana protein fragment SEQ ID NO: 36527.
 PN EPI033405-A2.
 PD 06-SEP-2000.
 Query Match 4.8%; Score 81.5; DB 3; Length 725;
 Best Local Similarity 20.6%; Pred. No. 77;
 RESULT 776
 ID AAG30537 standard; protein; 735 AA.
 DE Arabidopsis thaliana protein fragment SEQ ID NO: 36526.
 PN EPI033405-A2.
 PD 06-SEP-2000.
 Query Match 4.8%; Score 81.5; DB 3; Length 735;
 Best Local Similarity 20.6%; Pred. No. 79;
 RESULT 777
 ID AAG30536 standard; protein; 778 AA.
 DE Arabidopsis thaliana protein fragment SEQ ID NO: 36525.
 PN EPI033405-A2.
 PD 06-SEP-2000.
 Query Match 4.8%; Score 81.5; DB 3; Length 778;
 Best Local Similarity 20.6%; Pred. No. 86;
 RESULT 778
 ID ABU25347 standard; protein; 835 AA.
 DE Protein encoded by Prokaryotic essential gene #10874.
 PN WO200277183-A2.
 PD 03-OCT-2002.
 PA (ELIT) ELITRA PHARM INC.
 Query Match 4.8%; Score 81.5; DB 6; Length 835;
 Best Local Similarity 21.8%; Pred. No. 95;
 RESULT 779
 ID AAW22775 standard; protein; 1312 AA.
 DE Human RAD50.
 PN WO9727284-A2.
 PD 31-JUL-1997.
 PA (GENE) GENELABS TECHNOLOGIES INC.
 Query Match 4.8%; Score 81.5; DB 2; Length 1312;
 Best Local Similarity 23.1%; Pred. No. 1.8e+02;
 RESULT 780
 ID ABG12816 standard; protein; 388 AA.
 DE Novel human diagnostic protein #12807.
 PN WO200175067-A2.

PD 11-OCT-2001.
 PA (HYSE) HYSEQ INC.
 Query Match 4.8%; Score 81; DB 4; Length 388;
 Best Local Similarity 23.0%; Pred. No. 35;
 RESULT 781
 ID AAR15507 standard; protein; 485 AA.
 DE Tomato ACC synthase encoded by clone LE-ACC2.
 PN USN7579896-N.
 PD 12-NOV-1991.
 PA (USDA) US SEC OF AGRIC.
 Query Match 4.8%; Score 81; DB 2; Length 485;
 Best Local Similarity 19.7%; Pred. No. 49;
 RESULT 782
 ID AAM47314 standard; protein; 485 AA.
 DE Tomato ACC synthase LE-ACC2.
 PN US5723766-A.
 PD 03-MAR-1998.
 PA (USDA) US SEC OF AGRIC.
 Query Match 4.8%; Score 81; DB 2; Length 485;
 Best Local Similarity 19.7%; Pred. No. 49;
 RESULT 783
 ID AAE00984 standard; protein; 485 AA.
 DE Tomato 1-aminocyclopropane-1-carboxylic acid synthase, LE-ACC2.
 PN US6207881-B1.
 PD 27-MAR-2001.
 PA (USDA) US SEC OF AGRIC.
 Query Match 4.8%; Score 81; DB 4; Length 485;
 Best Local Similarity 19.7%; Pred. No. 49;
 RESULT 784
 ID AAB59720 standard; protein; 485 AA.
 DE Protein encoded by tomato ACC synthase gene LE-ACC 2.
 PN US6156956-A.
 PD 05-DEC-2000.
 PA (USDA) US DEPT OF AGRICULTURE.
 Query Match 4.8%; Score 81; DB 4; Length 485;
 Best Local Similarity 19.7%; Pred. No. 49;
 RESULT 785
 ID AAB59725 standard; protein; 485 AA.
 DE Tomato ACC synthase gene LE-ACC2(b) clone.
 PN US6156956-A.
 PD 05-DEC-2000.
 PA (USDA) US DEPT OF AGRICULTURE.
 Query Match 4.8%; Score 81; DB 4; Length 485;
 Best Local Similarity 19.7%; Pred. No. 49;
 RESULT 786
 ID ABU0678 standard; protein; 504 AA.
 DE Protein encoded by Prokaryotic essential gene #6205.
 PN WO200277183-A2.
 PD 03-OCT-2002.
 PA (ELIT) ELITRA PHARM INC.
 Query Match 4.8%; Score 81; DB 6; Length 504;
 Best Local Similarity 25.5%; Pred. No. 52;
 RESULT 787
 ID AAB01117 standard; protein; 552 AA.
 DE Human gene 4 encoded secreted protein HSH186, SEQ ID NO:31.
 PN WO200134799-A1.
 PD 17-MAY-2001.
 PA (HUMA) HUMAN GENOME SCI INC.
 Query Match 4.8%; Score 81; DB 4; Length 552;
 Best Local Similarity 19.4%; Pred. No. 59;
 RESULT 788
 ID ABG64586 standard; protein; 552 AA.
 DE Human albumin fusion protein #1261.
 PN WO200177137-A1.
 PD 18-OCT-2001.
 PA (HUMA) HUMAN GENOME SCI INC.
 Query Match 4.8%; Score 81; DB 5; Length 552;
 Best Local Similarity 19.4%; Pred. No. 59;
 RESULT 789
 ID ADL77853 standard; protein; 552 AA.
 DE Albumin fusion protein related therapeutic protein X, SEQ ID NO 1335.
 PN US2004010134-A1.
 PD 15-JAN-2004.

PA (ROSE/) ROSEN C A.
PA (HASE/) HASELTINE W A.
Query Match 4.8%; Score 81; DB 8; Length 552;
Best Local Similarity 19.4%; Pred. No. 59;
RESULT 790
ID AAB65970 standard; protein; 754 AA.
DE Human secreted protein BLAST search protein SEQ ID NO: 110.
PN WO200077023-A1.
PD 21-DEC-2000.
PA (HIMA-) HUMAN GENOME SCI INC.
Query Match 4.8%; Score 81; DB 4; Length 754;
Best Local Similarity 20.0%; Pred. No. 92;
RESULT 791
ID ADS28536 standard; protein; 848 AA.
DE Bacterial polypeptide #17569.
PN US200333675-A1.
PD 18-DEC-2003.
PA (CAOY/) CAO Y.
PA (HINK/) HINKER G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
Query Match 4.8%; Score 81; DB 8; Length 848;
Best Local Similarity 27.0%; Pred. No. 1.1e+02;
RESULT 792
ID ADR95699 standard; protein; 959 AA.
DE Novel S. pneumoniae protein sequence, SEQ ID 4334.
PN US6800744-B1.
PD 05-OCT-2004.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 4.8%; Score 81; DB 8; Length 959;
Best Local Similarity 23.4%; Pred. No. 1.3e+02;
RESULT 793
ID ABH01981 standard; protein; 1032 AA.
DE S. pneumoniae type 4 strain protein from coding region #1558.
PN WO200277021-A2.
PD 03-OCT-2002.
PA (CHIR-) CHIRON SPA.
PA (GENO-) INST GENOMIC RES.
Query Match 4.8%; Score 81; DB 6; Length 1032;
Best Local Similarity 23.4%; Pred. No. 1.4e+02;
RESULT 794
ID ADR6851 standard; protein; 1032 AA.
DE Streptococcus pneumoniae protein, Seq ID No 3366.
PN US6699703-B1.
PD 02-MAR-2004.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 4.8%; Score 81; DB 8; Length 1032;
Best Local Similarity 23.4%; Pred. No. 1.4e+02;
RESULT 795
ID AAM50898 standard; protein; 1609 AA.
DE Human laminin G1 chain.
PN WO9815179-A1.
PD 16-APR-1998.
PA (UNIW) UNIV WASHINGTON.
Query Match 4.8%; Score 81; DB 2; Length 1609;
Best Local Similarity 22.1%; Pred. No. 2.7e+02;
RESULT 796
ID ADL61261 standard; protein; 1609 AA.
DE Human protein tyrosine kinase biomarker laminin gamma 1 protein.
PN WO2004020583-A2.
PD 11-MAR-2004.
PA (BRIM) BRISTOL-MYERS SQUIBB CO.
Query Match 4.8%; Score 81; DB 8; Length 1609;
Best Local Similarity 22.1%; Pred. No. 2.7e+02;
RESULT 797
ID ADR87632 standard; protein; 1609 AA.
DE Human laminin beta 2, SEQ ID 36.
PN WO2004075835-A2.
PD 10-SEP-2004.
PA (GETH) GENENTECH INC.
Query Match 4.8%; Score 81; DB 8; Length 1609;
Best Local Similarity 22.1%; Pred. No. 2.7e+02;

RESULT 798
ID ADD55738 standard; protein; 661 AA.
DE Thalecress environmental stress-related protein #48.
PN US200331386-A1.
PD 10-JUL-2003.
PA (SAMA/) SAMARA R.
PA (HEAR/) HEARD J.
PA (JIAN/) JIANG C.
PA (PINE/) PINEDA O.
PA (REUB/) REUBER L.
PA (RIEC/) RIECHMANN J L.
PA (YUGG/) YU G.
PA (KEDD/) KEDDIE J.
PA (RATC/) RATCLIFFE O.
PA (PIIG/) PILGRIM M.
PA (ADAM/) ADAM L.
PA (BROU/) BROUIN P.
PA (ZHAN/) ZHANG J.
Query Match 4.8%; Score 80.5; DB 7; Length 661;
Best Local Similarity 20.5%; Pred. No. 86;
RESULT 799
ID ADO01835 standard; protein; 661 AA.
DE Thalecress transcription factor protein #124.
PN US2004045049-A1.
PD 04-MAR-2004.
PA (ZHAN/) ZHANG J.
PA (FROM/) FROM M E.
PA (HEAR/) HEARD J E.
PA (RIEC/) RIECHMANN J L.
PA (ADAM/) ADAM L J.
PA (BROU/) BROUIN P E.
PA (PINE/) PINEDA O.
PA (REUB/) REUBER T L.
PA (KEDD/) KEDDIE J S.
PA (YUGG/) YU G.
PA (JIAN/) JIANG C.
PA (SAMA/) SAMARA R S.
PA (PIIG/) PILGRIM M L.
PA (CREE/) CREELMAN R A.
PA (DUBE/) DUBELL A N.
PA (RATC/) RATCLIFFE O.
PA (KDMT/) KOMIMOTO R.
PA (SHER/) SHERMAN B K.
Query Match 4.8%; Score 80.5; DB 8; Length 661;
Best Local Similarity 20.5%; Pred. No. 86;
RESULT 800
ID ABB65439 standard; protein; 1377 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 23109.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 4.8%; Score 80.5; DB 4; Length 1377;
Best Local Similarity 21.9%; Pred. No. 2.5e+02;
RESULT 801
ID ADCS1662 standard; protein; 2273 AA.
DE Human MEGF8 protein #2.
PN JP2002360254-A.
PD 17-DEC-2002.
PA (KAZU-) ZH KAZUSA DNA KENKYUSHO.
Query Match 4.8%; Score 80.5; DB 7; Length 2273;
Best Local Similarity 34.2%; Pred. No. 5.1e+02;
RESULT 802
ID ADCS1660 standard; protein; 2778 AA.
DE Human MEGF8 protein #1.
PN JP2002360254-A.
PD 17-DEC-2002.
PA (KAZU-) ZH KAZUSA DNA KENKYUSHO.
Query Match 4.8%; Score 80.5; DB 7; Length 2778;
Best Local Similarity 34.2%; Pred. No. 6.8e+02;
RESULT 803
ID ADG75733 standard; protein; 2789 AA.
DE Human protein modification and maintenance molecule polypeptide SeqID57.
PN WO2003083084-A2.

PD 09-OCT-2003.
PA (INCY-) INCYTE CORP.
Query Match 4.7%; Score 80.5; DB 7; Length 2789;
Best Local Similarity 34.2%; Pred. No. 6.8e+02;
RESULT 804
ID ABB82209 standard; protein; 213 AA.
DE Tumour-associated antigenic target (TAT) polypeptide PRO83130, SEQ:5694.
PN WO2004030615-A2.
PD 15-APR-2004.
PA (GERTH) GENENTECH INC.
Query Match 4.7%; Score 80; DB 8; Length 213;
Best Local Similarity 22.9%; Pred. No. 19;
RESULT 805
ID ADA35158 standard; protein; 305 AA.
DE Acinetobacter baumannii protein #319.
PN US562958-B1.
PD 13-MAY-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 4.7%; Score 80; DB 6; Length 305;
Best Local Similarity 23.1%; Pred. No. 32;
RESULT 806
ID ABB63183 standard; protein; 575 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 16341.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 4.7%; Score 80; DB 4; Length 575;
Best Local Similarity 25.9%; Pred. No. 79;
RESULT 807
ID ABB22494 standard; protein; 604 AA.
DE Novel human diagnostic protein #22485.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match 4.7%; Score 80; DB 4; Length 604;
Best Local Similarity 20.4%; Pred. No. 85;
RESULT 808
ID AAR48627 standard; protein; 1122 AA.
DE Protein-tyrosine-kinase tek.
PN WO9404694-A1.
PD 03-MAR-1994.
PA (MOUN) MOUNT SINAI HOSPITAL CORP.
Query Match 4.7%; Score 80; DB 2; Length 1122;
Best Local Similarity 20.3%; Pred. No. 2.1e+02;
RESULT 809
ID AAB19805 standard; protein; 1605 AA.
DE Mouse laminin 2 gamma-1 chain.
PN WO200066730-A2.
PD 09-NOV-2000.
PA (UNIV-) UNIV NEW JERSEY MEDICINE & DENTISTRY.
Query Match 4.7%; Score 80; DB 3; Length 1605;
Best Local Similarity 22.5%; Pred. No. 3.5e+02;
RESULT 810
ID AAB48454 standard; protein; 1605 AA.
DE Mouse laminin 8 polypeptide, SEQ ID NO: 26.
PN WO200066732-A2.
PD 09-NOV-2000.
PA (BIOS-) BIOSRATUM INC.
Query Match 4.7%; Score 80; DB 3; Length 1605;
Best Local Similarity 22.5%; Pred. No. 3.5e+02;
RESULT 811
ID ABB81596 standard; protein; 1605 AA.
DE Mouse laminin 10 third chain protein sequence SEQ ID NO:18.
PN WO200250111-A2.
PD 27-JUN-2002.
PA (BIOS-) BIOSRATUM INC.
Query Match 4.7%; Score 80; DB 5; Length 1605;
Best Local Similarity 22.5%; Pred. No. 3.5e+02;
RESULT 812
ID ADT49890 standard; protein; 1605 AA.
DE Murine J02930 SEQ ID NO:97.
PN WO2004083241-A2.
PD 30-SEP-2004.

PA (TAKE) TAKEDA CHEM IND LTD.
Query Match 4.7%; Score 80; DB 8; Length 1605;
Best Local Similarity 22.5%; Pred. No. 3.5e+02;
RESULT 813
ID ABB12113 standard; protein; 1887 AA.
DE Human protein modification and maintenance molecule (PMOD) #10.
PN WO200281636-A2.
PD 17-OCT-2002.
PA (INCY-) INCYTE GENOMICS INC.
Query Match 4.7%; Score 80; DB 6; Length 1887;
Best Local Similarity 26.3%; Pred. No. 4.4e+02;
RESULT 814
ID ABB80242 standard; protein; 1887 AA.
DE Human subtilase.
PN WO2003060109-A2.
PD 24-JUL-2003.
PA (FARB) BAYER AG.
Query Match 4.7%; Score 80; DB 7; Length 1887;
Best Local Similarity 26.3%; Pred. No. 4.4e+02;
RESULT 815
ID ADM29324 standard; protein; 1887 AA.
DE Human novel protein NOV10a.
PN WO2003064628-A2.
PD 07-AUG-2003.
PA (CURA-) CURAGEN CORP.
Query Match 4.7%; Score 80; DB 7; Length 1887;
Best Local Similarity 26.3%; Pred. No. 4.4e+02;
RESULT 816
ID ADH48732 standard; protein; 2854 AA.
DE NOV7 protein sequence, SEQ ID 16.
PN WO200268652-A2.
PD 06-SEP-2002.
PA (CURA-) CURAGEN CORP.
Query Match 4.7%; Score 80; DB 5; Length 2854;
Best Local Similarity 31.7%; Pred. No. 8e+02;
RESULT 817
ID AAB38614 standard; protein; 395 AA.
DE Mouse thymidylate kinase protein.
PN WO2003064642-A1.
PD 07-AUG-2003.
PA (FARB) BAYER AG.
Query Match 4.7%; Score 79.5; DB 7; Length 395;
Best Local Similarity 21.3%; Pred. No. 52;
RESULT 818
ID ADT76250 standard; protein; 395 AA.
DE Marker gene related amino acid sequence SEQ ID NO:1502.
PN EP1394274-A2.
PD 03-MAR-2004.
PA (GENO-) GENOX RES INC.
Query Match 4.7%; Score 79.5; DB 8; Length 395;
Best Local Similarity 21.3%; Pred. No. 52;
RESULT 819
ID ABB25076 standard; protein; 415 AA.
DE Protein encoded by Prokaryotic essential gene #10603.
PN WO20027183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 4.7%; Score 79.5; DB 6; Length 415;
Best Local Similarity 22.0%; Pred. No. 56;
RESULT 820
ID AAR15506 standard; protein; 485 AA.
DE Tomato ACC synthase encoded by clone pTACCL.
PN USN579896-N.
PD 12-NOV-1991.
PA (USDA) US SEC OF AGRIC.
Query Match 4.7%; Score 79.5; DB 2; Length 485;
Best Local Similarity 22.6%; Pred. No. 70;
RESULT 821
ID AAW47313 standard; protein; 485 AA.
DE Tomato ACC synthase.
PN US5723766-A.
PD 03-MAR-1998.
PA (USDA) US SEC OF AGRIC.

Query Match 4.7%; Score 79.5; DB 2; Length 485;
Best Local Similarity 22.6%; Pred. No. 70;
RESULT 822
ID AAE00983 standard; protein; 485 AA.
DE Tomato 1-aminocyclopropane-1-carboxylic acid synthase (ACC).
FN US6207881-B1.
PD 27-MAR-2001.
PA (USDA) US SEC OF AGRIC.
Query Match 4.7%; Score 79.5; DB 4; Length 485;
Best Local Similarity 22.6%; Pred. No. 70;
RESULT 823
ID AAB59719 standard; protein; 485 AA.
DE Tomato ACC synthase.
FN US6156956-A.
PD 05-DEC-2000.
PA (USDA) US DEPT OF AGRICULTURE.
Query Match 4.7%; Score 79.5; DB 4; Length 485;
Best Local Similarity 22.6%; Pred. No. 70;
RESULT 824
ID ADR10465 standard; protein; 682 AA.
DE Human protein useful for treating neurological disease Seq 3971.
FN EPI447413-A2.
PD 18-AUG-2004.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
Query Match 4.7%; Score 79.5; DB 8; Length 682;
Best Local Similarity 24.3%; Pred. No. 1.1e+02;
RESULT 825
ID AAG81808 standard; protein; 701 AA.
DE S. epidermidis open reading frame protein sequence SEQ ID NO:710.
FN WO200134809-A2.
PD 17-MAY-2001.
PA (GLAX) GLAXO GROUP LTD.
Query Match 4.7%; Score 79.5; DB 4; Length 701;
Best Local Similarity 21.9%; Pred. No. 1.2e+02;
RESULT 826
ID ABP8170 standard; protein; 703 AA.
DE Staphylococcus epidermidis ORF amino acid sequence SEQ ID NO:3015.
FN US6380370-B1.
PD 30-APR-2002.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 4.7%; Score 79.5; DB 5; Length 703;
Best Local Similarity 21.9%; Pred. No. 1.2e+02;
RESULT 827
ID ADS04687 standard; protein; 703 AA.
DE Staphylococcus epidermis polypeptide seqid 3982.
FN US200414734-A1.
PD 29-JUL-2004.
PA (DOUC/) DOUCETTE-STAMM L.
PA (BUSH/) BUSH D.
Query Match 4.7%; Score 79.5; DB 8; Length 703;
Best Local Similarity 21.9%; Pred. No. 1.2e+02;
RESULT 828
ID AAO16642 standard; protein; 919 AA.
DE Human extracellular messenger protein #2.
FN WO2003002610-A1.
PD 09-JAN-2003.
PA (INCY-) INCYTE GENOMICS INC.
Query Match 4.7%; Score 79.5; DB 6; Length 919;
Best Local Similarity 24.3%; Pred. No. 1.8e+02;
RESULT 829
ID ADI27626 standard; protein; 919 AA.
DE Human SCUBE2 protein.
FN US200319813-A1.
PD 27-NOV-2003.
PA (MILL-) MILLENIUM PHARM INC.
Query Match 4.7%; Score 79.5; DB 8; Length 919;
Best Local Similarity 24.3%; Pred. No. 1.8e+02;
RESULT 830
ID ADO66056 standard; protein; 971 AA.
DE Novel human protein sequence #1029.
FN EPI440981-A2.
PD 28-JUL-2004.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.

Query Match 4.7%; Score 79.5; DB 8; Length 971;
Best Local Similarity 24.3%; Pred. No. 1.9e+02;
RESULT 831
ID ABP69329 standard; protein; 999 AA.
DE Human polypeptide SEQ ID NO 1376.
FN WO200270539-A2.
PD 12-SEP-2002.
PA (HYSE-) HYSEQ INC.
Query Match 4.7%; Score 79.5; DB 5; Length 999;
Best Local Similarity 24.3%; Pred. No. 2e+02;
RESULT 832
ID ABG61893 standard; protein; 999 AA.
DE Prostate cancer-associated protein #94.
FN WO200230268-A2.
PD 18-APR-2002.
PA (EOSB-) EOS BIOTECHNOLOGY INC.
Query Match 4.7%; Score 79.5; DB 5; Length 999;
Best Local Similarity 24.3%; Pred. No. 2e+02;
RESULT 833
ID ABB80926 standard; protein; 999 AA.
DE Human breast cancer modulating protein BCO2.
FN WO200255988-A2.
PD 18-JUL-2002.
PA (EOSB-) EOS BIOTECHNOLOGY INC.
Query Match 4.7%; Score 79.5; DB 5; Length 999;
Best Local Similarity 24.3%; Pred. No. 2e+02;
RESULT 834
ID ABJ05567 standard; protein; 999 AA.
DE Breast cancer-associated protein 32.
FN WO200259377-A2.
PD 01-AUG-2002.
PA (EOSB-) EOS BIOTECHNOLOGY INC.
Query Match 4.7%; Score 79.5; DB 5; Length 999;
Best Local Similarity 24.3%; Pred. No. 2e+02;
RESULT 835
ID ABJ19815 standard; protein; 999 AA.
DE Androgen-independent prostate cancer-related protein - SEQ ID No 42.
FN WO200298358-A2.
PD 12-DEC-2002.
PA (EOSB-) EOS BIOTECHNOLOGY INC.
Query Match 4.7%; Score 79.5; DB 6; Length 999;
Best Local Similarity 24.3%; Pred. No. 2e+02;
RESULT 836
ID ABR47407 standard; protein; 999 AA.
DE Breast cancer associated protein sequence SEQ ID NO:45.
FN WO2003004989-A2.
PD 16-JAN-2003.
PA (MILL-) MILLENIUM PHARM INC.
Query Match 4.7%; Score 79.5; DB 7; Length 999;
Best Local Similarity 24.3%; Pred. No. 2e+02;
RESULT 837
ID ADN39416 standard; protein; 999 AA.
DE Cancer/angiogenesis/fibrosis-related polypeptide, SEQ ID NO:A16.
FN WO2003042661-A2.
PD 22-MAY-2003.
PA (EOSB-) EOS BIOTECHNOLOGY INC.
Query Match 4.7%; Score 79.5; DB 7; Length 999;
Best Local Similarity 24.3%; Pred. No. 2e+02;
RESULT 838
ID ADN38734 standard; protein; 999 AA.
DE Cancer/angiogenesis/fibrosis-related polypeptide, SEQ ID NO:52.
FN WO2003042661-A2.
PD 22-MAY-2003.
PA (EOSB-) EOS BIOTECHNOLOGY INC.
Query Match 4.7%; Score 79.5; DB 7; Length 999;
Best Local Similarity 24.3%; Pred. No. 2e+02;
RESULT 839
ID ADN39569 standard; protein; 999 AA.
DE Cancer/angiogenesis/fibrosis-related polypeptide, SEQ ID NO:A169.
FN WO2003042661-A2.
PD 22-MAY-2003.
PA (EOSB-) EOS BIOTECHNOLOGY INC.
Query Match 4.7%; Score 79.5; DB 7; Length 999;

Best Local Similarity 24.3%; Pred. No. 2e+02;
 RESULT 840
 ID AD127636 standard; protein; 999 AA.
 DE SCUBE2 homologous protein.
 PN US2003219813-A1.
 PD 27-NOV-2003.
 PA (MILL-) MILLENNIUM PHARM INC.
 Query Match 4.7%; Score 79.5; DB 8; Length 999;
 Best Local Similarity 24.3%; Pred. No. 2e+02;
 RESULT 841
 ID AAR5316 standard; protein; 1117 AA.
 DE Mouse tyrosine kinase ("tek") expressed during cardiogenesis.
 PN CA2085291-A.
 PD 31-JAN-1994.
 PA (MOUN) MOUNT SINAI HOSPITAL CORP.
 Query Match 4.7%; Score 79.5; DB 2; Length 1117;
 Best Local Similarity 20.0%; Pred. No. 2.3e+02;
 RESULT 842
 ID ADP47905 standard; protein; 1866 AA.
 DE Human inflammation/cancer-related CATERPILLER NOD27 protein.
 PN WO2004034093-A2.
 PD 22-APR-2004.
 PA (UNNC-) UNIV NORTH CAROLINA.
 Query Match 4.7%; Score 79.5; DB 8; Length 1866;
 Best Local Similarity 23.0%; Pred. No. 4.9e+02;
 RESULT 843
 ID ADP12959 standard; protein; 1866 AA.
 DE Protein encoding reference mRNA sequence #44.
 PN WO2004042346-A2.
 PD 21-MAY-2004.
 PA (EXPR-) EXPRESSION DIAGNOSTICS INC.
 Query Match 4.7%; Score 79.5; DB 8; Length 1866;
 Best Local Similarity 23.0%; Pred. No. 4.9e+02;
 RESULT 844
 ID AAB38635 standard; protein; 251 AA.
 DE Human secreted protein sequence encoded by gene 38 SEQ ID NO:172.
 PN WO200056882-A1.
 PD 28-SEP-2000.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match 4.7%; Score 79; DB 3; Length 251;
 Best Local Similarity 21.0%; Pred. No. 31;
 RESULT 845
 ID AAB38633 standard; protein; 259 AA.
 DE Human secreted protein sequence encoded by gene 38 SEQ ID NO:170.
 PN WO200056882-A1.
 PD 28-SEP-2000.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match 4.7%; Score 79; DB 3; Length 259;
 Best Local Similarity 21.0%; Pred. No. 32;
 RESULT 846
 ID AAB38631 standard; protein; 259 AA.
 DE Human secreted protein sequence encoded by gene 38 SEQ ID NO:168.
 PN WO200056882-A1.
 PD 28-SEP-2000.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match 4.7%; Score 79; DB 3; Length 259;
 Best Local Similarity 21.0%; Pred. No. 32;
 RESULT 847
 ID AAB38629 standard; protein; 259 AA.
 DE Human secreted protein sequence encoded by gene 38 SEQ ID NO:166.
 PN WO200056882-A1.
 PD 28-SEP-2000.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match 4.7%; Score 79; DB 3; Length 259;
 Best Local Similarity 21.0%; Pred. No. 32;
 RESULT 848
 ID ADR41503 standard; protein; 565 AA.
 DE Human CD-1-like molecule HFKFH60, SEQ ID NO:302.
 PN WO200226930-A2.
 PD 04-APR-2002.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match 4.7%; Score 79; DB 5; Length 565;
 Best Local Similarity 21.0%; Pred. No. 98;
 RESULT 849
 ID ABM83037 standard; protein; 889 AA.
 DE Human diagnostic and therapeutic pproteain SEQ ID NO:3286.
 PN WO2004023973-A2.
 PD 25-MAR-2004.
 PA (INCY-) INCYTE CORP.
 Query Match 4.7%; Score 79; DB 8; Length 889;
 Best Local Similarity 24.5%; Pred. No. 1.9e+02;
 RESULT 850
 ID AAY59046 standard; protein; 1118 AA.
 DE Mouse receptor tyrosine kinase protein.
 PN US5998187-A.
 PD 07-DEC-1999.
 PA (MOUN) MOUNT SINAI HOSPITAL CORP.
 Query Match 4.7%; Score 79; DB 3; Length 1118;
 Best Local Similarity 20.3%; Pred. No. 2.6e+02;
 RESULT 851
 ID AAY59048 standard; protein; 1122 AA.
 DE Mouse tek receptor tyrosine kinase protein.
 PN US5998187-A.
 PD 07-DEC-1999.
 PA (MOUN) MOUNT SINAI HOSPITAL CORP.
 Query Match 4.7%; Score 79; DB 3; Length 1122;
 Best Local Similarity 20.3%; Pred. No. 2.6e+02;
 RESULT 852
 ID AAR73951 standard; protein; 1123 AA.
 DE Mouse tie-2 receptor tyrosine kinase protein.
 PN WO9513387-A1.
 PD 18-MAY-1995.
 PA (PLAC) MAX PLANCK GES FOERDERUNG WISSENSCHAFTEN.
 Query Match 4.7%; Score 79; DB 2; Length 1123;
 Best Local Similarity 20.3%; Pred. No. 2.6e+02;
 RESULT 853
 ID AAR67391 standard; protein; 1123 AA.
 DE Murine tyrosine kinase receptor tie-2.
 PN JP06315382-A.
 PD 15-NOV-1994.
 PA (SUDA/) SUDA T.
 PA (YAMA) YAMANOUCHI PHARM CO LTD.
 Query Match 4.7%; Score 79; DB 2; Length 1123;
 Best Local Similarity 20.3%; Pred. No. 2.6e+02;
 RESULT 854
 ID ABU07840 standard; protein; 1125 AA.
 DE Murine Tie receptor tyrosine kinase 2 (Tie 2).
 PN WO2003004529-A2.
 PD 16-JAN-2003.
 PA (LTCN) LICENTIA LTD.
 Query Match 4.7%; Score 79; DB 6; Length 1125;
 Best Local Similarity 20.3%; Pred. No. 2.6e+02;
 RESULT 855
 ID AAY14208 standard; peptide; 229 AA.
 DE HIV-1 gp120 peptide.
 PN WO9924065-A1.
 PD 20-MAY-1999.
 PA (UYCO) UNIV COLUMBIA NEW YORK.
 PA (DAND) DANA FARBEN CANCER INST INC.
 PA (SMIK) SMITHKLINE BEECHAM CORP.
 Query Match 4.6%; Score 78.5; DB 2; Length 229;
 Best Local Similarity 25.7%; Pred. No. 30;
 RESULT 856
 ID AAY14212 standard; peptide; 229 AA.
 DE HIV gp120 protein fragment.
 PN WO9924553-A2.
 PD 20-MAY-1999.
 PA (UYCO) UNIV COLUMBIA NEW YORK.
 PA (DAND) DANA FARBEN CANCER INST INC.
 Query Match 4.6%; Score 78.5; DB 2; Length 229;
 Best Local Similarity 25.7%; Pred. No. 30;
 RESULT 857
 ID ABG22503 standard; protein; 410 AA.
 DE Novel human diagnostic protein #22494.
 PN WO200175067-A2.
 PD 11-OCT-2001.

PA (HYSE-) HYSEQ INC.
Query Match 4.6%; Score 78.5; DB 4; Length 410;
Best Local Similarity 20.5%; Pred. No. 70;
RESULT 858
ID AAB07666 standard; protein; 785 AA.
DE Amino acid sequence of TARI, a surface layer protein.
PN EPI026248-A2.
PD 09-AUG-2000.
PA (UYRA-) UNIV RAMOT APPLIED RES & IND DEV LTD.
Query Match 4.6%; Score 78.5; DB 3; Length 785;
Best Local Similarity 21.8%; Pred. No. 1.8e+02;
RESULT 859
ID ABB65359 standard; protein; 1087 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 228659.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 4.6%; Score 78.5; DB 4; Length 1087;
Best Local Similarity 22.3%; Pred. No. 2.8e+02;
RESULT 860
ID ABB65358 standard; protein; 1087 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 22866.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 4.6%; Score 78.5; DB 4; Length 1087;
Best Local Similarity 22.3%; Pred. No. 2.8e+02;
RESULT 861
ID AAW71295 standard; protein; 1312 AA.
DE Human homologue of yeast RAD50.
PN WO9838306-A1.
PD 03-SEP-1998.
PA (GENE-) GENELABS TECHNOLOGIES INC.
Query Match 4.6%; Score 78.5; DB 2; Length 1312;
Best Local Similarity 22.5%; Pred. No. 3.7e+02;
RESULT 862
ID ABG30373 standard; protein; 356 AA.
DE Novel human diagnostic protein #30364.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match 4.6%; Score 78; DB 4; Length 356;
Best Local Similarity 20.0%; Pred. No. 64;
RESULT 863
ID ADM99266 standard; protein; 408 AA.
DE Cochliobolus heterostrophus strain C4 protease protein SegID 149.
PN WO2004033668-A2.
PD 22-APR-2004.
PA (DIYE-) DIVERSA CORP.
Query Match 4.6%; Score 78; DB 8; Length 408;
Best Local Similarity 22.0%; Pred. No. 78;
RESULT 864
ID ADM99268 standard; protein; 408 AA.
DE Cochliobolus heterostrophus strain C4 protease protein SegID 151.
PN WO2004033668-A2.
PD 22-APR-2004.
PA (DIYE-) DIVERSA CORP.
Query Match 4.6%; Score 78; DB 8; Length 408;
Best Local Similarity 22.0%; Pred. No. 78;
RESULT 865
ID AAB13632 standard; protein; 880 AA.
DE C. trachomatis pmpl gene protein.
PN WO20034483-A2.
PD 15-JUN-2000.
PA (CORI-) CORIXA CORP.
Query Match 4.6%; Score 78; DB 3; Length 880;
Best Local Similarity 23.5%; Pred. No. 2.4e+02;
RESULT 866
ID AAG83200 standard; protein; 880 AA.
DE Protein encoded by Chlamydia trachomatis pmpl gene.
PN WO200140474-A2.
PD 07-JUN-2001.
PA (CORI-) CORIXA CORP.

Query Match 4.6%; Score 78; DB 4; Length 880;
Best Local Similarity 23.5%; Pred. No. 2.4e+02;
RESULT 867
ID ABB94171 standard; protein; 880 AA.
DE Chlamydia protein sequence SEQ ID NO:175.
PN WO200208267-A2.
PD 31-JAN-2002.
PA (CORI-) CORIXA CORP.
Query Match 4.6%; Score 78; DB 5; Length 880;
Best Local Similarity 23.5%; Pred. No. 2.4e+02;
RESULT 868
ID ADE62841 standard; protein; 324 AA.
DE Rat Protein P97578, SEQ ID NO 8775.
PN WO2003016475-A2.
PD 27-FEB-2003.
PA (GENO) GEN HOSPITAL CORP.
PA (PARB) BAYER AG.
Query Match 4.6%; Score 77.5; DB 7; Length 324;
Best Local Similarity 20.8%; Pred. No. 63;
RESULT 869
ID ABG61528 standard; protein; 363 AA.
DE Iron uptake ABC transporter polypeptide #35.
PN WO200234773-A2.
PD 02-MAY-2002.
PA (IMCO-) IMPERIAL COLLEGE INNOVATIONS LTD.
Query Match 4.6%; Score 77.5; DB 5; Length 363;
Best Local Similarity 19.9%; Pred. No. 74;
RESULT 870
ID ADN27279 standard; protein; 394 AA.
DE Bacterial polypeptide #9932.
PN US2003233675-A1.
PD 18-DEC-2003.
PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
Query Match 4.6%; Score 77.5; DB 8; Length 394;
Best Local Similarity 27.3%; Pred. No. 84;
RESULT 871
ID ADA84087 standard; protein; 414 AA.
DE Human HMLA2 protein.
PN WO2002103028-A2.
PD 27-DEC-2002.
PA (BIOM-) BIOMEDICAL CENT.
Query Match 4.6%; Score 77.5; DB 6; Length 414;
Best Local Similarity 16.7%; Pred. No. 90;
RESULT 872
ID ADQ60374 standard; protein; 414 AA.
DE HERV-H LTR-associating 2 protein.
PN WO2004063709-A2.
PD 29-JUL-2004.
PA (BRIM) BRISTOL-MYERS SQUIBB CO.
Query Match 4.6%; Score 77.5; DB 8; Length 414;
Best Local Similarity 16.7%; Pred. No. 90;
RESULT 873
ID AAU79177 standard; protein; 425 AA.
DE Mouse tandem PH-domain-containing protein-2 (TAPP2) protein.
PN WO200212276-A2.
PD 14-FEB-2002.
PA (MEDIC-) MEDICAL RES COUNCIL.
Query Match 4.6%; Score 77.5; DB 5; Length 425;
Best Local Similarity 21.8%; Pred. No. 93;
RESULT 874
ID ABR40241 standard; protein; 425 AA.
DE Murine TAPP2.
PN WO2003011901-A1.
PD 13-FEB-2003.
PA (UYDU-) UNIV DUNDEE.
Query Match 4.6%; Score 77.5; DB 6; Length 425;
Best Local Similarity 21.8%; Pred. No. 93;
RESULT 875
ID ADJ95156 standard; protein; 451 AA.

DE Novel NOVX protein sequence #192.
PN WO2003040325-A2.
PD 15-MAY-2003.
PA (CURA-) CURAGEN CORP.
Query Match 4.6%; Score 77.5; DB 7; Length 451;
Best Local Similarity 26.0%; Pred. No. 1e+02;
RESULT 876
ID AAR31186 standard; protein; 462 AA.
DE GABA-A receptor alpha-5 subunit.
PN WO9222652-A1.
PD 23-DEC-1992.
PA (MERI) MERCK SHARP & DOHME LTD.
Query Match 4.6%; Score 77.5; DB 2; Length 462;
Best Local Similarity 26.0%; Pred. No. 1.1e+02;
RESULT 877
ID AAR59864 standard; protein; 462 AA.
DE Human GABA receptor alpha5 subunit.
PN WO9413799-A1.
PD 23-JUN-1994.
PA (MERI) MERCK SHARP & DOHME LTD.
Query Match 4.6%; Score 77.5; DB 2; Length 462;
Best Local Similarity 26.0%; Pred. No. 1.1e+02;
RESULT 878
ID ADB78624 standard; protein; 462 AA.
DE Human GABA receptor subunit mutant SEQ ID NO:168.
PN WO2003008574-A1.
PD 30-JAN-2003.
PA (BION-) BIONOMICS LTD.
Query Match 4.6%; Score 77.5; DB 7; Length 462;
Best Local Similarity 26.0%; Pred. No. 1.1e+02;
RESULT 879
ID AAW26428 standard; protein; 530 AA.
DE Swinepox virus HindIII C encoded protein C18L.
PN US5651972-A.
PD 29-JUL-1997.
PA (UYFL) UNIV FLORIDA RES FOUND INC.
Query Match 4.6%; Score 77.5; DB 2; Length 530;
Best Local Similarity 24.3%; Pred. No. 1.3e+02;
RESULT 880
ID AAB68249 standard; protein; 530 AA.
DE Protein encoded by reverse complement of HindIII C fragment of SPV.
PN US6217882-B1.
PD 17-APR-2001.
PA (UYFL) UNIV FLORIDA RES FOUND INC.
Query Match 4.6%; Score 77.5; DB 4; Length 530;
Best Local Similarity 24.3%; Pred. No. 1.3e+02;
RESULT 881
ID AAG92916 standard; protein; 657 AA.
DE C glutamicum protein fragment SEQ ID NO: 6670.
PN EP1108790-A2.
PD 20-JUN-2001.
PA (KYOW) KYOWA HAKKO KOGYO KK.
Query Match 4.6%; Score 77.5; DB 4; Length 657;
Best Local Similarity 20.4%; Pred. No. 1.7e+02;
RESULT 882
ID ABB93142 standard; protein; 669 AA.
DE Hebdicidally active polypeptide SEQ ID NO 2353.
PN WO200210210-A2.
PD 07-FEB-2002.
PA (FARB) BAYER AG.
Query Match 4.6%; Score 77.5; DB 5; Length 669;
Best Local Similarity 23.3%; Pred. No. 1.8e+02;
RESULT 883
ID ADJ76177 standard; protein; 761 AA.
DE Marker gene related amino acid sequence SEQ ID NO:1429.
PN EP1394274-A2.
PD 03-MAR-2004.
PA (GENO-) GENOX RES INC.
Query Match 4.6%; Score 77.5; DB 8; Length 761;
Best Local Similarity 21.8%; Pred. No. 2.2e+02;
RESULT 884
ID AAU79822 standard; protein; 836 AA.
DE OSF-2 protein associated protein #1.
PN WO200220055-A1.
PD 14-MAR-2002.
PA (SUNR) SUNTORY LTD.
Query Match 4.6%; Score 77.5; DB 5; Length 836;
Best Local Similarity 19.8%; Pred. No. 2.5e+02;
RESULT 885
ID ABU48219 standard; protein; 890 AA.
DE Protein encoded by Prokaryotic essential gene #33746.
PN WO200277185-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 4.6%; Score 77.5; DB 6; Length 890;
Best Local Similarity 22.4%; Pred. No. 2.7e+02;
RESULT 886
ID ABG22502 standard; protein; 1016 AA.
DE Novel human diagnostic protein #22493.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match 4.6%; Score 77.5; DB 4; Length 1016;
Best Local Similarity 22.1%; Pred. No. 3.3e+02;
RESULT 887
ID ABB61252 standard; protein; 1078 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 10548.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 4.6%; Score 77.5; DB 4; Length 1078;
Best Local Similarity 20.0%; Pred. No. 3.6e+02;
RESULT 888
ID AAY41654 standard; protein; 210 AA.
DE Zea mays XIAP associated factor 1 protein.
PN WO9947688-A1.
PD 23-SEP-1999.
PA (DUPO) DU PONT DE NEMOURS & CO E I.
Query Match 4.5%; Score 77; DB 2; Length 210;
Best Local Similarity 26.0%; Pred. No. 38;
RESULT 889
ID ABU49577 standard; protein; 330 AA.
DE Protein encoded by Prokaryotic essential gene #35104.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 4.5%; Score 77; DB 6; Length 330;
Best Local Similarity 20.9%; Pred. No. 73;
RESULT 890
ID AAR83406 standard; protein; 402 AA.
DE Humicola insolens endoglucanase variant N89Q + N247Q.
PN WO9524471-A1.
PD 14-SEP-1995.
PA (NOVO) NOVO-NORDISK AS.
Query Match 4.5%; Score 77; DB 2; Length 402;
Best Local Similarity 18.2%; Pred. No. 97;
RESULT 891
ID ADH87596 standard; protein; 489 AA.
DE Enterococcus faecalis polypeptide #2076.
PN US6617156-B1.
PD 09-SEP-2003.
PA (DOUC/) DOUCETTE-STAMM L A.
Query Match 4.5%; Score 77; DB 7; Length 489;
Best Local Similarity 20.4%; Pred. No. 1.3e+02;
RESULT 892
ID ABM68570 standard; protein; 600 AA.
DE Photorhabdus luminescens protein sequence #1667.
PN WO200294867-A2.
PD 28-NOV-2002.
PA (INSP) INST PASTEUR.
Query Match 4.5%; Score 77; DB 6; Length 600;
Best Local Similarity 24.8%; Pred. No. 1.7e+02;

RESULT 893
ID ADH09924 standard; protein; 620 AA.
DE Human host factor protein, SEQ ID No 452.
PN WO2003094847-A2.
PD 20-NOV-2003.
PA (UYEM-) UNIV EMORY.
Query Match
Best Local Similarity 4.5%; Score 77; DB 8; Length 620;
Pred. No. 1.8e+02;
RESULT 894
ID ADN19438 standard; protein; 789 AA.
DE Bacterial polypeptide #2091.
PN US2003233675-A1.
PD 18-DEC-2003.
PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
Query Match
Best Local Similarity 4.5%; Score 77; DB 8; Length 789;
Pred. No. 2.6e+02;
RESULT 895
ID AAB58428 standard; protein; 848 AA.
DE Lung cancer associated polypeptide sequence SEQ ID 766.
PN WO20005180-A2.
PD 21-SEP-2000.
PA (HUMA-) HUMAN GENOME SCI INC.
PA (ROSE/) ROSEN C A.
Query Match
Best Local Similarity 4.5%; Score 77; DB 3; Length 848;
Pred. No. 2.8e+02;
RESULT 896
ID ABR64269 standard; protein; 858 AA.
DE Angiogenesis protein BMO367.
PN WO2003027285-A1.
PD 03-APR-2003.
PA (BION-) BIONOMICS LTD.
Query Match
Best Local Similarity 4.5%; Score 77; DB 6; Length 858;
Pred. No. 2.9e+02;
RESULT 897
ID ADE54205 standard; protein; 858 AA.
DE Human Protein Q92598, SEQ ID No 8.
PN WO2003016475-A2.
PD 27-FEB-2003.
PA (GEHO-) GEN HOSPITAL CORP.
PA (FARB-) BAYER AG.
Query Match
Best Local Similarity 4.5%; Score 77; DB 7; Length 858;
Pred. No. 2.9e+02;
RESULT 898
ID ADE54209 standard; protein; 858 AA.
DE Human Protein Q92598, SEQ ID No 12.
PN WO2003016475-A2.
PD 27-FEB-2003.
PA (GEHO-) GEN HOSPITAL CORP.
PA (FARB-) BAYER AG.
Query Match
Best Local Similarity 4.5%; Score 77; DB 7; Length 858;
Pred. No. 2.9e+02;
RESULT 899
ID ADH09935 standard; protein; 858 AA.
DE Human host factor protein, SEQ ID No 463.
PN WO2003094847-A2.
PD 20-NOV-2003.
PA (UYEM-) UNIV EMORY.
Query Match
Best Local Similarity 4.5%; Score 77; DB 8; Length 858;
Pred. No. 2.9e+02;
RESULT 900
ID ADH09936 standard; protein; 858 AA.
DE Human host factor protein, SEQ ID No 464.
PN WO2003094847-A2.
PD 20-NOV-2003.
PA (UYEM-) UNIV EMORY.
Query Match
Best Local Similarity 4.5%; Score 77; DB 8; Length 858;
Pred. No. 2.9e+02;
RESULT 901
ID ADH09925 standard; protein; 858 AA.

DE Human host factor protein, SEQ ID No 453.
PN WO2003094847-A2.
PD 20-NOV-2003.
PA (UYEM-) UNIV EMORY.
Query Match
Best Local Similarity 4.5%; Score 77; DB 8; Length 858;
Pred. No. 2.9e+02;
RESULT 902
ID ADL22530 standard; protein; 858 AA.
DE Human cancer antigen-related hepl05 protein.
PN WO200402624-A1.
PD 11-MAR-2004.
PA (KUMA-) KUMAMOTO TECHNOLOGY & IND FOUND.
Query Match
Best Local Similarity 4.5%; Score 77; DB 8; Length 858;
Pred. No. 2.9e+02;
RESULT 903
ID AAY07110 standard; protein; 872 AA.
DE Colon cancer associated antigen precursor sequence.
PN WO9904265-A2.
PD 28-JAN-1999.
PA (LUDW-) LUDWIG INST CANCER RES.
Query Match
Best Local Similarity 4.5%; Score 77; DB 2; Length 872;
Pred. No. 3e+02;
RESULT 904
ID ADH09926 standard; protein; 872 AA.
DE Human host factor protein, SEQ ID No 454.
PN WO2003094847-A2.
PD 20-NOV-2003.
PA (UYEM-) UNIV EMORY.
Query Match
Best Local Similarity 4.5%; Score 77; DB 8; Length 872;
Pred. No. 3e+02;
RESULT 905
ID ABG91020 standard; protein; 878 AA.
DE Chlamydia trachomatis outer membrane protein I protein.
PN WO200262380-A2.
PD 15-AUG-2002.
PA (SMRK-) SMITHKLINE BEECHAM BIOLOGICALS.
Query Match
Best Local Similarity 4.5%; Score 77; DB 5; Length 878;
Pred. No. 3e+02;
RESULT 906
ID AAE23454 standard; protein; 878 AA.
DE Chlamydia trachomatis I2 Pmp1 protein.
PN WO200228998-A2.
PD 11-APR-2002.
PA (ANTE-) ANTEEX BIOLOGICS INC.
Query Match
Best Local Similarity 4.5%; Score 77; DB 5; Length 878;
Pred. No. 3e+02;
RESULT 907
ID ADP43790 standard; protein; 878 AA.
DE Chlamydia trachomatis immunogenic protein, SEQ ID No 85.
PN WO2003049762-A2.
PD 19-JUN-2003.
PA (CHIR-) CHIRON SPA.
Query Match
Best Local Similarity 4.5%; Score 77; DB 7; Length 878;
Pred. No. 3e+02;
RESULT 908
ID ADP43792 standard; protein; 878 AA.
DE Chlamydia trachomatis immunogenic protein, SEQ ID No 87.
PN WO2003049762-A2.
PD 19-JUN-2003.
PA (CHIR-) CHIRON SPA.
Query Match
Best Local Similarity 4.5%; Score 77; DB 7; Length 878;
Pred. No. 3e+02;
RESULT 909
ID ADP43728 standard; protein; 878 AA.
DE Chlamydia trachomatis immunogenic protein, SEQ ID No 23.
PN WO2003049762-A2.
PD 19-JUN-2003.
PA (CHIR-) CHIRON SPA.
Query Match
Best Local Similarity 4.5%; Score 77; DB 7; Length 878;
Pred. No. 3e+02;
RESULT 910
ID ADP43712 standard; protein; 878 AA.
DE Chlamydia trachomatis immunogenic protein, SEQ ID No 7.

PN WO2003049762-A2.
 PD 19-JUN-2003.
 PA (CHIR-) CHIRON SPA.
 Query Match 4.5%; Score 77; DB 7; Length 878;
 Best Local Similarity 23.5%; Pred. No. 3e+02;
 RESULT 911
 ID ABG19855 standard; protein; 1018 AA.
 DE Novel human diagnostic protein #19846.
 PN WO200175067-A2.
 PD 11-OCT-2001.
 PA (HYSE-) HYSEQ INC.
 Query Match 4.5%; Score 77; DB 4; Length 1018;
 Best Local Similarity 20.8%; Pred. No. 3.7e+02;
 RESULT 912
 ID ADB62754 standard; protein; 1085 AA.
 DE Human Protein NP_005063, SEQ ID NO 8687.
 PN WO2003016475-A2.
 PD 27-FEB-2003.
 PA (GEHO-) GEN HOSPITAL CORP.
 PA (FARB-) BAYER AG.
 Query Match 4.5%; Score 77; DB 7; Length 1085;
 Best Local Similarity 17.5%; Pred. No. 4.1e+02;
 RESULT 913
 ID ADB62758 standard; protein; 1085 AA.
 DE Human Protein NP_005063, SEQ ID NO 8691.
 PN WO2003016475-A2.
 PD 27-FEB-2003.
 PA (GEHO-) GEN HOSPITAL CORP.
 PA (FARB-) BAYER AG.
 Query Match 4.5%; Score 77; DB 7; Length 1085;
 Best Local Similarity 17.5%; Pred. No. 4.1e+02;
 RESULT 914
 ID ADB62762 standard; protein; 1085 AA.
 DE Human Protein NP_005063, SEQ ID NO 8695.
 PN WO2003016475-A2.
 PD 27-FEB-2003.
 PA (GEHO-) GEN HOSPITAL CORP.
 PA (FARB-) BAYER AG.
 Query Match 4.5%; Score 77; DB 7; Length 1085;
 Best Local Similarity 17.5%; Pred. No. 4.1e+02;
 RESULT 915
 ID ABM81779 standard; protein; 1085 AA.
 DE Tumeur-associated antigenic target (TAT) polypeptide PRO4814, SEQ:4582.
 PN WO2004030615-A2.
 PD 15-APR-2004.
 PA (GEHT-) GENENTECH INC.
 Query Match 4.5%; Score 77; DB 8; Length 1085;
 Best Local Similarity 17.5%; Pred. No. 4.1e+02;
 RESULT 916
 ID AAM83160 standard; protein; 1101 AA.
 DE Rat orphan tyrosine kinase receptor protein Rtk-7 (Tie-2).
 PN US5843749-A.
 PD 01-DEC-1998.
 PA (REGE-) REGENERON PHARM INC.
 Query Match 4.5%; Score 77; DB 2; Length 1101;
 Best Local Similarity 19.9%; Pred. No. 4.1e+02;
 RESULT 917
 ID AA45613 standard; protein; 1293 AA.
 DE Arabidopsis thaliana protein fragment SEQ ID NO: 57287.
 PN EP1033405-A2.
 PD 06-SEP-2000.
 Query Match 4.5%; Score 77; DB 3; Length 1293;
 Best Local Similarity 20.3%; Pred. No. 5.2e+02;
 RESULT 918
 ID AA45612 standard; protein; 1304 AA.
 DE Arabidopsis thaliana protein fragment SEQ ID NO: 57286.
 PN EP1033405-A2.
 PD 06-SEP-2000.
 Query Match 4.5%; Score 77; DB 3; Length 1304;
 Best Local Similarity 20.3%; Pred. No. 5.3e+02;
 RESULT 919
 ID AA45611 standard; protein; 1324 AA.
 DE Arabidopsis thaliana protein fragment SEQ ID NO: 57285.

PN EP1033405-A2.
 PD 06-SEP-2000.
 Query Match 4.5%; Score 77; DB 3; Length 1324;
 Best Local Similarity 20.3%; Pred. No. 5.4e+02;
 RESULT 920
 ID AAW19784 standard; protein; 1726 AA.
 DE Human multiple regulatory protein SPR6.
 PN WO9703087-A1.
 PD 30-JAN-1997.
 PA (UNMT-) UNIV MICHIGAN.
 Query Match 4.5%; Score 77; DB 2; Length 1726;
 Best Local Similarity 22.4%; Pred. No. 7.9e+02;
 RESULT 921
 ID AAU17511 standard; protein; 131 AA.
 DE Novel signal transduction pathway protein, Seq ID 1076.
 PN WO200154733-A1.
 PD 02-AUG-2001.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match 4.5%; Score 76.5; DB 4; Length 131;
 Best Local Similarity 25.2%; Pred. No. 22;
 RESULT 922
 ID ABO27216 standard; protein; 131 AA.
 DE Human signal transduction pathway component HMCFB47.
 PN US2003036505-A1.
 PD 20-FEB-2003.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match 4.5%; Score 76.5; DB 6; Length 131;
 Best Local Similarity 25.2%; Pred. No. 22;
 RESULT 923
 ID ADB94219 standard; protein; 131 AA.
 DE Human novel protein #453.
 PN US2002168711-A1.
 PD 14-NOV-2002.
 PA (ROSE/) ROSEN C A.
 PA (RUBE/) RUBEN S M.
 PA (BARA/) BARASH S C.
 Query Match 4.5%; Score 76.5; DB 7; Length 131;
 Best Local Similarity 25.2%; Pred. No. 22;
 RESULT 924
 ID AAG38906 standard; protein; 287 AA.
 DE Arabidopsis thaliana protein fragment SEQ ID NO: 48065.
 PN EP1033405-A2.
 PD 06-SEP-2000.
 Query Match 4.5%; Score 76.5; DB 3; Length 287;
 Best Local Similarity 22.0%; Pred. No. 67;
 RESULT 925
 ID AAG38905 standard; protein; 305 AA.
 DE Arabidopsis thaliana protein fragment SEQ ID NO: 48064.
 PN EP1033405-A2.
 PD 06-SEP-2000.
 Query Match 4.5%; Score 76.5; DB 3; Length 305;
 Best Local Similarity 22.0%; Pred. No. 74;
 RESULT 926
 ID AAG38904 standard; protein; 312 AA.
 DE Arabidopsis thaliana protein fragment SEQ ID NO: 48063.
 PN EP1033405-A2.
 PD 06-SEP-2000.
 Query Match 4.5%; Score 76.5; DB 3; Length 312;
 Best Local Similarity 22.0%; Pred. No. 76;
 RESULT 927
 ID AAG05059 standard; protein; 383 AA.
 DE Arabidopsis thaliana protein fragment SEQ ID NO: 1320.
 PN EP1033405-A2.
 PD 06-SEP-2000.
 Query Match 4.5%; Score 76.5; DB 3; Length 383;
 Best Local Similarity 21.3%; Pred. No. 1e+02;
 RESULT 928
 ID ABO63725 standard; protein; 396 AA.
 DE Klebsiella pneumoniae polypeptide seqid 10242.
 PN US610836-B1.
 PD 26-AUG-2003.
 PA (GENO-) GENOME THERAPEUTICS CORP.
 Query Match 4.5%; Score 76.5; DB 7; Length 396;

Best Local Similarity 25.0%; Pred. No. 1.1e+02;
RESULT 929
ID AAB80371 standard; protein; 414 AA.
DE Secreted protein encoded by gene #1.
PN WO200107459-A1.
PD 01-FEB-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 4.5%; Score 76.5; DB 4; Length 414;
Best Local Similarity 16.7%; Pred. No. 1.1e+02;
RESULT 930
ID ABG65290 standard; protein; 414 AA.
DE Human albumin fusion protein #1965.
PN WO200177137-A1.
PD 18-OCT-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 4.5%; Score 76.5; DB 5; Length 414;
Best Local Similarity 16.7%; Pred. No. 1.1e+02;
RESULT 931
ID ADL78557 standard; protein; 414 AA.
DE Albumin fusion protein related therapeutic protein X, SEQ ID No 2039.
PN US2004010134-A1.
PD 15-JUN-2004.
PA (ROSE/) ROSEN C A.
Query Match 4.5%; Score 76.5; DB 8; Length 414;
Best Local Similarity 16.7%; Pred. No. 1.1e+02;
RESULT 932
ID AAG05058 standard; protein; 449 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 1319.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 4.5%; Score 76.5; DB 3; Length 449;
Best Local Similarity 21.3%; Pred. No. 1.3e+02;
RESULT 933
ID AAG05057 standard; protein; 462 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 1318.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 4.5%; Score 76.5; DB 3; Length 462;
Best Local Similarity 21.3%; Pred. No. 1.3e+02;
RESULT 934
ID AAB38626 standard; protein; 471 AA.
DE Gene 38 human secreted protein homologous amino acid sequence #163.
PN WO200056882-A1.
PD 28-SEP-2000.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 4.5%; Score 76.5; DB 3; Length 471;
Best Local Similarity 19.3%; Pred. No. 1.4e+02;
RESULT 935
ID ADA55549 standard; protein; 570 AA.
DE Human protein, SEQ ID 3117.
PN EP1293569-A2.
PD 19-MAR-2003.
PA (HELI-) HELIX RES INST.
Query Match 4.5%; Score 76.5; DB 6; Length 570;
Best Local Similarity 20.5%; Pred. No. 1.8e+02;
RESULT 936
ID ADJ70708 standard; protein; 570 AA.
DE Human heat mitochondrial protein as a therapeutic target SeqID2514.
PN WO2003087768-A2.
PD 23-OCT-2003.
PA (MITO-) MITOKOR.
Query Match 4.5%; Score 76.5; DB 7; Length 570;
Best Local Similarity 20.5%; Pred. No. 1.8e+02;
RESULT 937
ID AAR32657 standard; protein; 657 AA.
DE PSI protein from C.melasecola ATCC 17965.
PN WO9303158-A1.
PD 18-FEB-1993.
PA (ORSA-) ORSAN.
Query Match 4.5%; Score 76.5; DB 2; Length 657;

Best Local Similarity 20.4%; Pred. No. 2.2e+02;
RESULT 938
ID ADM29350 standard; protein; 753 AA.
DE Human novel protein NOV19a.
PN WO2003064628-A2.
PD 07-AUG-2003.
PA (CURA-) CURAGEN CORP.
Query Match 4.5%; Score 76.5; DB 7; Length 753;
Best Local Similarity 21.7%; Pred. No. 2.7e+02;
RESULT 939
ID ADQ59433 standard; protein; 967 AA.
DE Human cancer-associated (CA) protein sequence SEQ ID NO:69.
PN WO2004058288-A1.
PD 15-JUL-2004.
PA (SAGR-) SAGRES DISCOVERY INC.
Query Match 4.5%; Score 76.5; DB 8; Length 967;
Best Local Similarity 19.3%; Pred. No. 3.9e+02;
RESULT 940
ID ADN19491 standard; protein; 1000 AA.
DE Bacterial polypeptide #2144.
PN US2003233675-A1.
PD 18-DEC-2003.
PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
Query Match 4.5%; Score 76.5; DB 8; Length 1000;
Best Local Similarity 26.4%; Pred. No. 4.1e+02;
RESULT 941
ID ABB61540 standard; protein; 1191 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 11412.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 4.5%; Score 76.5; DB 4; Length 1191;
Best Local Similarity 19.8%; Pred. No. 5.2e+02;
RESULT 942
ID ADH48824 standard; protein; 1356 AA.
DE NOV45B protein sequence, SEQ ID 108.
PN WO200268652-A2.
PD 06-SEP-2002.
PA (CURA-) CURAGEN CORP.
Query Match 4.5%; Score 76.5; DB 5; Length 1356;
Best Local Similarity 21.3%; Pred. No. 6.3e+02;
RESULT 943
ID ABB64069 standard; protein; 2009 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 18999.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 4.5%; Score 76.5; DB 4; Length 2009;
Best Local Similarity 21.0%; Pred. No. 1.1e+03;
RESULT 944
ID ADU11680 standard; protein; 265 AA.
DE Rice protein modulated by post-transcriptional gene silencing SeqID 316.
PN US2003135888-A1.
PD 17-JUL-2003.
PA (ZHU/) ZHU T.
PA (WANG/) WANG X.
PA (CHAN/) CHANG H.
PA (BRIG/) BRIGGS S P.
PA (COOP/) COOPER B.
PA (GLAZ/) GLAZEBROOK J.
PA (GOFF/) GOLF S A.
PA (KATA/) KATAGIRI F.
PA (KEEP/) KEEPS J.
PA (MOUG/) MOUGHAMER T.
PA (PROV/) PROVART N.
PA (RICK/) RICKER D.
Query Match 4.5%; Score 76; DB 7; Length 265;
Best Local Similarity 19.1%; Pred. No. 68;
RESULT 945

ID ABU15068 standard; protein; 277 AA.
 DE Protein encoded by Prokaryotic essential gene #595.
 PN WO20027183-A2.
 PD 03-OCT-2002.
 PA (ELIT-) ELITRA PHARM INC.
 Query Match 4.5%; Score 76; DB 6; Length 277;
 Best Local Similarity 23.6%; Pred. No. 72;
 RESULT 946
 ID ABG30302 standard; protein; 315 AA.
 DE Novel human diagnostic protein #30293.
 PN WO200175067-A2.
 PD 11-OCT-2001.
 PA (HYSE-) HYSEQ INC.
 Query Match 4.5%; Score 76; DB 4; Length 315;
 Best Local Similarity 22.3%; Pred. No. 87;
 RESULT 947
 ID ABU10305 standard; protein; 357 AA.
 DE Chicken bves (cbves) carboxyl domain.
 PN US6503540-B1.
 PD 07-JAN-2003.
 PA (RESE/) RESE D E.
 PA (BADE/) BADER D M.
 Query Match 4.5%; Score 76; DB 7; Length 357;
 Best Local Similarity 23.2%; Pred. No. 1e+02;
 RESULT 948
 ID ABB49335 standard; protein; 375 AA.
 DE *Listeria monocytogenes* protein #2039.
 PN WO200177335-A2.
 PD 18-OCT-2001.
 PA (INSP) INST PASTEUR.
 Query Match 4.5%; Score 76; DB 5; Length 375;
 Best Local Similarity 22.2%; Pred. No. 1.1e+02;
 RESULT 949
 ID ABG10732 standard; protein; 380 AA.
 DE Novel human diagnostic protein #10723.
 PN WO200175067-A2.
 PD 11-OCT-2001.
 PA (HYSE-) HYSEQ INC.
 Query Match 4.5%; Score 76; DB 4; Length 380;
 Best Local Similarity 19.8%; Pred. No. 1.1e+02;
 RESULT 950
 ID AAR83416 standard; protein; 402 AA.
 DE *Humicola insolens* endoglucanase variant I310D.
 PN WO9524471-A1.
 PD 14-SEP-1995.
 PA (NOVO) NOVO-NORDISK AS.
 Query Match 4.5%; Score 76; DB 2; Length 402;
 Best Local Similarity 18.5%; Pred. No. 1.2e+02;
 RESULT 951
 ID ABB61459 standard; protein; 450 AA.
 DE *Drosophila melanogaster* polypeptide SEQ ID NO 11169.
 PN WO200171042-A2.
 PD 27-SEP-2001.
 PA (PEKE) PE CORP NY.
 Query Match 4.5%; Score 76; DB 4; Length 450;
 Best Local Similarity 19.7%; Pred. No. 1.5e+02;
 RESULT 952
 ID ABR39455 standard; protein; 462 AA.
 DE *Staphylococcus epidermidis* ORF amino acid sequence SEQ ID NO:4300.
 PN US6380370-B1.
 PD 30-APR-2002.
 PA (GENO-) GENOME THERAPEUTICS CORP.
 Query Match 4.5%; Score 76; DB 5; Length 462;
 Best Local Similarity 23.5%; Pred. No. 1.5e+02;
 RESULT 953
 ID ADS05296 standard; protein; 466 AA.
 DE *Staphylococcus epidermis* polypeptide seqid 4591.
 PN US2004147734-A1.
 PD 29-JUN-2004.
 PA (DOUC/) DOUCETTE-STAMM L.
 PA (BUSH/) BUSH D.
 Query Match 4.5%; Score 76; DB 8; Length 462;
 Best Local Similarity 23.5%; Pred. No. 1.5e+02;
 RESULT 954
 ID ABU10301 standard; protein; 487 AA.
 DE Fragment of chicken bves (cbves).
 PN US6503540-B1.
 PD 07-JAN-2003.
 PA (RESE/) RESE D E.
 PA (BADE/) BADER D M.
 Query Match 4.5%; Score 76; DB 7; Length 487;
 Best Local Similarity 23.2%; Pred. No. 1.6e+02;
 RESULT 955
 ID AAB00158 standard; protein; 507 AA.
 DE sCD4-SCFv(17b) HIV single chain antibody fusion protein.
 PN WO200055207-A1.
 PD 21-SEP-2000.
 PA (USSH) US NAT INST OF HEALTH.
 Query Match 4.5%; Score 76; DB 3; Length 507;
 Best Local Similarity 27.8%; Pred. No. 1.7e+02;
 RESULT 956
 ID AAY37049 standard; protein; 518 AA.
 DE Protein involved in intermediate metabolism of sugars and/or cofactors.
 PN WO9928475-A2.
 PD 10-JUN-1999.
 PA (GEST) GENSET.
 Query Match 4.5%; Score 76; DB 2; Length 518;
 Best Local Similarity 20.8%; Pred. No. 1.8e+02;
 RESULT 957
 ID ABB61505 standard; protein; 608 AA.
 DE *Drosophila melanogaster* polypeptide SEQ ID NO 11307.
 PN WO200171042-A2.
 PD 27-SEP-2001.
 PA (PEKE) PE CORP NY.
 Query Match 4.5%; Score 76; DB 4; Length 608;
 Best Local Similarity 18.8%; Pred. No. 2.2e+02;
 RESULT 958
 ID ADR05763 standard; protein; 770 AA.
 DE Mouse Notch2-like protein.
 PN US2004152120-A1.
 PD 05-AUG-2004.
 PA (APPL-) APPLERA CORP.
 Query Match 4.5%; Score 76; DB 8; Length 770;
 Best Local Similarity 20.2%; Pred. No. 3.1e+02;
 RESULT 959
 ID ADN26806 standard; protein; 783 AA.
 DE Bacterial polypeptide #9459.
 PN US200323675-A1.
 PD 18-DEC-2003.
 PA (CAOY/) CAO Y.
 PA (HINK/) HINKLE G J.
 PA (SLAT/) SLATER S C.
 PA (CHEN/) CHEN X.
 PA (GOLD/) GOLDMAN B S.
 Query Match 4.5%; Score 76; DB 8; Length 783;
 Best Local Similarity 27.1%; Pred. No. 3.2e+02;
 RESULT 960
 ID AAR41867 standard; protein; 811 AA.
 DE Mouse OSF-2.
 PN EP562508-A2.
 PD 29-SEP-1993.
 PA (PARH) HOECHST JAPAN LTD.
 Query Match 4.5%; Score 76; DB 2; Length 811;
 Best Local Similarity 20.5%; Pred. No. 3.4e+02;
 RESULT 961
 ID AAU79824 standard; protein; 811 AA.
 DE OSF-2 protein associated protein #2.
 PN WO200220055-A1.
 PD 14-MAR-2002.
 PA (SUNR) SUNTORY LTD.
 PA (SUNR) SUNTORY BIOMEDICAL RES LTD.
 Query Match 4.5%; Score 76; DB 5; Length 811;
 Best Local Similarity 20.5%; Pred. No. 3.4e+02;
 RESULT 962
 ID ADU76125 standard; protein; 811 AA.
 DE Marker gene related amino acid sequence SEQ ID NO:1377.

PN EPI394274-A2.
PD 03-MAR-2004.
PA (GENO-) GENOX RES INC. 4.5%; Score 76; DB 8; Length 811;
Query Match
Best Local Similarity 20.5%; Pred. No. 3.4e+02;
RESULT 963
ID ADN19903 standard; protein; 1474 AA.
DE Bacterial polypeptide #556.
PN US200323675-A1.
PD 18-DEC-2003.
PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
Query Match
Best Local Similarity 4.5%; Score 76; DB 8; Length 1474;
Best Local Similarity 21.4%; Pred. No. 8e+02;
RESULT 964
ID ABR47539 standard; protein; 1855 AA.
DE Breast cancer associated protein sequence SEQ ID NO:315.
PN WO2003004989-A2.
PD 16-JAN-2003.
PA (MITL-) MILLENTUM PHARM INC.
Query Match
Best Local Similarity 4.5%; Score 76; DB 6; Length 1855;
Best Local Similarity 22.8%; Pred. No. 1.1e+03;
RESULT 965
ID ADN04056 standard; protein; 1855 AA.
DE Antiproliferic protein sequence #223.
PN WO2004028479-A2.
PD 08-APR-2004.
PA (GENTH) GENENTECH INC.
Query Match
Best Local Similarity 4.5%; Score 76; DB 8; Length 1855;
Best Local Similarity 22.8%; Pred. No. 1.1e+03;
RESULT 966
ID AAU04090 standard; protein; 2008 AA.
DE Human cadherin-like asymmetry protein, CLASP-4.
PN WO200142294-A2.
PD 14-JUN-2001.
PA (ARBO-) ARBOR VITA CORP.
Query Match
Best Local Similarity 4.5%; Score 76; DB 4; Length 2008;
Best Local Similarity 17.2%; Pred. No. 1.2e+03;
RESULT 967
ID ABG61703 standard; protein; 2008 AA.
DE Human cadherin-like asymmetry protein-4 (CLASP-4).
PN WO20023117-A2.
PD 18-APR-2002.
PA (ARBO-) ARBOR VITA CORP.
PA (GARM/) GARMAN J D.
PA (CAND/) CANDIA A F.
Query Match
Best Local Similarity 4.5%; Score 76; DB 5; Length 2008;
Best Local Similarity 17.2%; Pred. No. 1.2e+03;
RESULT 968
ID ABR43636 standard; protein; 2008 AA.
DE Human CLASP-4 protein SEQ ID NO:29.
PN WO2003025120-A2.
PD 27-MAR-2003.
PA (ARBO-) ARBOR VITA CORP.
Query Match
Best Local Similarity 4.5%; Score 76; DB 6; Length 2008;
Best Local Similarity 17.2%; Pred. No. 1.2e+03;
RESULT 969
ID ADC79417 standard; protein; 2008 AA.
DE Human CLASP-4 full-length protein.
PN US2002068302-A1.
PD 06-JUN-2002.
PA (LUPS/) LUT P S.
PA (GARM/) GARMAN J D.
PA (CAND/) CANDIA A F.
Query Match
Best Local Similarity 4.5%; Score 76; DB 7; Length 2008;
Best Local Similarity 17.2%; Pred. No. 1.2e+03;
RESULT 970
ID ABB59371 standard; protein; 4601 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 4905.
PN WO200171042-A2.

PD 27-SEP-2001.
PA (PERE) PE CORP NY.
Query Match
Best Local Similarity 4.5%; Score 76; DB 4; Length 4601;
RESULT 971
ID ABB44610 standard; protein; 137 AA.
DE Human wound healing related polypeptide SEQ ID NO 93.
PN CA2325226-A1.
PD 17-MAY-2001.
PA (SWIT-) SWITCH BIOTECH AG.
Query Match
Best Local Similarity 4.5%; Score 75.5; DB 4; Length 137;
Best Local Similarity 29.5%; Pred. No. 30;
RESULT 972
ID ADJ92183 standard; protein; 137 AA.
DE Human hair keratin-associated-protein SEQ ID NO:42.
PN WO2001042387-A1.
PD 22-MAY-2003.
PA (UYKE-) UNIV KEIO.
PA (NIPI-) JAPAN SOC PROMOTION SCI.
Query Match
Best Local Similarity 4.5%; Score 75.5; DB 7; Length 137;
Best Local Similarity 29.5%; Pred. No. 30;
RESULT 973
ID ABU26522 standard; protein; 213 AA.
DE Protein encoded by Prokaryotic essential gene #12049.
PN WO200271183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match
Best Local Similarity 4.5%; Score 75.5; DB 6; Length 213;
Best Local Similarity 24.2%; Pred. No. 56;
RESULT 974
ID AAU79178 standard; protein; 304 AA.
DE Human partial tandem PH-domain-containing protein-2 (TAPP2) protein.
PN WO200212276-A2.
PD 14-FEB-2002.
PA (MEDT-) MEDICAL RES COUNCIL.
Query Match
Best Local Similarity 4.5%; Score 75.5; DB 5; Length 304;
Best Local Similarity 25.2%; Pred. No. 93;
RESULT 975
ID AAY96079 standard; protein; 323 AA.
DE Secretible angiogenesis inhibitor p27(25-93)-p16 fusion W9.
PN WO200052158-A1.
PD 08-SEP-2000.
PA (CEML-) CELLS GENESYS INC.
PA (MITO-) MITOXIN INC.
Query Match
Best Local Similarity 4.5%; Score 75.5; DB 3; Length 323;
Best Local Similarity 24.0%; Pred. No. 1e+02;
RESULT 976
ID ABR40240 standard; protein; 355 AA.
DE Human TAPP2.
PN WO2003011901-A1.
PD 13-FEB-2003.
PA (UYDU-) UNIV DUNDEE.
Query Match
Best Local Similarity 4.5%; Score 75.5; DB 6; Length 355;
Best Local Similarity 25.2%; Pred. No. 1.2e+02;
RESULT 977
ID AAU79175 standard; protein; 357 AA.
DE Partial human tandem PH-domain-containing protein-2 (TAPP2) protein.
PN WO200212276-A2.
PD 14-FEB-2002.
PA (MEDT-) MEDICAL RES COUNCIL.
Query Match
Best Local Similarity 4.5%; Score 75.5; DB 5; Length 357;
Best Local Similarity 25.2%; Pred. No. 1.2e+02;
RESULT 978
ID ABU00587 standard; protein; 363 AA.
DE S. pneumoniae type 4 strain protein from coding region #154.
PN WO200277021-A2.
PD 03-OCT-2002.
PA (CHIR-) CHIRON SPA.
PA (GENO-) INST GENOMIC RES.
Query Match
Best Local Similarity 4.5%; Score 75.5; DB 6; Length 363;
Best Local Similarity 19.9%; Pred. No. 1.2e+02;
RESULT 979
ID ADW92069 standard; protein; 363 AA.

DE S pneumoniae antigenic protein sequence SegID266.
 PN WO2004020609-A2.
 PD 11-MAR-2004.
 PA (TUFT) UNIV TUFTS.
 Query Match 4.5%; Score 75.5; DB 8; Length 363;
 Best Local Similarity 19.9%; Pred. No. 1.2e+02;
 RESULT 980
 ID AAY81674 standard; protein; 364 AA.
 DE Streptococcus pneumoniae protein sequence ID211 - 4127.2.
 PN WO200006737-A2.
 PD 10-FEB-2000.
 PA (MICR-) MICROBIAL TECHNIQS LTD.
 Query Match 4.5%; Score 75.5; DB 3; Length 364;
 Best Local Similarity 19.9%; Pred. No. 1.2e+02;
 RESULT 981
 ID ADX34683 standard; protein; 376 AA.
 DE Acinetobacter baumannii protein #1844.
 PN US6562958-B1.
 PD 13-MAY-2003.
 PA (GENO-) GENOME THERAPEUTICS CORP.
 Query Match 4.5%; Score 75.5; DB 6; Length 376;
 Best Local Similarity 21.1%; Pred. No. 1.3e+02;
 RESULT 982
 ID AAG29637 standard; protein; 403 AA.
 DE Arabidopsis thaliana protein fragment SEQ ID NO: 35297.
 PN EP1033405-A2.
 PD 06-SEP-2000.
 PA
 Query Match 4.5%; Score 75.5; DB 3; Length 403;
 Best Local Similarity 21.5%; Pred. No. 1.4e+02;
 RESULT 983
 ID AAG29636 standard; protein; 410 AA.
 DE Arabidopsis thaliana protein fragment SEQ ID NO: 35296.
 PN EP1033405-A2.
 PD 06-SEP-2000.
 PA
 Query Match 4.5%; Score 75.5; DB 3; Length 410;
 Best Local Similarity 21.5%; Pred. No. 1.4e+02;
 RESULT 984
 ID ABB91777 standard; protein; 414 AA.
 DE Hericicidally active polypeptide SEQ ID NO 988.
 PN WO200210210-A2.
 PD 07-FEB-2002.
 PA (FARB) BAYER AG.
 Query Match 4.5%; Score 75.5; DB 5; Length 414;
 Best Local Similarity 21.8%; Pred. No. 1.4e+02;
 RESULT 985
 ID ABB81055 standard; protein; 525 AA.
 DE Tumour-associated antigenic target (TAT) polypeptide PRO81759, SEQ:2729.
 PN WO2004030615-A2.
 PD 15-APR-2004.
 PA (GETH) GENENTECH INC.
 Query Match 4.5%; Score 75.5; DB 8; Length 525;
 Best Local Similarity 22.6%; Pred. No. 2e+02;
 RESULT 986
 ID ADB40118 standard; protein; 690 AA.
 DE Human NOV9a protein - SEQ ID 24.
 PN WO2003064589-A2.
 PD 07-AUG-2003.
 PA (CURA-) CURAGEN CORP.
 Query Match 4.5%; Score 75.5; DB 7; Length 690;
 Best Local Similarity 23.6%; Pred. No. 3e+02;
 RESULT 987
 ID ADM19103 standard; protein; 754 AA.
 DE Bacterial polypeptide #1736.
 PN US2003233675-A1.
 PD 18-DEC-2003.
 PA (CAOY/) CAO Y.
 PA (HINK/) HINKLE G J.
 PA (SLAT/) SLATER S C.
 PA (CHEN/) CHEN X.
 PA (GOLD/) GOLDMAN B S.
 Query Match 4.5%; Score 75.5; DB 8; Length 754;
 Best Local Similarity 18.5%; Pred. No. 3.4e+02;
 RESULT 988

ID ADI45095 standard; protein; 1162 AA.
 DE Rice isoprenoid biosynthesis-associated protein #13.
 PN US2004010815-A1.
 PD 15-JAN-2004.
 PA (LANG/) LANGE B M.
 PA (GHAS/) GHASSEMIAN M.
 PA (BRIG/) BRIGGS S P.
 PA (COOP/) COOPER B.
 PA (GLAZ/) GLAZERBOOK J.
 PA (GOLF/) GOLF S A.
 PA (KATA/) KATAGIRI F.
 PA (KREP/) KREPS J.
 PA (MOUG/) MUGHAMER T.
 PA (PROV/) PROVART N.
 PA (RICK/) RICK D.
 PA (ZHUT/) ZHU T.
 Query Match 4.5%; Score 75.5; DB 8; Length 1162;
 Best Local Similarity 18.4%; Pred. No. 6.4e+02;
 RESULT 989
 ID ADS44198 standard; protein; 1264 AA.
 DE Bacterial polypeptide #22628.
 PN US2003233675-A1.
 PD 18-DEC-2003.
 PA (CAOY/) CAO Y.
 PA (HINK/) HINKLE G J.
 PA (SLAT/) SLATER S C.
 PA (CHEN/) CHEN X.
 PA (GOLD/) GOLDMAN B S.
 Query Match 4.5%; Score 75.5; DB 8; Length 1264;
 Best Local Similarity 20.7%; Pred. No. 7.4e+02;
 RESULT 990
 ID AAY37230 standard; protein; 148 AA.
 DE Chlamydia trachomatis cellular envelope protein.
 PN WO9928475-A2.
 PD 10-JUN-1999.
 PA (BEST) GENSET.
 Query Match 4.4%; Score 75; DB 2; Length 148;
 Best Local Similarity 29.2%; Pred. No. 37;
 RESULT 991
 ID AAW79397 standard; protein; 226 AA.
 DE Staphylococcus aureus protein.
 PN WO9823738-A2.
 PD 04-JUN-1998.
 PA (SMIK) SMITHKLINE BEECHAM CORP.
 Query Match 4.4%; Score 75; DB 2; Length 226;
 Best Local Similarity 24.3%; Pred. No. 68;
 RESULT 992
 ID ABU16213 standard; protein; 293 AA.
 DE Protein encoded by Prokaryotic essential gene #1740.
 PN WO200277183-A2.
 PD 03-OCT-2002.
 PA (ELIT-) ELITRA PHARM INC.
 Query Match 4.4%; Score 75; DB 6; Length 293;
 Best Local Similarity 24.3%; Pred. No. 99;
 RESULT 993
 ID ABM72927 standard; protein; 293 AA.
 DE Staphylococcus aureus protein #2167.
 PN WO200294868-A2.
 PD 28-NOV-2002.
 PA (CHIR-) CHIRON SPA.
 Query Match 4.4%; Score 75; DB 6; Length 293;
 Best Local Similarity 24.3%; Pred. No. 99;
 RESULT 994
 ID ABB71061 standard; protein; 345 AA.
 DE Drosophila melanogaster polypeptide SEQ ID NO 39975.
 PN WO2001171042-A2.
 PD 27-SEP-2001.
 PA (PEKE) PE CORP NY.
 Query Match 4.4%; Score 75; DB 4; Length 345;
 Best Local Similarity 21.1%; Pred. No. 1.3e+02;
 RESULT 995
 ID AAR83405 standard; protein; 402 AA.
 DE Humicola insolens endoglucanase variant N890.

PN W09524471-A1.
PD 14-SEP-1995.
PA (NOVO) NOVO-NORDISK AS.
Query Match 4.4%; Score 75; DB 2; Length 402;
Best Local Similarity 18.2%; Pred. No. 1.6e+02;
RESULT 996
ID AAR83398 standard; protein; 402 AA.
DE Humicola insolens endoglucanase.
PN W09524471-A1.
PD 14-SEP-1995.
PA (NOVO) NOVO-NORDISK AS.
Query Match 4.4%; Score 75; DB 2; Length 402;
Best Local Similarity 18.2%; Pred. No. 1.6e+02;
RESULT 997
ID AAR83411 standard; protein; 402 AA.
DE Humicola insolens endoglucanase variant S37W + P39W.
PN W09524471-A1.
PD 14-SEP-1995.
PA (NOVO) NOVO-NORDISK AS.
Query Match 4.4%; Score 75; DB 2; Length 402;
Best Local Similarity 18.2%; Pred. No. 1.6e+02;
RESULT 998
ID AAR83410 standard; protein; 402 AA.
DE Humicola insolens endoglucanase variant E202A.
PN W09524471-A1.
PD 14-SEP-1995.
PA (NOVO) NOVO-NORDISK AS.
Query Match 4.4%; Score 75; DB 2; Length 402;
Best Local Similarity 18.2%; Pred. No. 1.6e+02;
RESULT 999
ID AAR83417 standard; protein; 402 AA.
DE Humicola insolens endoglucanase variant E150Q.
PN W09524471-A1.
PD 14-SEP-1995.
PA (NOVO) NOVO-NORDISK AS.
Query Match 4.4%; Score 75; DB 2; Length 402;
Best Local Similarity 18.2%; Pred. No. 1.6e+02;
RESULT 1000
ID AAR83409 standard; protein; 402 AA.
DE Humicola insolens endoglucanase variant Q399N.
PN W09524471-A1.
PD 14-SEP-1995.
PA (NOVO) NOVO-NORDISK AS.
Query Match 4.4%; Score 75; DB 2; Length 402;
Best Local Similarity 18.2%; Pred. No. 1.6e+02;
RESULT 1001
ID AAR83419 standard; protein; 402 AA.
DE Humicola insolens endoglucanase variant M198L.
PN W09524471-A1.
PD 14-SEP-1995.
PA (NOVO) NOVO-NORDISK AS.
Query Match 4.4%; Score 75; DB 2; Length 402;
Best Local Similarity 18.2%; Pred. No. 1.6e+02;
RESULT 1002
ID AAR83407 standard; protein; 402 AA.
DE Humicola insolens endoglucanase variant H123N.
PN W09524471-A1.
PD 14-SEP-1995.
PA (NOVO) NOVO-NORDISK AS.
Query Match 4.4%; Score 75; DB 2; Length 402;
Best Local Similarity 18.2%; Pred. No. 1.6e+02;
RESULT 1003
ID AAR83412 standard; protein; 402 AA.
DE Humicola insolens endoglucanase variant M142E.
PN W09524471-A1.
PD 14-SEP-1995.
PA (NOVO) NOVO-NORDISK AS.
Query Match 4.4%; Score 75; DB 2; Length 402;
Best Local Similarity 18.2%; Pred. No. 1.6e+02;
RESULT 1004
ID AAR83418 standard; protein; 402 AA.
DE Humicola insolens endoglucanase variant E334K.
PN W09524471-A1.

PD 14-SEP-1995.
PA (NOVO) NOVO-NORDISK AS.
Query Match 4.4%; Score 75; DB 2; Length 402;
Best Local Similarity 18.2%; Pred. No. 1.6e+02;
RESULT 1005
ID AAR83408 standard; protein; 402 AA.
DE Humicola insolens endoglucanase variant T385N.
PN W09524471-A1.
PD 14-SEP-1995.
PA (NOVO) NOVO-NORDISK AS.
Query Match 4.4%; Score 75; DB 2; Length 402;
Best Local Similarity 18.2%; Pred. No. 1.6e+02;
RESULT 1006
ID AAV67390 standard; protein; 415 AA.
DE Endoglucanase enzyme protein sequence for use in a liquid detergent.
PN EP63311-A1.
PD 11-JAN-1995.
PA (PROC) PROCTER & GAMBLE CO.
Query Match 4.4%; Score 75; DB 2; Length 415;
Best Local Similarity 17.6%; Pred. No. 1.6e+02;
RESULT 1007
ID AAM17926 standard; protein; 415 AA.
DE Abrading endoglucanase.
PN W09718286-A1.
PD 22-MAY-1997.
PA (NOVO) NOVO-NORDISK AS.
Query Match 4.4%; Score 75; DB 2; Length 415;
Best Local Similarity 18.2%; Pred. No. 1.6e+02;
RESULT 1008
ID AAY56385 standard; protein; 415 AA.
DE Cellulolytic enzyme EGI amino acid sequence.
PN W09957260-A1.
PD 11-NOV-1999.
PA (PROC) PROCTER & GAMBLE CO.
Query Match 4.4%; Score 75; DB 3; Length 415;
Best Local Similarity 17.6%; Pred. No. 1.6e+02;
RESULT 1009
ID AAM17928 standard; protein; 435 AA.
DE Streak-reducing endoglucanase.
PN W09718286-A1.
PD 22-MAY-1997.
PA (NOVO) NOVO-NORDISK AS.
Query Match 4.4%; Score 75; DB 2; Length 435;
Best Local Similarity 17.6%; Pred. No. 1.8e+02;
RESULT 1010
ID AAG90523 standard; protein; 453 AA.
DE C glucanucum protein fragment SEQ ID NO: 4277.
PN EP1108790-A2.
PD 20-JUN-2001.
PA (KYOW) KYOWA HAKKO KOGYO KK.
Query Match 4.4%; Score 75; DB 4; Length 453;
Best Local Similarity 29.7%; Pred. No. 1.9e+02;
RESULT 1011
ID ABB53743 standard; protein; 461 AA.
DE Lactococcus lactis protein yeeG.
PN FR2807446-A1.
PD 12-OCT-2001.
PA (INRG) INRA INST NAT RECH AGRONOMICUE.
Query Match 4.4%; Score 75; DB 5; Length 461;
Best Local Similarity 20.8%; Pred. No. 1.9e+02;
RESULT 1012
ID ADB64684 standard; protein; 467 AA.
DE Human protein encoded by clone NESOP20004520.
PN EP1308459-A2.
PD 07-MAY-2003.
PA (HELT-) HELIX RES INST.
Query Match 4.4%; Score 75; DB 7; Length 467;
Best Local Similarity 21.2%; Pred. No. 1.9e+02;
RESULT 1013
ID ABB70728 standard; protein; 472 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 38976.
PN W0200171042-A2.

PD 27-SEP-2001.
PA (PERKE) PE CORP NY.
Query Match 4.4%; Score 75; DB 4; Length 472;
Best Local Similarity 20.2%; Pred. No. 2e+02;
RESULT 1014
ID AAB3136 standard; protein; 536 AA.
DE Macaca mulatta rhadinovirus 17577 RRV ORF17 protein SEQ ID NO:29.
PD WO200028040-A2.
PD 18-MAY-2000.
PA (UNOR-) UNIV OREGON HEALTH SCI.
Query Match 4.4%; Score 75; DB 3; Length 536;
Best Local Similarity 23.9%; Pred. No. 2.4e+02;
RESULT 1015
ID ADA5568 standard; protein; 536 AA.
DE Human protein, SEQ ID 3136.
PD EP1293569-A2.
PD 19-MAR-2003.
PA (HELI-) HELIX RES INST.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
Query Match 4.4%; Score 75; DB 6; Length 536;
Best Local Similarity 20.0%; Pred. No. 2.4e+02;
RESULT 1016
ID AAB12455 standard; protein; 617 AA.
DE Human HSLY1 protein SEQ ID NO:6.
PD CN1250095-A.
PD 12-APR-2000.
PA (XINH-) XINHUNGPU FUDAN GENE ENG CO LTD SHANGHA.
Query Match 4.4%; Score 75; DB 3; Length 617;
Best Local Similarity 23.0%; Pred. No. 2.9e+02;
RESULT 1017
ID AAM4162 standard; protein; 637 AA.
DE Novel protein from rat primary culture astrocyte.
PD JP10025300-A.
PD 27-JAN-1998.
PA (DAIN) DAINIPPON PHARM CO LTD.
PA (TOYA/) TOYAMA M.
Query Match 4.4%; Score 75; DB 2; Length 637;
Best Local Similarity 23.2%; Pred. No. 3e+02;
RESULT 1018
ID AAB12456 standard; protein; 637 AA.
DE RSLYIN protein sequence.
PD CN1250095-A.
PD 12-APR-2000.
PA (XINH-) XINHUNGPU FUDAN GENE ENG CO LTD SHANGHA.
Query Match 4.4%; Score 75; DB 3; Length 637;
Best Local Similarity 23.2%; Pred. No. 3e+02;
RESULT 1019
ID AAY76597 standard; protein; 645 AA.
DE Human ovarian tumor EST fragment encoded protein 93.
PD DE19817557-A1.
PD 21-OCT-1999.
PA (META-) METAGEN GBS GENOMFORSCHUNG MBH.
Query Match 4.4%; Score 75; DB 2; Length 645;
Best Local Similarity 23.0%; Pred. No. 3.1e+02;
RESULT 1020
ID ABG07430 standard; protein; 661 AA.
DE Novel human diagnostic protein #7421.
PD WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match 4.4%; Score 75; DB 4; Length 661;
Best Local Similarity 20.7%; Pred. No. 3.2e+02;
RESULT 1021
ID AAB13638 standard; protein; 866 AA.
DE C. trachomatis pmp1 gene amino terminus minus signal sequence protein.
PD WO200034483-A2.
PD 15-JUN-2000.
PA (CORI-) CORIXA CORP.
Query Match 4.4%; Score 75; DB 3; Length 866;
Best Local Similarity 29.2%; Pred. No. 4.7e+02;
RESULT 1022
ID AAG83206 standard; protein; 866 AA.
DE Protein encoded by Chlamydia trachomatis pmp1 gene.
PD WO200140474-A2.
PD 07-JUN-2001.
PA (CORI-) CORIXA CORP.
Query Match 4.4%; Score 75; DB 4; Length 866;
Best Local Similarity 29.2%; Pred. No. 4.7e+02;
RESULT 1023
ID ABB94177 standard; protein; 866 AA.
DE Chlamydia protein sequence SEQ ID NO:189.
PD WO200208267-A2.
PD 31-JAN-2002.
PA (CORI-) CORIXA CORP.
Query Match 4.4%; Score 75; DB 5; Length 866;
Best Local Similarity 29.2%; Pred. No. 4.7e+02;
RESULT 1024
ID ABB91601 standard; protein; 970 AA.
DE Herbicidially active polypeptide SEQ ID NO 812.
PD WO200210210-A2.
PD 07-FEB-2002.
PA (FARB) BAYER AG.
Query Match 4.4%; Score 75; DB 5; Length 970;
Best Local Similarity 19.7%; Pred. No. 5.6e+02;
RESULT 1025
ID ABG25739 standard; protein; 1155 AA.
DE Novel human diagnostic protein #25730.
PD WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match 4.4%; Score 75; DB 4; Length 1155;
Best Local Similarity 20.7%; Pred. No. 7.2e+02;
RESULT 1026
ID AAB24892 standard; peptide; 1199 AA.
DE Plant SDF encoded polypeptide sequence SEQ List 1 NO:403.
PD WO200040695-A2.
PD 13-JUL-2000.
PA (CERE-) CERES INC.
Query Match 4.4%; Score 75; DB 3; Length 1199;
Best Local Similarity 19.7%; Pred. No. 7.5e+02;
RESULT 1027
ID AAB24891 standard; peptide; 1210 AA.
DE Plant SDF encoded polypeptide sequence SEQ List 1 NO:402.
PD WO200040695-A2.
PD 13-JUL-2000.
PA (CERE-) CERES INC.
Query Match 4.4%; Score 75; DB 3; Length 1210;
Best Local Similarity 19.7%; Pred. No. 7.6e+02;
RESULT 1028
ID AAM19783 standard; protein; 1248 AA.
DE Human multiple regulatory protein SPR6.
PD WO9703087-A1.
PD 30-JAN-1997.
PA (UNMI) UNIV MICHIGAN.
Query Match 4.4%; Score 75; DB 2; Length 1248;
Best Local Similarity 22.4%; Pred. No. 8e+02;
RESULT 1029
ID AAB24890 standard; peptide; 1276 AA.
DE Plant SDF encoded polypeptide sequence SEQ List 1 NO:401.
PD WO200040695-A2.
PD 13-JUL-2000.
PA (CERE-) CERES INC.
Query Match 4.4%; Score 75; DB 3; Length 1276;
Best Local Similarity 19.7%; Pred. No. 8.3e+02;
RESULT 1030
ID ADN20691 standard; protein; 1310 AA.
DE Bacterial polypeptide #3344.
PD US200333675-A1.
PD 18-DEC-2003.
PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (GHEH/) CHEN X.
PA (GOLD/) GOLDMAN B S.
Query Match 4.4%; Score 75; DB 8; Length 1310;
Best Local Similarity 17.8%; Pred. No. 8.6e+02;

RESULT 1031
ID ABG14462 standard; protein; 353 AA.
DE Novel human diagnostic protein #14453.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match 4.4%; Score 74.5; DB 4; Length 353;
Best Local Similarity 20.5%; Pred. No. 1.5e+02;
RESULT 1032
ID AAM69428 standard; protein; 378 AA.
DE Human secreted protein dp537_4.
PN WO9840404-A2.
PD 17-SEP-1998.
PA (GEMV-) GENNETICS INST INC.
Query Match 4.4%; Score 74.5; DB 2; Length 378;
Best Local Similarity 18.8%; Pred. No. 1.6e+02;
RESULT 1033
ID ABU24050 standard; protein; 437 AA.
DE Protein encoded by prokaryotic essential gene #9577.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 4.4%; Score 74.5; DB 6; Length 437;
Best Local Similarity 19.7%; Pred. No. 2e+02;
RESULT 1034
ID ABR57280 standard; protein; 525 AA.
DE Human coronin 2A protein Coronin_2A.
PN WO2003040296-A2.
PD 15-MAY-2003.
PA (DEVE-) DEVELOGEN ENTWICKLUNGSBIOLOGISCHE FORSCH.
PA (HARD-) HARDER T.
Query Match 4.4%; Score 74.5; DB 6; Length 525;
Best Local Similarity 22.6%; Pred. No. 2.6e+02;
RESULT 1035
ID ABU03730 standard; protein; 539 AA.
DE Human expressed protein tag (EPT) #396.
PN WO200278524-A2.
PD 10-OCT-2002.
PA (ZYCO-) ZYCOS INC.
Query Match 4.4%; Score 74.5; DB 6; Length 539;
Best Local Similarity 23.3%; Pred. No. 2.7e+02;
RESULT 1036
ID ABU03731 standard; protein; 539 AA.
DE Human expressed protein tag (EPT) #397.
PN WO200278524-A2.
PD 10-OCT-2002.
PA (ZYCO-) ZYCOS INC.
Query Match 4.4%; Score 74.5; DB 6; Length 539;
Best Local Similarity 23.3%; Pred. No. 2.7e+02;
RESULT 1037
ID ABU03729 standard; protein; 539 AA.
DE Human expressed protein tag (EPT) #395.
PN WO200278524-A2.
PD 10-OCT-2002.
PA (ZYCO-) ZYCOS INC.
Query Match 4.4%; Score 74.5; DB 6; Length 539;
Best Local Similarity 23.3%; Pred. No. 2.7e+02;
RESULT 1038
ID ABU03732 standard; protein; 539 AA.
DE Human expressed protein tag (EPT) #398.
PN WO200278524-A2.
PD 10-OCT-2002.
PA (ZYCO-) ZYCOS INC.
Query Match 4.4%; Score 74.5; DB 6; Length 539;
Best Local Similarity 23.3%; Pred. No. 2.7e+02;
RESULT 1039
ID ADM05790 standard; protein; 595 AA.
DE Human protein of the invention SEQ ID NO:4475.
PN EP1347046-A1.
PD 24-SEP-2003.
PA (REMS-) RES ASSOC BIOTECHNOLOGY.
Query Match 4.4%; Score 74.5; DB 7; Length 595;
Best Local Similarity 23.5%; Pred. No. 3.1e+02;

RESULT 1040
ID AAE26672 standard; protein; 717 AA.
DE Human 59914 protein.
PN EP136739-A2.
PD 04-SEP-2002.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 4.4%; Score 74.5; DB 5; Length 717;
Best Local Similarity 23.0%; Pred. No. 4.1e+02;
RESULT 1041
ID ADB65311 standard; protein; 717 AA.
DE Human protein encoded by clone TEST120070400.
PN EP1308459-A2.
PD 07-MAY-2003.
PA (HELI-) HELIX RES INST.
PA (REMS-) RES ASSOC BIOTECHNOLOGY.
Query Match 4.4%; Score 74.5; DB 7; Length 717;
Best Local Similarity 23.0%; Pred. No. 4.1e+02;
RESULT 1042
ID ADH51689 standard; protein; 717 AA.
DE Human 59914 protein amino acid sequence.
PN US2003219806-A1.
PD 27-NOV-2003.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 4.4%; Score 74.5; DB 8; Length 717;
Best Local Similarity 23.0%; Pred. No. 4.1e+02;
RESULT 1043
ID ADR44908 standard; protein; 717 AA.
DE Polypeptide 59914 amino acid sequence.
PN WO2004071411-A2.
PD 26-AUG-2004.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 4.4%; Score 74.5; DB 8; Length 717;
Best Local Similarity 23.0%; Pred. No. 4.1e+02;
RESULT 1044
ID AAM70899 standard; protein; 761 AA.
DE Protein encoded by tumour suppressor gene IB3089A.
PN WO9854318-A1.
PD 03-DEC-1998.
PA (CUR1-) CURIE RES INST MARIE.
Query Match 4.4%; Score 74.5; DB 2; Length 761;
Best Local Similarity 21.1%; Pred. No. 4.4e+02;
RESULT 1045
ID AAY44704 standard; protein; 761 AA.
DE Human tumour suppressor protein IB3089A.
PN WO200001816-A1.
PD 13-JAN-2000.
PA (IMCR-) IMPERIAL CANCER RES TECHNOLOGY.
Query Match 4.4%; Score 74.5; DB 3; Length 761;
Best Local Similarity 21.1%; Pred. No. 4.4e+02;
RESULT 1046
ID ADU75380 standard; protein; 761 AA.
DE Marker gene related amino acid sequence SEQ ID NO:632.
PD 03-MAR-2004.
PA (GENO-) GENOX RES INC.
Query Match 4.4%; Score 74.5; DB 8; Length 761;
Best Local Similarity 21.1%; Pred. No. 4.4e+02;
RESULT 1047
ID ADQ20487 standard; protein; 761 AA.
DE Human soft tissue sarcoma-upregulated protein - SEQ ID 3307.
PN WO2004048938-A2.
PD 10-JUN-2004.
PA (PROT-) PROTEIN DESIGN LABS INC.
Query Match 4.4%; Score 74.5; DB 8; Length 761;
Best Local Similarity 21.1%; Pred. No. 4.4e+02;
RESULT 1048
ID ADR14427 standard; protein; 761 AA.
DE Human NF-kappaB pathway-associated protein SeqID428.
PN WO2004065577-A2.
PD 05-AUG-2004.
PA (BRIM-) BRISTOL-MYERS SQUIBB CO.
Query Match 4.4%; Score 74.5; DB 8; Length 761;
Best Local Similarity 21.1%; Pred. No. 4.4e+02;

RESULT 1049
ID AAB33158 standard; protein; 823 AA.
DE Human ORFX ORF2922 polypeptide sequence SEQ ID NO:5844.
PN WO200058473-A2.
PD 05-OCT-2000.
PA (CORA-) CORAGEN CORP.
Query Match
Best Local Similarity 23.1%; Pred. No. 4.9e+02;
ID ADB64439 standard; protein; 833 AA.
DE Human KM-HN-1 protein used to treat head and neck cancer Seqid 1.
PN JP2004147649-A.
PD 27-MAY-2004.
PA (KOMA-) ZH KUMAMOTO TECHNO SANGYO ZAIDAN.
Query Match
Best Local Similarity 23.5%; Pred. No. 5e+02;
RESULT 1051
ID AAO84380 standard; protein; 1009 AA.
DE Novel human secreted or membrane-associated protein #19.
PN WO200204600-A2.
PD 17-JAN-2002.
PA (SMIK) SMITHKLINE BEECHAM CORP.
PA (SMIK) SMITHKLINE BEECHAM PLC.
PA (GLAX) GLAXO GROUP LTD.
Query Match
Best Local Similarity 23.1%; Pred. No. 6.6e+02;
RESULT 1052
ID AAE25387 standard; protein; 1009 AA.
DE Human NZMS-11 protein.
PN WO200246385-A2.
PD 13-JUN-2002.
PA (INCY-) INCYTE GENOMICS INC.
Query Match
Best Local Similarity 23.1%; Pred. No. 6.6e+02;
LENGTH 1009;
RESULT 1053
ID ADC26201 standard; protein; 1022 AA.
DE Human NOV5 protein.
PN WO2003004687-A2.
PD 16-JAN-2003.
PA (CORA-) CORAGEN CORP.
Query Match
Best Local Similarity 23.1%; Pred. No. 6.8e+02;
LENGTH 1022;
RESULT 1054
ID ADN49840 standard; protein; 1125 AA.
DE Turkey astrovirus (Thetv) ORF1a encoded serine protease.
PN US696562-B1.
PD 24-FEB-2004.
PA (USDA) US SEC OF AGRIC.
PA (UYGE-) UNIV GEORGIA RES FOUND INC.
Query Match
Best Local Similarity 20.7%; Pred. No. 7.8e+02;
LENGTH 1125;
RESULT 1055
ID ABO35640 standard; protein; 1139 AA.
DE Protein encoded by Prokaryotic essential gene #21167.
PN WO20027183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match
Best Local Similarity 23.2%; Pred. No. 7.9e+02;
LENGTH 1139;
RESULT 1056
ID ABO23514 standard; protein; 1139 AA.
DE Mycoplasma genitalium outlier protein #1.
PN US2003039863-A1.
PD 27-FEB-2003.
PA (BRAH/) BRAHMACHARI S K.
PA (RAMA/) RAMACHANDRAN S.
PA (NAND/) NANDI T.
PA (BHIM/) BHIMARAO C.
Query Match
Best Local Similarity 23.2%; Pred. No. 7.9e+02;
LENGTH 1139;
RESULT 1057
ID AAR8453 standard; protein; 1342 AA.
DE erDB-3 polypeptide.
PN US5480968-A.
PD 02-JAN-1996.
PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
Query Match
Best Local Similarity 21.4%; Pred. No. 1e+03;
LENGTH 1342;
RESULT 1058
ID AAM69406 standard; protein; 1342 AA.
DE Erdb-3 glycoprotein clone E3-16.
PN US5820859-A.
PD 13-OCT-1998.
PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
Query Match
Best Local Similarity 21.4%; Pred. No. 1e+03;
LENGTH 1342;
RESULT 1059
ID AAY16594 standard; protein; 1342 AA.
DE erDB-3 protein encoded by the E3-16 CDNA clone.
PN US5916755-A.
PD 29-JUN-1999.
PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
Query Match
Best Local Similarity 21.4%; Pred. No. 1e+03;
LENGTH 1342;
RESULT 1060
ID ADA37256 standard; protein; 1342 AA.
DE Human Erdb3 amino acid sequence SEQ ID NO:6.
PN WO2003066677-A1.
PD 14-AUG-2003.
PA (NISC-) JAPAN SCI & TECHNOLOGY CORP.
PA (RIKE) RIKEN KK.
PA (MOCH) MOCHIDA PHARM CO LTD.
Query Match
Best Local Similarity 21.4%; Pred. No. 1e+03;
LENGTH 1342;
RESULT 1061
ID ADD52685 standard; protein; 1342 AA.
DE Human erdb-3.
PN US6639060-B1.
PD 28-OCT-2003.
PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
Query Match
Best Local Similarity 21.4%; Pred. No. 1e+03;
LENGTH 1342;
RESULT 1062
ID ADE62708 standard; protein; 1342 AA.
DE Human Protein P21860, SEQ ID NO 8640.
PN WO2003016475-A2.
PD 27-FEB-2003.
PA (GEHO) GEN HOSPITAL CORP.
PA (FARB) BAYER AG.
Query Match
Best Local Similarity 21.4%; Pred. No. 1e+03;
LENGTH 1342;
RESULT 1063
ID ADE36712 standard; protein; 1342 AA.
DE Human Erdb-3 amino acid sequence SEQ ID NO:1.
PN WO2003080835-A1.
PD 02-OCT-2003.
PA (ZENS-) ZENSON SHANGHAI SCI TECH LTD.
Query Match
Best Local Similarity 21.4%; Pred. No. 1e+03;
LENGTH 1342;
RESULT 1064
ID ADM10301 standard; protein; 1342 AA.
DE Human epidermal growth factor receptor (EGFR) polypeptide #1.
PN US2003053995-A1.
PD 20-MAR-2003.
PA (HUNG/) HUNG M.
PA (LINS/) LIN S.
Query Match
Best Local Similarity 21.4%; Pred. No. 1e+03;
LENGTH 1342;
RESULT 1065
ID ADU66656 standard; protein; 1342 AA.
DE Her3 protein for anti-cancer protein complex.
PN WO2004009622-A2.
PD 29-JAN-2004.
PA (CEIL-) CELLZOME AG.
Query Match
Best Local Similarity 21.4%; Pred. No. 1e+03;
LENGTH 1342;

RESULT 1066
ID ADO56208 standard; protein; 1342 AA.
DE Human ErbB-3.
PN US2004063140-A1.
PD 01-APR-2004.
PA (KRAU/) KRAUS M H.
PA (AARCO/) AARONSON S A.
Query Match 4.4%; Score 74.5; DB 8; Length 1342;
Best Local Similarity 21.4%; Pred. No. 1e+03;
RESULT 1067
ID AAR12608 standard; protein; 1343 AA.
DE EGRF-R erB-3 clone E3-16 product.
PN WO9108214-A.
PD 13-JUN-1991.
PA (USDC) US SEC OF COMMERCE.
PA (USSH) NAT INST OF HEALTH.
Query Match 4.4%; Score 74.5; DB 2; Length 1343;
Best Local Similarity 21.4%; Pred. No. 1e+03;
RESULT 1068
ID ADH48822 standard; protein; 1426 AA.
DE NOV45A protein sequence, SEQ ID 106.
PN WO200266852-A2.
PD 06-SEP-2002.
PA (CUBA-) CUBAGEN CORP.
Query Match 4.4%; Score 74.5; DB 5; Length 1426;
Best Local Similarity 21.3%; Pred. No. 1.1e+03;
RESULT 1069
ID ABB63592 standard; protein; 1513 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 17568.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 4.4%; Score 74.5; DB 4; Length 1513;
Best Local Similarity 18.5%; Pred. No. 1.2e+03;
RESULT 1070
ID ABB44550 standard; protein; 1630 AA.
DE Human wound healing related polypeptide SEQ ID NO 7.
PN CA2325226-A1.
PD 17-MAY-2001.
PA (SWIT-) SWITCH BIOTECH AG.
Query Match 4.4%; Score 74.5; DB 4; Length 1630;
Best Local Similarity 22.6%; Pred. No. 1.3e+03;
RESULT 1071
ID ABB98331 standard; protein; 1630 AA.
DE Amino acid sequence of human HECT domain protein HECT17.
PN FR2828209-A1.
PD 07-FEB-2003.
PA (CYTO-) CYTOMICS SYSTEMS SA.
Query Match 4.4%; Score 74.5; DB 6; Length 1630;
Best Local Similarity 22.6%; Pred. No. 1.3e+03;
RESULT 1072
ID AAM39023 standard; protein; 1632 AA.
DE Human polypeptide SEQ ID NO 2168.
PN WO200153312-A1.
PD 26-JUL-2001.
PA (HYSE-) HYSEQ INC.
Query Match 4.4%; Score 74.5; DB 4; Length 1632;
Best Local Similarity 22.6%; Pred. No. 1.3e+03;
RESULT 1073
ID ADC99058 standard; protein; 2171 AA.
DE Human KRP protein - SEQ ID 11.
PN WO2003033660-A2.
PD 24-APR-2003.
PA (INCY-) INCYTE GENOMICS INC.
Query Match 4.4%; Score 74.5; DB 7; Length 2171;
Best Local Similarity 22.6%; Pred. No. 2e+03;
RESULT 1074
ID AAR72826 standard; protein; 2482 AA.
DE Human mitotin.
PN WO9511309-A2.
PD 27-APR-1995.
PA (TEXA-) UNIV TEXAS SYSTEM.
Query Match 4.4%; Score 74.5; DB 2; Length 2482;

Best Local Similarity 22.0%; Pred. No. 2.4e+03;
RESULT 1075
ID AAW23996 standard; protein; 2482 AA.
DE Human mitotin amino acid sequence.
PN US5710022-A.
PD 20-JAN-1998.
PA (TEXA-) UNIV TEXAS SYSTEM.
Query Match 4.4%; Score 74.5; DB 2; Length 2482;
Best Local Similarity 22.0%; Pred. No. 2.4e+03;
RESULT 1076
ID ABG21509 standard; protein; 2955 AA.
DE Novel human diagnostic protein #21500.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match 4.4%; Score 74.5; DB 4; Length 2955;
Best Local Similarity 22.6%; Pred. No. 3.1e+03;
RESULT 1077
ID ABB44617 standard; protein; 2988 AA.
DE Human wound healing related polypeptide SEQ ID NO 106.
PN CA2325226-A1.
PD 17-MAY-2001.
PA (SWIT-) SWITCH BIOTECH AG.
Query Match 4.4%; Score 74.5; DB 4; Length 2988;
Best Local Similarity 22.6%; Pred. No. 3.2e+03;
RESULT 1078
ID ADN95402 standard; protein; 3113 AA.
DE Human BEC/LBC-related protein sequence SegID325.
PN WO2003080640-A1.
PD 02-OCT-2003.
PA (LUDW-) LUDWIG INST CANCER RES.
PA (LICN) LICENTIA LTD.
Query Match 4.4%; Score 74.5; DB 7; Length 3113;
Best Local Similarity 22.0%; Pred. No. 3.4e+03;
RESULT 1079
ID ADK70220 standard; protein; 3113 AA.
DE Human oesophageal cancer antigen SEQ ID NO:16.
PN JP2003259872-A.
PD 16-SEP-2003.
PA (KAGAKU) KAGAKU GIUTSU SHINKO JIGYODAN.
Query Match 4.4%; Score 74.5; DB 8; Length 3113;
Best Local Similarity 22.0%; Pred. No. 3.4e+03;
RESULT 1080
ID ADL72172 standard; protein; 3113 AA.
DE Human solid-cancer antigen peptide mitotin.
PN WO2004018518-A1.
PD 04-MAR-2004.
PA (NISC-) NIPAN SCI & TECHNOLOGY CORP.
Query Match 4.4%; Score 74.5; DB 8; Length 3113;
Best Local Similarity 22.0%; Pred. No. 3.4e+03;
RESULT 1081
ID ADQ18045 standard; protein; 3113 AA.
DE Human soft tissue sarcoma-upregulated protein - SEQ ID 862.
PN WO2004048938-A2.
PD 10-JUN-2004.
PA (PROT-) PROTEIN DESIGN LABS INC.
Query Match 4.4%; Score 74.5; DB 8; Length 3113;
Best Local Similarity 22.0%; Pred. No. 3.4e+03;
RESULT 1082
ID ABU07438 standard; protein; 3210 AA.
DE Protein differentially regulated in prostate cancer #41.
PN WO200281638-A2.
PD 17-OCT-2002.
PA (ORIG-) ORIGENE TECHNOLOGIES INC.
Query Match 4.4%; Score 74.5; DB 6; Length 3210;
Best Local Similarity 22.0%; Pred. No. 3.5e+03;
RESULT 1083
ID ADU66483 standard; protein; 3210 AA.
DE Cenp-F kinetochore protein for anti-cancer protein complex.
PN WO2004009622-A2.
PD 29-JAN-2004.
PA (CELL-) CELLZONE AG.
Query Match 4.4%; Score 74.5; DB 8; Length 3210;

Best Local Similarity 22.0%; Pred. No. 3.5e+03;
 RESULT 1084
 ID AAR9795 standard; protein: 3248 AA.
 DE Kinetochore protein CENP-F.
 PN WO9617867-A1.
 PD 13-JUN-1996.
 PA (FOXK-) FOX CHASE CANCER CENT.
 PA (UYTE-) UNIV TECHNOLOGIES INT INC.
 Query Match
 Best Local Similarity 4.4%; Score 74.5; DB 2; Length 3248;
 RESULT 1085
 ID ABB49452 standard; protein: 243 AA.
 DE *Listeria monocytogenes* protein #2156.
 PN WO200177335-A2.
 PD 18-OCT-2001.
 PA (INSP-) INST PASTEUR.
 Query Match
 Best Local Similarity 4.4%; Score 74; DB 5; Length 243;
 RESULT 1086
 ID AUB32775 standard; protein: 243 AA.
 DE Protein encoded by Prokaryotic essential gene #18302.
 PN WO200277183-A2.
 PD 03-OCT-2002.
 PA (ELIT-) ELITRA PHARM INC.
 Query Match
 Best Local Similarity 4.4%; Score 74; DB 6; Length 243;
 RESULT 1087
 ID AUA34096 standard; protein: 286 AA.
 DE *Staphylococcus aureus* cellular proliferation protein #372.
 PN WO200170955-A2.
 PD 27-SEP-2001.
 PA (ELIT-) ELITRA PHARM INC.
 Query Match
 Best Local Similarity 4.4%; Score 74; DB 4; Length 286;
 RESULT 1088
 ID AUA36606 standard; protein: 293 AA.
 DE *Staphylococcus aureus* cellular proliferation protein #776.
 PN WO200170955-A2.
 PD 27-SEP-2001.
 PA (ELIT-) ELITRA PHARM INC.
 Query Match
 Best Local Similarity 4.4%; Score 74; DB 4; Length 293;
 RESULT 1089
 ID ADN72441 standard; protein: 354 AA.
 DE Thale cress protein upregulated in E2Fa/Dpa expressing plants SegID 336.
 PN WO2004035798-A2.
 PD 29-APR-2004.
 PA (CROP-) CROPPDESIGN NV.
 Query Match
 Best Local Similarity 4.4%; Score 74; DB 8; Length 354;
 RESULT 1090
 ID ADN19574 standard; protein: 423 AA.
 DE Bacterial polypeptide #2227.
 PN US2003233675-A1.
 PD 18-DEC-2003.
 PA (CAOY/) CAO Y.
 PA (HINK/) HINKLE G J.
 PA (SLAT/) SLATER S C.
 PA (CHEN/) CHEN X.
 PA (GOLD/) GOLDMAN B S.
 Query Match
 Best Local Similarity 4.4%; Score 74; DB 8; Length 423;
 RESULT 1091
 ID ABB60937 standard; protein: 511 AA.
 DE Bos tauus thioresdoxin reductase SEQ ID NO:286.
 PN WO200250289-A1.
 PD 27-JUN-2002.
 PA (SEMB-) SEMBIOSYS GENETICS INC.
 PA (STGN-) STINGENTA PARTICIPATIONS AG.
 Query Match
 Best Local Similarity 4.4%; Score 74; DB 5; Length 511;
 RESULT 1092
 ID ABB07606 standard; protein: 557 AA.
 DE Novel human diagnostic protein #7597.
 PN WO200175067-A2.
 PD 11-OCT-2001.
 PA (HYSE-) HYSEQ INC.
 Query Match
 Best Local Similarity 4.4%; Score 74; DB 4; Length 557;
 RESULT 1093
 ID AAW85701 standard; protein: 628 AA.
 DE Pinene synthase of grand fir.
 PN WO9902030-A1.
 PD 21-JAN-1999.
 PA (UNIW-) UNIV WASHINGTON STATE RES FOUN.
 Query Match
 Best Local Similarity 4.4%; Score 74; DB 2; Length 628;
 RESULT 1094
 ID AAY90837 standard; protein: 628 AA.
 DE Grand fir pinene synthase protein sequence SEQ ID NO:20.
 PN WO200017327-A2.
 PD 30-MAR-2000.
 PA (KENT-) UNIV KENTUCKY RES DEPT.
 PA (SALK-) SALK INST BIOLOGICAL STUDIES.
 Query Match
 Best Local Similarity 4.4%; Score 74; DB 3; Length 628;
 RESULT 1095
 ID AAB69371 standard; protein: 628 AA.
 DE Grand fir (-)-pinene synthase SEQ ID NO: 4.
 PN WO200107565-A2.
 PD 01-FEB-2001.
 PA (UNIW-) UNIV WASHINGTON STATE RES FOUN.
 Query Match
 Best Local Similarity 4.4%; Score 74; DB 4; Length 628;
 RESULT 1096
 ID AAB83344 standard; protein: 682 AA.
 DE Human diagnostic and therapeutic pproteins SEQ ID NO:3593.
 PN WO2004023973-A2.
 PD 25-MAR-2004.
 PA (INCY-) INCYTE CORP.
 Query Match
 Best Local Similarity 4.4%; Score 74; DB 8; Length 682;
 RESULT 1097
 ID ABB37047 standard; protein: 696 AA.
 DE Human breast cancer / ovarian cancer related protein #23.
 PN WO2003000012-A2.
 PD 03-JAN-2003.
 PA (MILL-) MILLENNIUM PHARM INC.
 Query Match
 Best Local Similarity 4.4%; Score 74; DB 6; Length 696;
 RESULT 1098
 ID AUA35000 standard; protein: 764 AA.
 DE *Enterococcus faecalis* cellular proliferation protein #287.
 PN WO200170955-A2.
 PD 27-SEP-2001.
 PA (ELIT-) ELITRA PHARM INC.
 Query Match
 Best Local Similarity 4.4%; Score 74; DB 4; Length 764;
 RESULT 1099
 ID AUA33453 standard; protein: 764 AA.
 DE *Enterococcus faecalis* cellular proliferation protein #89.
 PN WO200170955-A2.
 PD 27-SEP-2001.
 PA (ELIT-) ELITRA PHARM INC.
 Query Match
 Best Local Similarity 4.4%; Score 74; DB 4; Length 764;
 RESULT 1100
 ID ADN26543 standard; protein: 784 AA.
 DE Bacterial polypeptide #9196.
 PN US2003233675-A1.
 PD 18-DEC-2003.
 PA (CAOY/) CAO Y.
 PA (HINK/) HINKLE G J.
 PA (SLAT/) SLATER S C.
 PA (CHEN/) CHEN X.
 PA (GOLD/) GOLDMAN B S.

Query Match 4.4%; Score 74; DB 8; Length 784;
Best Local Similarity 26.4%; Pred. No. 5.2e+02;
RESULT 1101
ID AAE32797 standard; protein; 1033 AA.
DE Human CEA protein.
PN WO200290508-A2.
PD 14-NOV-2002.
PA (ALPH-) ALPHAGEN INC.
Query Match 4.4%; Score 74; DB 6; Length 1033;
Best Local Similarity 19.9%; Pred. No. 7.7e+02;
RESULT 1102
ID AAU75875 standard; protein; 1049 AA.
DE SRBP2-lacI fusion protein.
PN US633167-B1.
PD 25-DEC-2001.
PA (AMHP) AMERICAN HOME PROD CORP.
Query Match 4.4%; Score 74; DB 5; Length 1049;
Best Local Similarity 23.0%; Pred. No. 7.9e+02;
RESULT 1103
ID ADN22927 standard; protein; 1130 AA.
DE Bacterial polypeptide #5580.
PN US200323675-A1.
PD 18-DEC-2003.
PA (CAOY) CAO Y.
PA (HINK) HINKLE G J.
PA (SLAT) SLATER S C.
PA (CHEN) CHEN X.
PA (GOLD) GOLDMAN B S.
Query Match 4.4%; Score 74; DB 8; Length 1130;
Best Local Similarity 23.3%; Pred. No. 8.8e+02;
RESULT 1104
ID ADN22928 standard; protein; 1130 AA.
DE Bacterial polypeptide #5581.
PN US200323675-A1.
PD 18-DEC-2003.
PA (CAOY) CAO Y.
PA (HINK) HINKLE G J.
PA (SLAT) SLATER S C.
PA (CHEN) CHEN X.
PA (GOLD) GOLDMAN B S.
Query Match 4.4%; Score 74; DB 8; Length 1130;
Best Local Similarity 23.3%; Pred. No. 8.8e+02;
RESULT 1105
ID AAR66391 standard; protein; 1141 AA.
DE Human SRBP-2.
PN WO9426922-A2.
PD 24-NOV-1994.
PA (TEXA) UNIV TEXAS SYSTEM.
Query Match 4.4%; Score 74; DB 2; Length 1141;
Best Local Similarity 23.0%; Pred. No. 8.9e+02;
RESULT 1106
ID AAY50700 standard; protein; 1141 AA.
DE Human SRBP-2 protein.
PN DE19816902-A1.
PD 28-OCT-1999.
PA (KRON) KRONE W.
PA (MUEL) MUELLER-WIELAND D.
Query Match 4.4%; Score 74; DB 2; Length 1141;
Best Local Similarity 23.0%; Pred. No. 8.9e+02;
RESULT 1107
ID ABM62371 standard; protein; 1141 AA.
DE Tumour-associated antigenic target (TAT) polypeptide PRO83293, SEQ:6086.
PN WO2004030615-A2.
PD 15-APR-2004.
PA (GETH) GENENTECH INC.
Query Match 4.4%; Score 74; DB 8; Length 1141;
Best Local Similarity 23.0%; Pred. No. 8.9e+02;
RESULT 1108
ID ADQ39979 standard; protein; 1141 AA.
DE Human myocardial infarction-associated gene derived protein, SEQ ID 1642.
PN WO2004058052-A2.
PD 15-JUL-2004.
PA (APPL-) APPLERA CORP.

Query Match 4.4%; Score 74; DB 8; Length 1141;
Best Local Similarity 23.8%; Pred. No. 8.9e+02;
RESULT 1109
ID ADQ39980 standard; protein; 1141 AA.
DE Human myocardial infarction-associated gene derived protein, SEQ ID 1643.
PN WO2004058052-A2.
PD 15-JUL-2004.
PA (APPL-) APPLERA CORP.
Query Match 4.4%; Score 74; DB 8; Length 1141;
Best Local Similarity 23.8%; Pred. No. 8.9e+02;
RESULT 1110
ID ADD48653 standard; protein; 1216 AA.
DE Rat Protein P10687, SEQ ID NO 14359.
PN WO2003016475-A2.
PD 27-FEB-2003.
PA (GHO) GEN HOSPITAL CORP.
PA (FARB) BAYER AG.
Query Match 4.4%; Score 74; DB 7; Length 1216;
Best Local Similarity 19.3%; Pred. No. 9.8e+02;
RESULT 1111
ID AAU10540 standard; protein; 1478 AA.
DE Rat CIRL-2 variant BC (YSG2) polypeptide.
PN WO200175440-A2.
PD 11-OCT-2001.
PA (WELF-) WELFIDE CORP.
Query Match 4.4%; Score 74; DB 5; Length 1478;
Best Local Similarity 21.9%; Pred. No. 1.3e+03;
RESULT 1112
ID ADD46680 standard; protein; 1478 AA.
DE Rat Protein AAC62654, SEQ ID NO 12365.
PN WO2003016475-A2.
PD 27-FEB-2003.
PA (GHO) GEN HOSPITAL CORP.
PA (FARB) BAYER AG.
Query Match 4.4%; Score 74; DB 7; Length 1478;
Best Local Similarity 21.9%; Pred. No. 1.3e+03;
RESULT 1113
ID ADE55162 standard; protein; 1488 AA.
DE Rat Protein AF063102, SEQ ID NO 967.
PN WO2003016475-A2.
PD 27-FEB-2003.
PA (GHO) GEN HOSPITAL CORP.
PA (FARB) BAYER AG.
Query Match 4.4%; Score 74; DB 7; Length 1488;
Best Local Similarity 21.9%; Pred. No. 1.3e+03;
RESULT 1114
ID ADE55174 standard; protein; 1488 AA.
DE Rat Protein AF063102, SEQ ID NO 979.
PN WO2003016475-A2.
PD 27-FEB-2003.
PA (GHO) GEN HOSPITAL CORP.
PA (FARB) BAYER AG.
Query Match 4.4%; Score 74; DB 7; Length 1488;
Best Local Similarity 21.9%; Pred. No. 1.3e+03;
RESULT 1115
ID ADE55170 standard; protein; 1488 AA.
DE Rat Protein AF063102, SEQ ID NO 975.
PN WO2003016475-A2.
PD 27-FEB-2003.
PA (GHO) GEN HOSPITAL CORP.
PA (FARB) BAYER AG.
Query Match 4.4%; Score 74; DB 7; Length 1488;
Best Local Similarity 21.9%; Pred. No. 1.3e+03;
RESULT 1116
ID ADE55166 standard; protein; 1488 AA.
DE Rat Protein AF063102, SEQ ID NO 971.
PN WO2003016475-A2.
PD 27-FEB-2003.
PA (GHO) GEN HOSPITAL CORP.
PA (FARB) BAYER AG.
Query Match 4.4%; Score 74; DB 7; Length 1488;
Best Local Similarity 21.9%; Pred. No. 1.3e+03;
RESULT 1117

ID ABB70757 standard; protein; 143 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 39063.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 4.3%; Score 73.5; DB 4; Length 143;
Best Local Similarity 18.9%; Pred. No. 51;
RESULT 1118
ID ABB12711 standard; protein; 193 AA.
DE Novel human diagnostic protein #12702.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match 4.3%; Score 73.5; DB 4; Length 193;
Best Local Similarity 20.3%; Pred. No. 78;
RESULT 1119
ID ABB09966 standard; protein; 193 AA.
DE Novel protein-related contig polypeptide sequence #554.
PN WO2003054152-A2.
PD 03-JUL-2003.
PA (HYSE-) HYSEQ INC.
Query Match 4.3%; Score 73.5; DB 7; Length 193;
Best Local Similarity 20.3%; Pred. No. 78;
RESULT 1120
ID ABB13874 standard; protein; 287 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 13525.
PN EPI033405-A2.
PD 06-SEP-2000.
Query Match 4.3%; Score 73.5; DB 3; Length 287;
Best Local Similarity 22.0%; Pred. No. 1.4e+02;
RESULT 1121
ID ABB13873 standard; protein; 305 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 13524.
PN EPI033405-A2.
PD 06-SEP-2000.
Query Match 4.3%; Score 73.5; DB 3; Length 305;
Best Local Similarity 22.0%; Pred. No. 1.5e+02;
RESULT 1122
ID ABB13872 standard; protein; 312 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 13523.
PN EPI033405-A2.
PD 06-SEP-2000.
Query Match 4.3%; Score 73.5; DB 3; Length 312;
Best Local Similarity 22.0%; Pred. No. 1.6e+02;
RESULT 1123
ID ABB14871 standard; protein; 315 AA.
DE Novel human diagnostic protein #14862.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match 4.3%; Score 73.5; DB 4; Length 315;
Best Local Similarity 19.8%; Pred. No. 1.6e+02;
RESULT 1124
ID ABB22529 standard; protein; 358 AA.
DE Novel human diagnostic protein #22520.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match 4.3%; Score 73.5; DB 4; Length 358;
Best Local Similarity 19.8%; Pred. No. 1.9e+02;
RESULT 1125
ID ABB47464 standard; protein; 417 AA.
DE Listeria monocytogenes protein #168.
PN WO200177335-A2.
PD 18-OCT-2001.
PA (INSP) INST PASTEUR.
Query Match 4.3%; Score 73.5; DB 5; Length 417;
Best Local Similarity 20.4%; Pred. No. 2.4e+02;
RESULT 1126
ID ABB32595 standard; protein; 417 AA.
DE Protein encoded by Prokaryotic essential gene #18122.
PN WO200277183-A2.
PD 03-OCT-2002.

PA (ELIT-) ELITRA PHARM INC.
Query Match 4.3%; Score 73.5; DB 6; Length 417;
Best Local Similarity 20.4%; Pred. No. 2.4e+02;
RESULT 1127
ID ABB01895 standard; protein; 428 AA.
DE Novel human diagnostic protein #1886.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match 4.3%; Score 73.5; DB 4; Length 428;
Best Local Similarity 20.0%; Pred. No. 2.5e+02;
RESULT 1128
ID ABB1340 standard; protein; 467 AA.
DE Human novel secreted protein LP255 (b).
PN WO200214358-A2.
PD 21-FEB-2002.
PA (ELIT-) LITLY & CO ELI.
Query Match 4.3%; Score 73.5; DB 5; Length 467;
Best Local Similarity 27.5%; Pred. No. 2.8e+02;
RESULT 1129
ID ABB1308 standard; protein; 536 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 23820.
PN EPI033405-A2.
PD 06-SEP-2000.
Query Match 4.3%; Score 73.5; DB 3; Length 536;
Best Local Similarity 23.4%; Pred. No. 3.4e+02;
RESULT 1130
ID ABB17886 standard; protein; 833 AA.
DE Novel human diagnostic protein #17877.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match 4.3%; Score 73.5; DB 4; Length 833;
Best Local Similarity 19.6%; Pred. No. 6.4e+02;
RESULT 1131
ID ABB63245 standard; protein; 893 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 16527.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 4.3%; Score 73.5; DB 4; Length 893;
Best Local Similarity 22.6%; Pred. No. 7.1e+02;
RESULT 1132
ID ABB04054 standard; protein; 945 AA.
DE Human protein of the invention SEQ ID NO: 2739.
PN EPI347046-A1.
PD 24-SEP-2003.
PA (REMS-) RES ASSOC BIOTECHNOLOGY.
Query Match 4.3%; Score 73.5; DB 7; Length 945;
Best Local Similarity 19.1%; Pred. No. 7.7e+02;
RESULT 1133
ID ABB63754 standard; protein; 1019 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 18054.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 4.3%; Score 73.5; DB 4; Length 1019;
Best Local Similarity 22.1%; Pred. No. 8.6e+02;
RESULT 1134
ID ABB40820 standard; protein; 1212 AA.
DE Protein encoded by Prokaryotic essential gene #26347.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 4.3%; Score 73.5; DB 6; Length 1212;
Best Local Similarity 22.8%; Pred. No. 1.1e+03;
RESULT 1135
ID ABB08046 standard; protein; 2845 AA.
DE Mouse polypeptide #42.
PN US2004071700-A1.
PD 15-APR-2004.
PA (LIFE-) LIFE SCI DEV CORP.
Query Match 4.3%; Score 73.5; DB 8; Length 2845;

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Best Local Similarity 24.8%; Pred. No. 3.7e+03;
RESULT 1136
ID AAY56029 standard; protein; 3329 AA.
DE Human BRCA2 tumour suppressor protein.
PN WO9598135-A1.
PD 18-NOV-1999.
PA (SALK ) SALK INST BIOLOGICAL STUDIRS.
Query Match 4.3%; Score 73; DB 5; Length 3329;
Best Local Similarity 21.7%; Pred. No. 4.7e+03;
RESULT 1137
ID ABUS1002 standard; protein; 189 AA.
DE Helicobacter pylori selected interacting domain (SID) protein #345.
PN WO200266501-A2.
PD 29-AUG-2002.
PA (HYBR-) HYBRIGENICS.
PA (INSP ) INST PASTEUR.
Query Match 4.3%; Score 73; DB 5; Length 189;
Best Local Similarity 23.5%; Pred. No. 85;
RESULT 1138
ID AAG27830 standard; protein; 269 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 32820.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 4.3%; Score 73; DB 3; Length 269;
Best Local Similarity 22.2%; Pred. No. 1.4e+02;
RESULT 1139
ID ADQ19681 standard; protein; 276 AA.
DE Human soft tissue sarcoma-upregulated protein - SEQ ID 2500.
PN WO2004048938-A2.
PD 10-JUN-2004.
PA (PROT-) PROTEIN DESIGN LABS INC.
Query Match 4.3%; Score 73; DB 8; Length 276;
Best Local Similarity 19.4%; Pred. No. 1.5e+02;
RESULT 1140
ID AAG37829 standard; protein; 278 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 32819.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 4.3%; Score 73; DB 3; Length 278;
Best Local Similarity 22.2%; Pred. No. 1.5e+02;
RESULT 1141
ID AAG53263 standard; protein; 328 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 67794.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 4.3%; Score 73; DB 3; Length 328;
Best Local Similarity 21.5%; Pred. No. 1.9e+02;
RESULT 1142
ID ADS42868 standard; protein; 330 AA.
DE Bacterial polypeptide #1298.
PN US2003233675-A1.
PD 18-DEC-2003.
PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
Query Match 4.3%; Score 73; DB 8; Length 330;
Best Local Similarity 21.0%; Pred. No. 1.9e+02;
RESULT 1143
ID AAG53262 standard; protein; 346 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 67793.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 4.3%; Score 73; DB 3; Length 346;
Best Local Similarity 21.5%; Pred. No. 2e+02;
RESULT 1144
ID AAG53261 standard; protein; 351 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 67792.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 4.3%; Score 73; DB 3; Length 351;
Best Local Similarity 21.5%; Pred. No. 2.1e+02;

RESULT 1145
ID ABB60115 standard; protein; 362 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 7137.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE ) PE CORP NY.
Query Match 4.3%; Score 73; DB 4; Length 362;
Best Local Similarity 25.4%; Pred. No. 2.2e+02;
RESULT 1146
ID AAG7828 standard; protein; 376 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 32818.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 4.3%; Score 73; DB 3; Length 376;
Best Local Similarity 22.2%; Pred. No. 2.3e+02;
RESULT 1147
ID ADN26038 standard; protein; 385 AA.
DE Bacterial polypeptide #8691.
PN US2003233675-A1.
PD 18-DEC-2003.
PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
Query Match 4.3%; Score 73; DB 8; Length 385;
Best Local Similarity 19.9%; Pred. No. 2.4e+02;
RESULT 1148
ID ABU35522 standard; protein; 446 AA.
DE Protein encoded by prokaryotic essential gene #21049.
PN WO20027183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 4.3%; Score 73; DB 6; Length 446;
Best Local Similarity 21.1%; Pred. No. 2.9e+02;
RESULT 1149
ID ADB78618 standard; protein; 452 AA.
DE Human GABA receptor subunit mutant SEQ ID NO:162.
PN WO2003008574-A1.
PD 30-JAN-2003.
PA (BION-) BIONOMICS LTD.
PA (WALL/) WALLACE R W.
Query Match 4.3%; Score 73; DB 7; Length 452;
Best Local Similarity 25.9%; Pred. No. 3e+02;
RESULT 1150
ID AAY95938 standard; protein; 474 AA.
DE Porcine adenovirus 3 E1B-474R protein.
PN WO200050076-A1.
PD 31-AUG-2000.
PA (PURD ) PURDUE RES FOUND.
Query Match 4.3%; Score 73; DB 3; Length 474;
Best Local Similarity 21.6%; Pred. No. 3.2e+02;
RESULT 1151
ID ADS42170 standard; protein; 479 AA.
DE Bacterial polypeptide #20600.
PN US2003233675-A1.
PD 18-DEC-2003.
PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
Query Match 4.3%; Score 73; DB 8; Length 479;
Best Local Similarity 18.8%; Pred. No. 3.3e+02;
RESULT 1152
ID ADN23648 standard; protein; 494 AA.
DE Bacterial polypeptide #6301.
PN US2003233675-A1.
PD 18-DEC-2003.
PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
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PA (GOLD/) GOLDMAN B.S.
Query Match 4.3%; Score 73; DB 8; Length 494;
Best Local Similarity 19.0%; Pred. No. 3.4e+02;
RESULT 1153
ID ADF07358 standard; protein; 589 AA.
DE Bacterial polypeptide #3471.
PN US6605709-B1.
PD 12-AUG-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 4.3%; Score 73; DB 7; Length 589;
Best Local Similarity 21.6%; Pred. No. 4.4e+02;
RESULT 1154
ID ABB62805 standard; protein; 635 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 15207.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PERE) PE CORP NY.
Query Match 4.3%; Score 73; DB 4; Length 635;
Best Local Similarity 19.8%; Pred. No. 4.9e+02;
RESULT 1155
ID ABO69935 standard; protein; 679 AA.
DE Pseudomonas aeruginosa polypeptide #2110.
PN US6551795-B1.
PD 22-APR-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 4.3%; Score 73; DB 7; Length 679;
Best Local Similarity 19.4%; Pred. No. 5.4e+02;
RESULT 1156
ID ABB64835 standard; protein; 692 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 21297.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PERE) PE CORP NY.
Query Match 4.3%; Score 73; DB 4; Length 692;
Best Local Similarity 24.1%; Pred. No. 5.5e+02;
RESULT 1157
ID ADO09454 standard; protein; 961 AA.
DE Human protein useful for treating neurological disease Seq 2960.
PN EP1447413-A2.
PD 18-AUG-2004.
PA (REAS-) RRS ASSOC BIOTECHNOLOGY.
Query Match 4.3%; Score 73; DB 8; Length 961;
Best Local Similarity 18.4%; Pred. No. 8.9e+02;
RESULT 1158
ID ABR53657 standard; protein; 1014 AA.
DE EPI258494-A1.
PN EPI258494-A1.
PD 20-NOV-2002.
PA (CELL-) CELLZOME AG.
Query Match 4.3%; Score 73; DB 6; Length 1014;
Best Local Similarity 16.5%; Pred. No. 9.6e+02;
RESULT 1159
ID ADK64114 standard; protein; 1014 AA.
DE Disease treating protein complex-derived protein #1318.
PN EPI338608-A2.
PD 27-AUG-2003.
PA (CELL-) CELLZOME AG.
Query Match 4.3%; Score 73; DB 7; Length 1014;
Best Local Similarity 16.5%; Pred. No. 9.6e+02;
RESULT 1160
ID AAM80177 standard; protein; 1058 AA.
DE Human protein SEQ ID NO 3823.
PN WO200157190-A2.
PD 09-AUG-2001.
PA (HYSE-) HYSEQ INC.
Query Match 4.3%; Score 73; DB 4; Length 1058;
Best Local Similarity 18.4%; Pred. No. 1e+03;
RESULT 1161
ID AAM79193 standard; protein; 1216 AA.
DE Human protein SEQ ID NO 1855.
PN WO200157190-A2.
PD 09-AUG-2001.
PA (HYSE-) HYSEQ INC.

Query Match 4.3%; Score 73; DB 4; Length 1216;
Best Local Similarity 18.4%; Pred. No. 1.2e+03;
RESULT 1162
ID ABB08204 standard; protein; 1216 AA.
DE Human lipid metabolism enzyme-4 (LME-4).
PN WO200185956-A2.
PD 15-NOV-2001.
PA (INCY-) INCYTE GENOMICS INC.
Query Match 4.3%; Score 73; DB 5; Length 1216;
Best Local Similarity 18.4%; Pred. No. 1.2e+03;
RESULT 1163
ID ADI57184 standard; protein; 1216 AA.
DE Human PLC-beta1 protein SEQ ID NO:4.
PN WO2004007754-A2.
PD 22-JAN-2004.
PA (RIGE-) RIGEL PHARM INC.
Query Match 4.3%; Score 73; DB 8; Length 1216;
Best Local Similarity 18.4%; Pred. No. 1.2e+03;
RESULT 1164
ID AAM19785 standard; protein; 1244 AA.
DE Mouse multiple regulatory protein SPR6.
PN WO9703087-A1.
PD 30-JAN-1997.
PA (UNMI) UNIV MICHIGAN.
Query Match 4.3%; Score 73; DB 2; Length 1244;
Best Local Similarity 22.0%; Pred. No. 1.3e+03;
RESULT 1165
ID ADC71568 standard; protein; 1548 AA.
DE Mouse subtilisin-like protein convertase 6 (SPC6).
PN US2003093824-A1.
PD 15-MAY-2003.
PA (ALLE/) ALLEN K D.
Query Match 4.3%; Score 73; DB 7; Length 1548;
Best Local Similarity 25.8%; Pred. No. 1.8e+03;
RESULT 1166
ID ABB81171 standard; protein; 1603 AA.
DE Human putative chromatin structure regulator, SUPR6H sequence.
PN WO2002595606-A2.
PD 01-AUG-2002.
PA (GPCB-) GPC BIOTECH AG.
Query Match 4.3%; Score 73; DB 5; Length 1603;
Best Local Similarity 22.0%; Pred. No. 1.8e+03;
RESULT 1167
ID AD57844 standard; protein; 1603 AA.
DE MRB protein #16.
PN WO2004015072-A2.
PD 19-FEB-2004.
PA (EXEL-) EXELIXIS INC.
Query Match 4.3%; Score 73; DB 8; Length 1603;
Best Local Similarity 22.0%; Pred. No. 1.8e+03;
RESULT 1168
ID ABB60498 standard; protein; 1679 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 8286.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PERE) PE CORP NY.
Query Match 4.3%; Score 73; DB 4; Length 1679;
Best Local Similarity 23.6%; Pred. No. 2e+03;
RESULT 1169
ID ABB60502 standard; protein; 1679 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 8298.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PERE) PE CORP NY.
Query Match 4.3%; Score 73; DB 4; Length 1679;
Best Local Similarity 23.6%; Pred. No. 2e+03;
RESULT 1170
ID ADS96568 standard; protein; 1680 AA.
DE Drosophila melanogaster protein, SEQ ID 189.
PN WO2004039999-A2.
PD 13-MAY-2004.
PA (SYGN) SYNGENTA PARTICIPATIONS AG.

Query Match 4.3%; Score 73; DB 8; Length 1680;
Best Local Similarity 23.6%; Pred. No. 2e+03;
RESULT 1171
ID ADB79869 standard; protein; 1726 AA.
DE Rat putative chromatin structure regulator, SEQ ID 109.
FN EPI279744-A2.
PD 29-JAN-2003.
PA (WARN) WARNER LAMBERT CO.
Query Match 4.3%; Score 73; DB 7; Length 1726;
Best Local Similarity 22.0%; Pred. No. 2.1e+03;
RESULT 1172
ID ABB80243 standard; protein; 1877 AA.
DE Murine subtilase.
FN WO2003060109-A2.
PD 24-JUL-2003.
PA (FARB) BAYER AG.
Query Match 4.3%; Score 73; DB 7; Length 1877;
Best Local Similarity 25.8%; Pred. No. 2.3e+03;
RESULT 1173
ID AAB35264 standard; protein; 7036 AA.
DE Human P450RAI-3 protein #1.
FN WO200295034-A2.
PD 28-NOV-2002.
PA (CYTO-) CYTOCHROMA INC.
Query Match 4.3%; Score 73; DB 6; Length 7036;
Best Local Similarity 18.9%; Pred. No. 1.6e+04;
RESULT 1174
ID AAG98340 standard; protein; 204 AA.
DE Escherichia coli protein sequence SEQ ID NO:388.
FN WO200148209-A2.
PD 05-JUL-2001.
PA (ELIT-) ELITRA PHARM INC.
Query Match 4.3%; Score 72.5; DB 4; Length 204;
Best Local Similarity 28.2%; Pred. No. 1.1e+02;
RESULT 1175
ID ADS50663 standard; protein; 310 AA.
DE Bacterial polypeptide #19696.
FN US200333675-A1.
PD 18-DEC-2003.
PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
Query Match 4.3%; Score 72.5; DB 8; Length 310;
Best Local Similarity 22.9%; Pred. No. 2e+02;
RESULT 1176
ID AAG52385 standard; protein; 569 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 66583.
FN EPI033405-A2.
PD 06-SEP-2000.
Query Match 4.3%; Score 72.5; DB 3; Length 569;
Best Local Similarity 21.2%; Pred. No. 4.7e+02;
RESULT 1177
ID AAG52384 standard; protein; 639 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 66582.
FN EPI033405-A2.
PD 06-SEP-2000.
Query Match 4.3%; Score 72.5; DB 3; Length 639;
Best Local Similarity 21.2%; Pred. No. 5.5e+02;
RESULT 1178
ID ABP27691 standard; protein; 750 AA.
DE Streptococcus polypeptide SEQ ID NO 4558.
FN WO200234771-A2.
PD 02-MAY-2002.
PA (CHIR-) CHIRON SPA.
PA (GENO-) INST GENOMIC RES.
Query Match 4.3%; Score 72.5; DB 5; Length 750;
Best Local Similarity 20.4%; Pred. No. 7e+02;
RESULT 1179
ID AAG52383 standard; protein; 762 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 66581.
FN EPI033405-A2.

PD 06-SEP-2000.
Query Match 4.3%; Score 72.5; DB 3; Length 762;
Best Local Similarity 21.2%; Pred. No. 7.1e+02;
RESULT 1180
ID ADD78242 standard; protein; 912 AA.
DE Human CGDD-23.
FN WO200307875-A2.
PD 25-SEP-2003.
PA (INCY-) INCYTE GENOMICS INC.
Query Match 4.3%; Score 72.5; DB 7; Length 912;
Best Local Similarity 23.8%; Pred. No. 9.3e+02;
RESULT 1181
ID ABB11773 standard; peptide; 1011 AA.
DE Human TRAP95 homologue, SEQ ID NO:2143.
FN WO200157188-A2.
PD 09-AUG-2001.
PA (HYSE-) HYSEQ INC.
Query Match 4.3%; Score 72.5; DB 4; Length 1011;
Best Local Similarity 27.5%; Pred. No. 1.1e+03;
RESULT 1182
ID AAG68179 standard; protein; 1120 AA.
DE Mitotic spindle coiled-coil related protein SEQ ID NO:95.
FN WO20017327-A1.
PD 18-OCT-2001.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 4.3%; Score 72.5; DB 4; Length 1120;
Best Local Similarity 22.8%; Pred. No. 1.2e+03;
RESULT 1183
ID ABR41103 standard; protein; 1120 AA.
DE Human mitotic spindle coiled-coil gene DEEPEST protein product.
FN WO200292764-A2.
PD 21-NOV-2002.
PA (GENO-) GENOME THERAPEUTICS CORP.
PA (AMHP) WYETH.
Query Match 4.3%; Score 72.5; DB 6; Length 1120;
Best Local Similarity 22.8%; Pred. No. 1.2e+03;
RESULT 1184
ID ADB98723 standard; protein; 1120 AA.
DE Human mitotic spindle coiled-coil related protein.
FN WO200292000-A2.
PD 21-NOV-2002.
PA (GENO-) GENOME THERAPEUTICS CORP.
PA (AMHP) WYETH.
Query Match 4.3%; Score 72.5; DB 7; Length 1120;
Best Local Similarity 22.8%; Pred. No. 1.2e+03;
RESULT 1185
ID ADB82519 standard; protein; 1120 AA.
DE Human protein sequence related to the invention #9.
FN WO200292015-A2.
PD 21-NOV-2002.
PA (GENO-) GENOME THERAPEUTICS CORP.
PA (AMHP) WYETH.
Query Match 4.3%; Score 72.5; DB 7; Length 1120;
Best Local Similarity 22.8%; Pred. No. 1.2e+03;
RESULT 1186
ID ADN95291 standard; protein; 1120 AA.
DE Human BEC/LBC-related protein sequence SeqID213.
FN WO2003080640-A1.
PD 02-OCT-2003.
PA (LUDW-) LUDWIG INST CANCER RES.
PA (LICN) LICENTIA LTD.
Query Match 4.3%; Score 72.5; DB 7; Length 1120;
Best Local Similarity 22.8%; Pred. No. 1.2e+03;
RESULT 1187
ID ADF06193 standard; protein; 1213 AA.
DE Bacterial polypeptide #2306.
FN US6605709-B1.
PD 12-AUG-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 4.3%; Score 72.5; DB 7; Length 1213;
Best Local Similarity 22.8%; Pred. No. 1.4e+03;
RESULT 1188
ID AAM39120 standard; protein; 1246 AA.

DE Human polypeptide SEQ ID NO 2265.
PN WO200153312-A1.
PD 26-JUL-2001.
PA (HYSE-) HYSEQ INC.
ID AAM40906 standard; protein; 1294 AA.
DE Human polypeptide SEQ ID NO 5837.
PN WO200153312-A1.
PD 26-JUL-2001.
PA (HYSE-) HYSEQ INC.
Query Match 4.3%; Score 72.5; DB 4; Length 1294;
Best Local Similarity 20.1%; Pred. No. 1.5e+03;
RESULT 1190
ID AAR27819 standard; protein; 1451 AA.
DE CCYnaeavc spike protein.
PN EP510773-A1.
PD 28-OCT-1992.
PA (ALKU) AKZO NV.
PA (ALKU) AKZO NOBEL NV.
Query Match 4.3%; Score 72.5; DB 2; Length 1451;
Best Local Similarity 21.4%; Pred. No. 1.8e+03;
RESULT 1191
ID ADE14361 standard; protein; 1508 AA.
DE Human intracellular signalling (INTSIG) protein #9.
PN WO2003060064-A2.
PD 24-JUL-2003.
PA (INCY-) INCYTE GENOMICS INC.
Query Match 4.3%; Score 72.5; DB 7; Length 1508;
Best Local Similarity 20.1%; Pred. No. 1.9e+03;
RESULT 1192
ID ADN20474 standard; protein; 1970 AA.
DE Bacterial polypeptide #3127.
PN US2003233675-A1.
PD 18-DEC-2003.
PA (CAOY) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
Query Match 4.3%; Score 72.5; DB 8; Length 1970;
Best Local Similarity 24.7%; Pred. No. 2.8e+03;
RESULT 1193
ID ADO84848 standard; protein; 2402 AA.
DE S epidermidis surface anchored LPYTG protein SegID20.
PN WO2004025416-A2.
PD 25-MAR-2004.
PA (TEXA) UNIV TEXAS A & M SYSTEM.
PA (INHI-) INHIBITEX INC.
PA (UNBR-) UAB RES FOUND.
Query Match 4.3%; Score 72.5; DB 8; Length 2402;
Best Local Similarity 19.2%; Pred. No. 3.7e+03;
RESULT 1194
ID ADM05802 standard; protein; 278 AA.
DE Human protein of the invention SEQ ID NO:4487.
PN EP3347046-A1.
PD 24-SEP-2003.
PA (RNAS-) RBS ASSOC BIOTECHNOLOGY.
Query Match 4.3%; Score 72; DB 7; Length 278;
Best Local Similarity 19.0%; Pred. No. 1.9e+02;
RESULT 1195
ID AAG20312 standard; protein; 310 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 22450.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 4.3%; Score 72; DB 3; Length 310;
Best Local Similarity 21.5%; Pred. No. 2.2e+02;
RESULT 1196
ID AAG38738 standard; protein; 310 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 47835.
PN EP1033405-A2.
PD 06-SEP-2000.

Query Match 4.3%; Score 72; DB 3; Length 310;
Best Local Similarity 21.5%; Pred. No. 2.2e+02;
RESULT 1197
ID ABP8716 standard; protein; 315 AA.
DE Staphylococcus epidermidis ORF amino acid sequence SEQ ID NO:3561.
PN US6380370-B1.
PD 30-APR-2002.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 4.3%; Score 72; DB 5; Length 315;
Best Local Similarity 22.4%; Pred. No. 2.3e+02;
RESULT 1198
ID ADS05247 standard; protein; 315 AA.
DE Staphylococcus epidermis polypeptide seqid 4542.
PN US2004147734-A1.
PD 29-JUL-2004.
PA (DOUC/) DOUTETTE-STAMM L.
PA (BUSH/) BUSH D.
Query Match 4.3%; Score 72; DB 8; Length 315;
Best Local Similarity 22.4%; Pred. No. 2.3e+02;
RESULT 1199
ID ABB67153 standard; protein; 346 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 28251.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 4.3%; Score 72; DB 4; Length 346;
Best Local Similarity 37.9%; Pred. No. 2.6e+02;
RESULT 1200
ID ADS27474 standard; protein; 359 AA.
DE Bacterial polypeptide #16507.
PN US2003233675-A1.
PD 18-DEC-2003.
PA (CAOY) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
Query Match 4.3%; Score 72; DB 8; Length 359;
Best Local Similarity 19.8%; Pred. No. 2.7e+02;
RESULT 1201
ID AAM40215 standard; protein; 378 AA.
DE Human polypeptide SEQ ID NO 3360.
PN WO200153312-A1.
PD 26-JUL-2001.
PA (HYSE-) HYSEQ INC.
Query Match 4.3%; Score 72; DB 4; Length 378;
Best Local Similarity 20.2%; Pred. No. 2.9e+02;
RESULT 1202
ID ADN26620 standard; protein; 385 AA.
DE Bacterial polypeptide #9273.
PN US2003233675-A1.
PD 18-DEC-2003.
PA (CAOY) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
Query Match 4.3%; Score 72; DB 8; Length 385;
Best Local Similarity 19.6%; Pred. No. 3e+02;
RESULT 1203
ID ADS28708 standard; protein; 387 AA.
DE Bacterial polypeptide #17741.
PN US2003233675-A1.
PD 18-DEC-2003.
PA (CAOY) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
Query Match 4.3%; Score 72; DB 8; Length 387;
Best Local Similarity 19.6%; Pred. No. 3e+02;
RESULT 1204
ID ADR86186 standard; protein; 396 AA.

DE Aspergillus fumigatus essential gene protein #236.
 PN WO2004067709-A2.
 PD 12-AUG-2004.
 PA (ELIT-) ELITRA PHARM INC.
 PA (ELIT-) ELITRA CANADA LTD.
 Query Match 4.3%; Score 72; DB 8; Length 396;
 Best Local Similarity 20.6%; Pred. No. 3.1e+02;
 RESULT 1205
 ID AAR83413 standard; protein; 402 AA.
 DE Humicola insolens endoglucanase variant K217A.
 PN WO9524471-A1.
 PD 14-SEP-1995.
 PA (NOVO) NOVO-NORDISK AS.
 Query Match 4.3%; Score 72; DB 2; Length 402;
 Best Local Similarity 17.6%; Pred. No. 3.2e+02;
 RESULT 1206
 ID AAY35620 standard; protein; 430 AA.
 DE C. pneumoniae protein involved in metabolism of nucleic acids.
 PN WO9927105-A2.
 PD 03-JUN-1999.
 PA (GENST) GENSET.
 Query Match 4.3%; Score 72; DB 2; Length 430;
 Best Local Similarity 23.0%; Pred. No. 3.5e+02;
 RESULT 1207
 ID ABB93364 standard; protein; 450 AA.
 DE Herbicidically active polypeptide SEQ ID NO 2575.
 PN WO200210210-A2.
 PD 07-FEB-2002.
 PA (FARB) BAYER AG.
 Query Match 4.3%; Score 72; DB 5; Length 450;
 Best Local Similarity 20.1%; Pred. No. 3.8e+02;
 RESULT 1208
 ID ABB93037 standard; protein; 454 AA.
 DE Herbicidically active polypeptide SEQ ID NO 2248.
 PN WO200210210-A2.
 PD 07-FEB-2002.
 PA (FARB) BAYER AG.
 Query Match 4.3%; Score 72; DB 5; Length 454;
 Best Local Similarity 19.3%; Pred. No. 3.8e+02;
 RESULT 1209
 ID ABB93365 standard; protein; 464 AA.
 DE Herbicidically active polypeptide SEQ ID NO 2576.
 PN WO200210210-A2.
 PD 07-FEB-2002.
 PA (FARB) BAYER AG.
 Query Match 4.3%; Score 72; DB 5; Length 464;
 Best Local Similarity 18.3%; Pred. No. 3.9e+02;
 RESULT 1210
 ID ADN20815 standard; protein; 464 AA.
 DE Bacterial polypeptide #3468.
 PN US2003233675-A1.
 PD 18-DEC-2003.
 PA (CAOY) CAO Y.
 PA (HINK) HINKLE G J.
 PA (SLAT) SLATER S C.
 PA (CHEN) CHEN X.
 PA (GOLD) GOLDMAN B S.
 Query Match 4.3%; Score 72; DB 8; Length 464;
 Best Local Similarity 24.8%; Pred. No. 3.9e+02;
 RESULT 1211
 ID ADP47892 standard; protein; 470 AA.
 DE Human CATERPILLER 11.1 nucleotide binding domain (NBD) protein.
 PN WO2004034093-A2.
 PD 22-APR-2004.
 PA (UNIC) UNIV NORTH CAROLINA.
 Query Match 4.3%; Score 72; DB 8; Length 470;
 Best Local Similarity 20.9%; Pred. No. 4e+02;
 RESULT 1212
 ID ADN24068 standard; protein; 470 AA.
 DE Bacterial polypeptide #6721.
 PN US2003233675-A1.
 PD 18-DEC-2003.
 PA (CAOY) CAO Y.

PA (HINK) HINKLE G J.
 PA (SLAT) SLATER S C.
 PA (CHEN) CHEN X.
 PA (GOLD) GOLDMAN B S.
 Query Match 4.3%; Score 72; DB 8; Length 470;
 Best Local Similarity 20.7%; Pred. No. 4e+02;
 RESULT 1213
 ID AAW39422 standard; protein; 485 AA.
 DE ACC synthase protein.
 PN US5702933-A.
 PD 30-DEC-1997.
 PA (MONS) MONSANTO CO.
 Query Match 4.3%; Score 72; DB 2; Length 485;
 Best Local Similarity 20.3%; Pred. No. 4.2e+02;
 RESULT 1214
 ID ABG22476 standard; protein; 635 AA.
 DE Novel human diagnostic protein #22467.
 PN WO200175067-A2.
 PD 11-OCT-2001.
 PA (HYSE-) HYSEQ INC.
 Query Match 4.3%; Score 72; DB 4; Length 635;
 Best Local Similarity 20.2%; Pred. No. 6.2e+02;
 RESULT 1215
 ID AAO15588 standard; protein; 655 AA.
 DE Human PYRIN-7 protein #2.
 PN WO200261049-A2.
 PD 08-AUG-2002.
 PA (MILL-) MILLENNIUM PHARM INC.
 PA (AMHP) WYETH.
 Query Match 4.3%; Score 72; DB 5; Length 655;
 Best Local Similarity 20.9%; Pred. No. 6.5e+02;
 RESULT 1216
 ID ABB07264 standard; protein; 655 AA.
 DE Human APBG polypeptide (Incyte ID. 7474984CD1).
 PN WO200192527-A2.
 PD 06-DEC-2001.
 PA (INCY-) INCYTE GENOMICS INC.
 Query Match 4.3%; Score 72; DB 5; Length 655;
 Best Local Similarity 20.9%; Pred. No. 6.5e+02;
 RESULT 1217
 ID ADF94751 standard; protein; 655 AA.
 DE Human PYRIN-7 protein #2.
 PN WO2003089588-A2.
 PD 30-OCT-2003.
 PA (MILL-) MILLENNIUM PHARM INC.
 PA (AMHP) WYETH.
 Query Match 4.3%; Score 72; DB 7; Length 655;
 Best Local Similarity 20.9%; Pred. No. 6.5e+02;
 RESULT 1218
 ID ADJ19393 standard; protein; 655 AA.
 DE Human PANS PAD domain-containing full-length protein 2.
 PN US2004002593-A1.
 PD 01-JAN-2004.
 PA (REED) REED J C.
 PA (GODZ) GODZIK A.
 Query Match 4.3%; Score 72; DB 8; Length 655;
 Best Local Similarity 20.9%; Pred. No. 6.5e+02;
 RESULT 1219
 ID ABB61500 standard; protein; 677 AA.
 DE Drosophila melanogaster polypeptide SEQ ID NO 11292.
 PN WO200171042-A2.
 PD 27-SEP-2001.
 PA (PEKE) PE CORP NY.
 Query Match 4.3%; Score 72; DB 4; Length 677;
 Best Local Similarity 22.2%; Pred. No. 6.8e+02;
 RESULT 1220
 ID ABG22511 standard; protein; 692 AA.
 DE Novel human diagnostic protein #22502.
 PN WO200175067-A2.
 PD 11-OCT-2001.
 PA (HYSE-) HYSEQ INC.
 Query Match 4.3%; Score 72; DB 4; Length 692;
 Best Local Similarity 20.2%; Pred. No. 7e+02;

RESULT 1221
ID ABB53591 standard; protein; 712 AA.
DE Lactococcus lactis protein yjcC.
PN FR2807446-A1.
PD 12-OCT-2001.
PA (INRG) INRA INST NAT RECH AGRONOMIQUE.
Query Match 4.3%; Score 72; DB 5; Length 712;
Best Local Similarity 21.8%; Pred. No. 7.3e+02;
RESULT 1222
ID ABB68348 standard; protein; 751 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 31836.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 4.3%; Score 72; DB 4; Length 751;
Best Local Similarity 20.9%; Pred. No. 7.9e+02;
RESULT 1223
ID AAY77728 standard; protein; 1021 AA.
DE Human G protein-conjugated receptor HK05490.
PN WO200005264-A1.
PD 03-FEB-2000.
PA (TAKE) TAKEDA CHEM IND LTD.
PA (KAZU-) KAZUSA DNA RES INST.
Query Match 4.3%; Score 72; DB 3; Length 1021;
Best Local Similarity 21.7%; Pred. No. 1.2e+03;
RESULT 1224
ID ADE55164 standard; protein; 1021 AA.
DE Human Protein BAA34506, SEQ ID NO 969.
PN WO2003016475-A2.
PD 27-FEB-2003.
PA (GEHO) GEN HOSPITAL CORP.
PA (FARB) BAYER AG.
Query Match 4.3%; Score 72; DB 7; Length 1021;
Best Local Similarity 21.7%; Pred. No. 1.2e+03;
RESULT 1225
ID ADE55168 standard; protein; 1021 AA.
DE Human Protein BAA34506, SEQ ID NO 973.
PN WO2003016475-A2.
PD 27-FEB-2003.
PA (GEHO) GEN HOSPITAL CORP.
PA (FARB) BAYER AG.
Query Match 4.3%; Score 72; DB 7; Length 1021;
Best Local Similarity 21.7%; Pred. No. 1.2e+03;
RESULT 1226
ID ADE55172 standard; protein; 1021 AA.
DE Human Protein BAA34506, SEQ ID NO 977.
PN WO2003016475-A2.
PD 27-FEB-2003.
PA (GEHO) GEN HOSPITAL CORP.
PA (FARB) BAYER AG.
Query Match 4.3%; Score 72; DB 7; Length 1021;
Best Local Similarity 21.7%; Pred. No. 1.2e+03;
RESULT 1227
ID ADE55176 standard; protein; 1021 AA.
DE Human Protein BAA34506, SEQ ID NO 981.
PN WO2003016475-A2.
PD 27-FEB-2003.
PA (GEHO) GEN HOSPITAL CORP.
PA (FARB) BAYER AG.
Query Match 4.3%; Score 72; DB 7; Length 1021;
Best Local Similarity 21.7%; Pred. No. 1.2e+03;
RESULT 1228
ID ADI17023 standard; protein; 1056 AA.
DE Human NOVA protein homologue SegID 559.
PN WO200268649-A2.
PD 06-SEP-2002.
PA (CURA-) CURAGEN CORP.
Query Match 4.3%; Score 72; DB 5; Length 1056;
Best Local Similarity 22.4%; Pred. No. 1.3e+03;
RESULT 1229
ID AAY84034 standard; protein; 1109 AA.
DE Amino acid sequence of cancer associated polypeptide CH8-2a13-1.
PN WO200009655-A2.

PD 24-FEB-2000.
PA (CALP-) CALIFORNIA PACIFIC MEDICAL CENT RES INST.
PA (USGO) US GOVERNMENT.
Query Match 4.3%; Score 72; DB 3; Length 1109;
Best Local Similarity 19.6%; Pred. No. 1.4e+03;
RESULT 1230
ID ABJ29941 standard; protein; 1173 AA.
DE Protein encoded by Prokaryotic essential gene #15468.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 4.3%; Score 72; DB 6; Length 1173;
Best Local Similarity 21.4%; Pred. No. 1.5e+03;
RESULT 1231
ID ADC97053 standard; protein; 1183 AA.
DE E. faecium protein sequence SEQ ID 6680.
PN US6583275-B1.
PD 24-JUN-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 4.3%; Score 72; DB 7; Length 1183;
Best Local Similarity 21.4%; Pred. No. 1.5e+03;
RESULT 1232
ID ABC26275 standard; protein; 1459 AA.
DE Human NOV22 protein.
PN WO2003004687-A2.
PD 16-JAN-2003.
PA (CURA-) CURAGEN CORP.
Query Match 4.3%; Score 72; DB 7; Length 1459;
Best Local Similarity 21.7%; Pred. No. 2.1e+03;
RESULT 1233
ID ADM97582 standard; protein; 1488 AA.
DE Human calcium-independent alpha-latrotoxin receptor.
PN WO200403235-A1.
PD 15-APR-2004.
PA (FARB) BAYER HEALTHCARE AG.
Query Match 4.3%; Score 72; DB 8; Length 1488;
Best Local Similarity 21.7%; Pred. No. 2.1e+03;
RESULT 1234
ID ABG15534 standard; protein; 1909 AA.
DE Novel human diagnostic protein #15525.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match 4.3%; Score 72; DB 4; Length 1909;
Best Local Similarity 22.8%; Pred. No. 3e+03;
RESULT 1235
ID ABM84976 standard; protein; 2104 AA.
DE Human diagnostic and therapeutic pproteins SEQ ID NO:5225.
PN WO2004023973-A2.
PD 25-MAR-2004.
PA (INCY-) INCYTE CORP.
Query Match 4.3%; Score 72; DB 8; Length 2104;
Best Local Similarity 26.4%; Pred. No. 3.5e+03;
RESULT 1236
ID ABM83919 standard; protein; 3897 AA.
DE Human diagnostic and therapeutic pproteins SEQ ID NO:4168.
PN WO2004023973-A2.
PD 25-MAR-2004.
PA (INCY-) INCYTE CORP.
Query Match 4.3%; Score 72; DB 8; Length 3897;
Best Local Similarity 22.9%; Pred. No. 8.4e+03;
RESULT 1237
ID ABM83916 standard; protein; 3924 AA.
DE Human diagnostic and therapeutic pproteins SEQ ID NO:4165.
PN WO2004023973-A2.
PD 25-MAR-2004.
PA (INCY-) INCYTE CORP.
Query Match 4.3%; Score 72; DB 8; Length 3924;
Best Local Similarity 22.9%; Pred. No. 8.5e+03;
RESULT 1238
ID ABM83915 standard; protein; 3955 AA.
DE Human diagnostic and therapeutic pproteins SEQ ID NO:4164.
PN WO2004023973-A2.

PD 25-MAR-2004.
PA (INCY-) INCYTE CORP.
Query Match 4.3%; Score 72; DB 8; Length 3955;
Best Local Similarity 22.9%; Pred. No. 8.6e+03;
RESULT 1239
ID ABR63914 standard; protein; 3985 AA.
DE Human diagnostic and therapeutic pproteins SEQ ID NO:4163.
PN WO2004023973-A2.
PD 25-MAR-2004.
PA (INCY-) INCYTE CORP.
Query Match 4.3%; Score 72; DB 8; Length 3985;
Best Local Similarity 22.9%; Pred. No. 8.7e+03;
RESULT 1240
ID ABR63912 standard; protein; 4016 AA.
DE Human diagnostic and therapeutic pproteins SEQ ID NO:4161.
PN WO2004023973-A2.
PD 25-MAR-2004.
PA (INCY-) INCYTE CORP.
Query Match 4.3%; Score 72; DB 8; Length 4016;
Best Local Similarity 22.9%; Pred. No. 8.8e+03;
RESULT 1241
ID ABR63913 standard; protein; 4072 AA.
DE Human diagnostic and therapeutic pproteins SEQ ID NO:4162.
PN WO2004023973-A2.
PD 25-MAR-2004.
PA (INCY-) INCYTE CORP.
Query Match 4.3%; Score 72; DB 8; Length 4072;
Best Local Similarity 22.9%; Pred. No. 9e+03;
RESULT 1242
ID ABR63911 standard; protein; 4082 AA.
DE Human diagnostic and therapeutic pproteins SEQ ID NO:4160.
PN WO2004023973-A2.
PD 25-MAR-2004.
PA (INCY-) INCYTE CORP.
Query Match 4.3%; Score 72; DB 8; Length 4082;
Best Local Similarity 22.9%; Pred. No. 9e+03;
RESULT 1243
ID ADL94155 standard; protein; 105 AA.
DE Human RAP7 PHD domain amino acid sequence.
PN WO2004020581-A2.
PD 11-MAR-2004.
PA (FONC-) FUNCTIONAL GENETICS INC.
Query Match 4.2%; Score 71.5; DB 8; Length 105;
Best Local Similarity 25.7%; Pred. No. 52;
RESULT 1244
ID AAM94983 standard; protein; 118 AA.
DE Human reproductive system related antigen SEQ ID NO: 3641.
PN WO200155320-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 4.2%; Score 71.5; DB 4; Length 118;
Best Local Similarity 33.3%; Pred. No. 62;
RESULT 1245
ID ABR56561 standard; protein; 118 AA.
DE Human testicular antigen SEQ ID NO: 1075.
PN WO200155317-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 4.2%; Score 71.5; DB 4; Length 118;
Best Local Similarity 33.3%; Pred. No. 62;
RESULT 1246
ID ADH69160 standard; protein; 205 AA.
DE Human heat mitochondrial protein as a therapeutic target SegID966.
PN WO2003087768-A2.
PD 23-OCT-2003.
PA (MITO-) MITOKOR.
Query Match 4.2%; Score 71.5; DB 7; Length 205;
Best Local Similarity 22.8%; Pred. No. 1.4e+02;
RESULT 1247
ID ABR32501 standard; protein; 211 AA.
DE Novel human diagnostic protein #22492.
PN WO200175067-A2.

PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match 4.2%; Score 71.5; DB 4; Length 211;
Best Local Similarity 20.1%; Pred. No. 1.4e+02;
RESULT 1248
ID ADD94810 standard; protein; 245 AA.
DE Human TREM-4-alpha protein SEQ ID NO:4.
PN WO2003080667-A2.
PD 02-OCT-2003.
PA (BIOX-) BIOXEL SPA.
PA (THOM/) THOMAS N C.
Query Match 4.2%; Score 71.5; DB 7; Length 245;
Best Local Similarity 22.1%; Pred. No. 1.8e+02;
RESULT 1249
ID ABR94329 standard; protein; 261 AA.
DE Chlamydia pneumoniae protein sequence SEQ ID NO:517.
PN WO200208267-A2.
PD 31-JAN-2002.
PA (CORI-) CORIXA CORP.
Query Match 4.2%; Score 71.5; DB 5; Length 261;
Best Local Similarity 24.0%; Pred. No. 1.9e+02;
RESULT 1250
ID AA37752 standard; protein; 277 AA.
DE Amino acid sequence of a Chlamydia trachomatis protein.
PN WO9928475-A2.
PD 10-JUN-1999.
PA (GRST-) GENSET.
Query Match 4.2%; Score 71.5; DB 2; Length 277;
Best Local Similarity 22.1%; Pred. No. 2.1e+02;
RESULT 1251
ID AA442989 standard; protein; 280 AA.
DE Human ORF2753 polypeptide sequence SEQ ID NO:5506.
PN WO200058473-A2.
PD 05-OCT-2000.
PA (CURA-) CURAGEN CORP.
Query Match 4.2%; Score 71.5; DB 3; Length 280;
Best Local Similarity 21.3%; Pred. No. 2.1e+02;
RESULT 1252
ID ABR53624 standard; protein; 296 AA.
DE Protein sequence #SEQ ID 2113.
PN EP1238494-A1.
PD 20-NOV-2002.
PA (CELL-) CELLZOME AG.
Query Match 4.2%; Score 71.5; DB 6; Length 296;
Best Local Similarity 20.9%; Pred. No. 2.3e+02;
RESULT 1253
ID ADK64208 standard; protein; 296 AA.
DE Disease treating protein complex-derived protein #1271.
PN EP1338608-A2.
PD 27-AUG-2003.
PA (CELL-) CELLZOME AG.
Query Match 4.2%; Score 71.5; DB 6; Length 296;
Best Local Similarity 20.9%; Pred. No. 2.3e+02;
RESULT 1254
ID ABR68066 standard; protein; 298 AA.
DE Photoreceptor protein sequence #1163.
PN WO200294667-A2.
PD 28-NOV-2002.
PA (INSP-) INST PASTEUR.
PA (CNRS) CNRS CENT NAT RECH SCI.
Query Match 4.2%; Score 71.5; DB 6; Length 298;
Best Local Similarity 21.3%; Pred. No. 2.4e+02;
RESULT 1255
ID ADS45238 standard; protein; 322 AA.
DE Bacterial polypeptide #23668.
PN US200323675-A1.
PD 18-DEC-2003.
PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
Query Match 4.2%; Score 71.5; DB 8; Length 322;

Best Local Similarity 24.1%; Pred. No. 2.6e+02;
 RESULT 1256
 ID ADO62814 standard; protein; 350 AA.
 DE Pseudomonas fluorescens satracin protein Sacc.
 PN WO2004056898-A1.
 PD 08-JUL-2004.
 PA (PHAR-) PHARMA MAR SA.
 (RUFF/) RUFFLES G K.
 Query Match
 Best Local Similarity 22.4%; Pred. No. 3e+02; Length 350;
 RESULT 1257
 ID ADS24938 standard; protein; 372 AA.
 DE Bacterial polypeptide #13971.
 PN US200333675-A1.
 PD 18-DEC-2003.
 PA (CAOY/) CAO Y.
 (HINK/) HINKLE G J.
 (SLAT/) SLATER S C.
 (CHEN/) CHEN X.
 (GOLD/) GOLDMAN B S.
 Query Match
 Best Local Similarity 21.8%; Pred. No. 3.2e+02; Length 372;
 RESULT 1258
 ID AAG49938 standard; protein; 380 AA.
 DE Arabidopsis thaliana protein fragment SEQ ID NO: 63228.
 PN EPI033405-A2.
 PD 06-SEP-2000.
 Query Match
 Best Local Similarity 24.4%; Pred. No. 3.3e+02; Length 380;
 RESULT 1259
 ID AAG52338 standard; protein; 380 AA.
 DE Arabidopsis thaliana protein fragment SEQ ID NO: 66520.
 PN EPI033405-A2.
 PD 06-SEP-2000.
 Query Match
 Best Local Similarity 24.4%; Pred. No. 3.3e+02; Length 380;
 RESULT 1260
 ID ABUS4578 standard; protein; 457 AA.
 DE Human NOVX polypeptide #37.
 PN WO200281498-A2.
 PD 17-OCT-2002.
 PA (CORA-) CURAGEN CORP.
 Query Match
 Best Local Similarity 18.8%; Pred. No. 4.3e+02; Length 457;
 RESULT 1261
 ID ABB65348 standard; protein; 465 AA.
 DE Drosophila melanogaster polypeptide SEQ ID NO 22836.
 PN WO200171042-A2.
 PD 27-SEP-2001.
 PA (PEKE-) PE CORP NY.
 Query Match
 Best Local Similarity 20.6%; Pred. No. 4.5e+02; Length 465;
 RESULT 1262
 ID ADJ71966 standard; protein; 581 AA.
 DE Human PMM protein amino acid sequence SegID26.
 PN WO2004009797-A2.
 PD 29-JAN-2004.
 PA (INCY-) INCYTE CORP.
 Query Match
 Best Local Similarity 25.8%; Pred. No. 6.1e+02; Length 581;
 RESULT 1263
 ID ABR39836 standard; protein; 590 AA.
 DE Human SCAP polypeptide-incyte Id. 71231045CD1.
 PN WO2003008625-A2.
 PD 30-JAN-2003.
 PA (INCY-) INCYTE GENOMICS INC.
 Query Match
 Best Local Similarity 23.9%; Pred. No. 6.3e+02; Length 590;
 RESULT 1264
 ID ADO09827 standard; protein; 681 AA.
 DE Hamster SGLT homologue protein SEQ ID NO:50.
 PN WO2004039405-A1.
 PD 13-MAY-2004.

PA (TAKE) TAKEDA CHEM IND LTD.
 Query Match
 Best Local Similarity 4.2%; Score 71.5; DB 8; Length 681;
 RESULT 1265
 ID ABG71433 standard; protein; 683 AA.
 DE Human protease polypeptide.
 PN US200237180-A1.
 PD 26-SEP-2002.
 PA (GANW/) GAN W.
 (YEUJ/) YE J.
 (DFRA/) DI FRANCESCO V.
 (BEAS/) BEASLEY E M.
 Query Match
 Best Local Similarity 4.2%; Score 71.5; DB 6; Length 683;
 RESULT 1266
 ID ADG62973 standard; protein; 683 AA.
 DE Human protease protein.
 PN US2003054489-A1.
 PD 20-MAR-2003.
 PA (APPL-) APPLERA CORP.
 Query Match
 Best Local Similarity 24.0%; Pred. No. 7.8e+02; Length 683;
 RESULT 1267
 ID ABR33183 standard; protein; 691 AA.
 DE Protein sequence #SEQ ID 1231.
 PN EPI258494-A1.
 PD 20-NOV-2002.
 PA (CELI-) CELIZOME AG.
 Query Match
 Best Local Similarity 4.2%; Score 71.5; DB 6; Length 691;
 RESULT 1268
 ID ADK63218 standard; protein; 691 AA.
 DE Disease treating protein complex-derived protein #735.
 PN EPI338608-A2.
 PD 27-AUG-2003.
 PA (CELI-) CELIZOME AG.
 Query Match
 Best Local Similarity 22.2%; Pred. No. 7.9e+02; Length 691;
 RESULT 1269
 ID ABB69814 standard; protein; 712 AA.
 DE Human polypeptide SEQ ID NO 1861.
 PN WO200270539-A2.
 PD 12-SEP-2002.
 PA (HYSE-) HYSEQ INC.
 Query Match
 Best Local Similarity 4.2%; Score 71.5; DB 5; Length 712;
 RESULT 1270
 ID ABM83343 standard; protein; 719 AA.
 DE Human diagnostic and therapeutic pproteins SEQ ID NO:3592.
 PN WO2004023973-A2.
 PD 25-MAR-2004.
 PA (INCY-) INCYTE CORP.
 Query Match
 Best Local Similarity 24.0%; Pred. No. 8.3e+02; Length 719;
 RESULT 1271
 ID ABP97463 standard; protein; 737 AA.
 DE Mouse Delta/Notch-like BGF-related receptor (DNMR).
 PN WO2003029467-A1.
 PD 10-APR-2003.
 PA (NISC-) JAPAN SCI & TECHNOLOGY CORP.
 Query Match
 Best Local Similarity 20.5%; Pred. No. 8.7e+02; Length 737;
 RESULT 1272
 ID ABB59751 standard; protein; 773 AA.
 DE Drosophila melanogaster polypeptide SEQ ID NO 6045.
 PN WO200171042-A2.
 PD 27-SEP-2001.
 PA (PEKE-) PE CORP NY.
 Query Match
 Best Local Similarity 19.8%; Pred. No. 9.3e+02; Length 773;
 RESULT 1273
 ID AB145257 standard; protein; 784 AA.
 DE Rice isoprenoid biosynthesis-associated protein #94.

PN US2004010815-A1.
 PD 15-JAN-2004.
 PA (LANG/) LANGE B M.
 DE (GHAS/) GHASSEMIAN M.
 PN (BRIG/) BRIGGS S P.
 PD (COOP/) COOPER B.
 PA (GLAZ/) GLAZEBROOK J.
 DE (GOFF/) GOFF S A.
 PN (KATA/) KATAGIRI F.
 PD (KREP/) KREPS J.
 PA (MOUG/) MOUGHAMER T.
 DE (PROV/) PROVANT N.
 PN (RICK/) RICHE D.
 PD (ZHUT/) ZHU T.
 PA (ZHU/) ZHU T.
 Query Match
 Best Local Similarity 22.1%; Score 71.5; DB 8; Length 784;
 RESULT 1274
 ID ADD46952 standard; protein; 796 AA.
 DE Rat Protein AAA41983, SEQ ID NO 12638.
 PN WO2003016475-A2.
 PD 27-FEB-2003.
 PA (GEHO) GEN HOSPITAL CORP.
 DE (FARB) BAYER AG.
 Query Match
 Best Local Similarity 19.8%; Score 71.5; DB 7; Length 796;
 RESULT 1275
 ID ADN21143 standard; protein; 958 AA.
 DE Bacterial polypeptide #3796.
 PN US2003233675-A1.
 PD 18-DEC-2003.
 PA (CAOY/) CAO Y.
 DE (HINK/) HINKLE G J.
 PN (SLAT/) SLATER S C.
 PD (CHEN/) CHEN X.
 PA (GOLD/) GOLDMAN B S.
 Query Match
 Best Local Similarity 22.6%; Score 71.5; DB 8; Length 958;
 RESULT 1276
 ID ABR53536 standard; protein; 1056 AA.
 DE Protein sequence #SEQ ID 1937.
 PN EPI258494-A1.
 PD 20-NOV-2002.
 PA (CELL-) CELLZOME AG.
 Query Match
 Best Local Similarity 19.1%; Score 71.5; DB 6; Length 1056;
 RESULT 1277
 ID ADK64418 standard; protein; 1056 AA.
 DE Disease treating protein complex-derived protein #1166.
 PN EPI338608-A2.
 PD 27-AUG-2003.
 PA (CELL-) CELLZOME AG.
 Query Match
 Best Local Similarity 4.2%; Score 71.5; DB 7; Length 1056;
 RESULT 1278
 ID ABR35715 standard; protein; 1063 AA.
 DE Fungal ZBC protein sequence #141.
 PN WO200224865-A2.
 PD 28-MAR-2002.
 PA (MICR-) MICROBIA INC.
 Query Match
 Best Local Similarity 20.9%; Score 71.5; DB 5; Length 1063;
 RESULT 1279
 ID ABR35714 standard; protein; 1068 AA.
 DE Fungal ZBC protein sequence #140.
 PN WO200224865-A2.
 PD 28-MAR-2002.
 PA (MICR-) MICROBIA INC.
 Query Match
 Best Local Similarity 4.2%; Score 71.5; DB 5; Length 1068;
 RESULT 1280
 ID ADK63116 standard; protein; 1068 AA.
 DE Disease treating protein complex-derived protein #684.
 PN EPI338608-A2.

PD 27-AUG-2003.
 PA (CELL-) CELLZOME AG.
 Query Match
 Best Local Similarity 4.2%; Score 71.5; DB 7; Length 1068;
 RESULT 1281
 ID ADN23310 standard; protein; 1086 AA.
 DE Bacterial polypeptide #5963.
 PN US2003233675-A1.
 PD 18-DEC-2003.
 PA (CAOY/) CAO Y.
 DE (HINK/) HINKLE G J.
 PN (SLAT/) SLATER S C.
 PD (CHEN/) CHEN X.
 PA (GOLD/) GOLDMAN B S.
 Query Match
 Best Local Similarity 19.7%; Score 71.5; DB 8; Length 1086;
 RESULT 1282
 ID ADN21411 standard; protein; 1170 AA.
 DE Bacterial polypeptide #4064.
 PN US2003233675-A1.
 PD 18-DEC-2003.
 PA (CAOY/) CAO Y.
 DE (HINK/) HINKLE G J.
 PN (SLAT/) SLATER S C.
 PD (CHEN/) CHEN X.
 PA (GOLD/) GOLDMAN B S.
 Query Match
 Best Local Similarity 21.2%; Score 71.5; DB 8; Length 1170;
 RESULT 1283
 ID AAB62201 standard; protein; 1247 AA.
 DE Cell cycle protein Radh-Isoform 1.
 PN WO200121784-A2.
 PD 29-MAR-2001.
 PA (RIGE-) RIGEL PHARM INC.
 Query Match
 Best Local Similarity 22.8%; Score 71.5; DB 4; Length 1247;
 RESULT 1284
 ID ABE15099 standard; protein; 1607 AA.
 DE Novel human diagnostic protein #15090.
 PN WO200175067-A2.
 PD 11-OCT-2001.
 PA (HYSE-) HYSEQ INC.
 Query Match
 Best Local Similarity 4.2%; Score 71.5; DB 4; Length 1607;
 RESULT 1285
 ID AAO16433 standard; protein; 1712 AA.
 DE Human nucleic acid-associated protein (MAAP) - SEQ ID NO 30.
 PN WO200300864-A2.
 PD 03-JAN-2003.
 PA (INCY-) INCYTE GENOMICS INC.
 Query Match
 Best Local Similarity 4.2%; Score 71.5; DB 6; Length 1712;
 RESULT 1286
 ID ABE62532 standard; protein; 1713 AA.
 DE Human diagnostic and therapeutic pprotein SEQ ID NO:2781.
 PN WO2004023973-A2.
 PD 25-MAR-2004.
 PA (INCY-) INCYTE CORP.
 Query Match
 Best Local Similarity 19.1%; Score 71.5; DB 8; Length 1713;
 RESULT 1287
 ID AAY51843 standard; protein; 2427 AA.
 DE Murine embryo macrophage m18.1 protein.
 PN DE19839096-A1.
 PD 02-MAR-2000.
 PA (HOWA/) HOWARD J.
 DE (PREF/) PFEFFER K.
 Query Match
 Best Local Similarity 4.2%; Score 71.5; DB 3; Length 2427;
 RESULT 1288
 ID AAD70656 standard; protein; 2527 AA.
 DE Human heat mitochondrial protein as a therapeutic target SeqID2462.
 PN WO2003087768-A2.

PD 23-OCT-2003.
PA (MITO-) MITOKOR.
PA (BUCK-) BUCK INST AGE RES.
Query Match 4.2%; Score 71.5; DB 7; Length 2527;
RESULT 1289
ID AD699060 standard; protein; 2715 AA.
DE Human heat mitochondrial protein as a therapeutic target SegID866.
PN WO2003087768-A2.
PD 23-OCT-2003.
PA (MITO-) MITOKOR.
PA (BUCK-) BUCK INST AGE RES.
Query Match 4.2%; Score 71.5; DB 7; Length 2715;
RESULT 1290
ID AD645526 standard; protein; 3712 AA.
DE Pan troglodytes AKAP450 amino acid sequence.
PN WO2003102587-A1.
PD 11-DEC-2003.
PA (UYED-) UNIV EDINBURGH.
Query Match 4.2%; Score 71.5; DB 8; Length 3712;
RESULT 1291
ID ABB53996 standard; protein; 153 AA.
DE Lactococcus lactis protein ygiB.
PN FR2807446-A1.
PD 12-OCT-2001.
PA (INRG) INRA INST NAT RECH AGRONOMIQUE.
Query Match 4.2%; Score 71; DB 5; Length 153;
RESULT 1292
ID ABB13179 standard; protein; 165 AA.
DE Protein encoded by Prokaryotic essential gene #16906.
PN WO20027183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 4.2%; Score 71; DB 6; Length 165;
RESULT 1293
ID ABB62115 standard; protein; 182 AA.
DE Tumour-associated antigenic target (PAT) polypeptide PRO83035, SEQ:5464.
PN WO2004030615-A2.
PD 15-APR-2004.
PA (GERH) GENENTECH INC.
Query Match 4.2%; Score 71; DB 8; Length 182;
RESULT 1294
ID ABO58838 standard; protein; 191 AA.
DE Human genome derived single exon protein #5072.
PN US2003194704-A1.
PD 16-OCT-2003.
PA (PERN/) PERN S G.
PA (RANK/) RANK D R.
PA (HANK/) HANKEL D K.
Query Match 4.2%; Score 71; DB 8; Length 191;
RESULT 1295
ID ADN99615 standard; protein; 239 AA.
DE Novel human protein sequence #431.
PN WO2004038003-A2.
PD 06-MAY-2004.
PA (FIVE-) FIVE PRIME THERAPEUTICS INC.
Query Match 4.2%; Score 71; DB 8; Length 239;
RESULT 1296
ID ADN99614 standard; protein; 239 AA.
DE Novel human protein sequence #430.
PN WO2004038003-A2.
PD 06-MAY-2004.
PA (FIVE-) FIVE PRIME THERAPEUTICS INC.
Query Match 4.2%; Score 71; DB 8; Length 239;
RESULT 1297
ID ABB43241 standard; protein; 468 AA.
DE Human ORF3005 polypeptide sequence SEQ ID NO:6010.

ID ABO70063 standard; protein; 257 AA.
DE Pseudomonas aeruginosa polypeptide #238.
PN US6551795-B1.
PD 22-APR-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 4.2%; Score 71; DB 7; Length 257;
RESULT 1298
ID AAG31375 standard; protein; 322 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 37668.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 4.2%; Score 71; DB 3; Length 322;
RESULT 1299
ID AAG31374 standard; protein; 327 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 37667.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 4.2%; Score 71; DB 3; Length 327;
RESULT 1300
ID ABB8449 standard; peptide; 327 AA.
DE Siah-related protein atSina2.
PN WO200262838-A1.
PD 15-AUG-2002.
PA (MACC-) MACC-LLM CANCER INST MEDICAL RES.
PA (SVTN-) ST VINCENTS INST MEDICAL RES.
Query Match 4.2%; Score 71; DB 5; Length 327;
RESULT 1301
ID ADF07575 standard; protein; 330 AA.
DE Bacterial polypeptide #3688.
PN US6605709-B1.
PD 12-AUG-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 4.2%; Score 71; DB 7; Length 330;
RESULT 1302
ID ABB68964 standard; protein; 399 AA.
DE Human long-chain prenyl diphosphate synthase-related protein.
PN WO200270539-A2.
PD 12-SEP-2002.
PA (HYSE-) HYSEQ INC.
Query Match 4.2%; Score 71; DB 5; Length 399;
RESULT 1303
ID ABB70710 standard; protein; 399 AA.
DE Human long-chain prenyl diphosphate synthase-related protein.
PN WO200292811-A1.
PD 21-NOV-2002.
PA (KANF-) KANEXA CORP.
Query Match 4.2%; Score 71; DB 6; Length 399;
RESULT 1304
ID AAR83415 standard; protein; 402 AA.
DE Humicola insolens endoglucanase variant R245G.
PN WO9524471-A1.
PD 14-SEP-1995.
PA (NOVO) NOVO-NORDISK AS.
Query Match 4.2%; Score 71; DB 2; Length 402;
RESULT 1305
ID ADO29463 standard; protein; 410 AA.
DE Mouse GPCR GPRC5B, SEQ ID NO:565.
PN WO2004040000-A2.
PD 13-MAY-2004.
PA (PRIM-) PRIMAL INC.
Query Match 4.2%; Score 71; DB 8; Length 410;
RESULT 1306
ID AAB43241 standard; protein; 468 AA.
DE Human ORF3005 polypeptide sequence SEQ ID NO:6010.

PN WO200058473-A2.
 PD 05-OCT-2000.
 PA (CURA-) CURAGEN CORP.
 Query Match 4.2%; Score 71; DB 3; Length 469;
 Best Local Similarity 18.8%; Pred. No. 5.1e+02;
 RESULT 1307
 ID AD669084 standard; protein; 468 AA.
 DE Human heat mitochondrial protein as a therapeutic target SeqID890.
 PN WO2003087768-A2.
 PD 23-OCT-2003.
 PA (MITO-) MITOKOR.
 PA (BUCK-) BUCK INST AGE RES.
 Query Match 4.2%; Score 71; DB 7; Length 468;
 Best Local Similarity 18.8%; Pred. No. 5.1e+02;
 RESULT 1308
 ID ABU49321 standard; protein; 511 AA.
 DE Protein encoded by Prokaryotic essential gene #34848.
 PN WO20027183-A2.
 PD 03-OCT-2002.
 PA (ELIT-) ELITRA PHARM INC.
 Query Match 4.2%; Score 71; DB 6; Length 511;
 Best Local Similarity 20.4%; Pred. No. 5.8e+02;
 RESULT 1309
 ID ABR53129 standard; protein; 566 AA.
 DE Protein sequence #SEQ ID 1123.
 PN EPI258494-A1.
 PD 20-NOV-2002.
 PA (CELL-) CELLZOME AG.
 Query Match 4.2%; Score 71; DB 6; Length 566;
 Best Local Similarity 18.8%; Pred. No. 6.7e+02;
 RESULT 1310
 ID AD662560 standard; protein; 566 AA.
 DE Disease treating protein complex-derived protein #406.
 PN EPI338608-A2.
 PD 27-AUG-2003.
 PA (CELL-) CELLZOME AG.
 Query Match 4.2%; Score 71; DB 7; Length 566;
 Best Local Similarity 18.8%; Pred. No. 6.7e+02;
 RESULT 1311
 ID AD128044 standard; protein; 579 AA.
 DE ECMCAD protein 4148119CD1.
 PN WO200202634-A2.
 PD 10-JAN-2002.
 PA (INCY-) INCYTE GENOMICS INC.
 Query Match 4.2%; Score 71; DB 5; Length 579;
 Best Local Similarity 19.3%; Pred. No. 6.9e+02;
 RESULT 1312
 ID ADP04513 standard; protein; 657 AA.
 DE Sea squirt protein with tissue specific expression in development Seq108.
 PN JP2004057129-A.
 PD 26-FEB-2004.
 PA (KAGA-) KAGAKU GIUTSU SHINKO JIGYODAN.
 Query Match 4.2%; Score 71; DB 8; Length 657;
 Best Local Similarity 19.3%; Pred. No. 8.3e+02;
 RESULT 1313
 ID AD117120 standard; protein; 666 AA.
 DE Human NOVX protein homologue SeqID 656.
 PN WO200268649-A2.
 PD 06-SEP-2002.
 PA (CURA-) CURAGEN CORP.
 Query Match 4.2%; Score 71; DB 5; Length 666;
 Best Local Similarity 22.3%; Pred. No. 8.4e+02;
 RESULT 1314
 ID AD117121 standard; protein; 669 AA.
 DE Human NOVX protein homologue SeqID 657.
 PN WO200268649-A2.
 PD 06-SEP-2002.
 PA (CURA-) CURAGEN CORP.
 Query Match 4.2%; Score 71; DB 5; Length 669;
 Best Local Similarity 22.3%; Pred. No. 8.5e+02;
 RESULT 1315
 ID ADQ89136 standard; protein; 669 AA.
 DE Human urologic disorder related protein 14303 SEQ:88.

PN WO2004065576-A2.
 PD 05-AUG-2004.
 PA (MILL-) MILLENNIUM PHARM INC.
 Query Match 4.2%; Score 71; DB 8; Length 669;
 Best Local Similarity 22.3%; Pred. No. 8.5e+02;
 RESULT 1316
 ID AD844922 standard; protein; 669 AA.
 DE Polypeptide 14303 amino acid sequence.
 PN WO2004071411-A2.
 PD 26-AUG-2004.
 PA (MILL-) MILLENNIUM PHARM INC.
 Query Match 4.2%; Score 71; DB 8; Length 669;
 Best Local Similarity 22.3%; Pred. No. 8.5e+02;
 RESULT 1317
 ID ABB71254 standard; protein; 685 AA.
 DE Drosophila melanogaster polypeptide SEQ ID NO 40554.
 PN WO200171042-A2.
 PD 27-SEP-2001.
 PA (PEKE-) PE CORP NY.
 Query Match 4.2%; Score 71; DB 4; Length 685;
 Best Local Similarity 20.1%; Pred. No. 8.8e+02;
 RESULT 1318
 ID ABB68912 standard; protein; 716 AA.
 DE Photorhabdus luminescens protein sequence #2009.
 PN WO200294867-A2.
 PD 28-NOV-2002.
 PA (INSP-) INST. PASTEUR.
 PA (CNRS-) CNRS CENT NAT RECH SCI.
 Query Match 4.2%; Score 71; DB 6; Length 716;
 Best Local Similarity 22.6%; Pred. No. 9.4e+02;
 RESULT 1319
 ID ADS29971 standard; protein; 751 AA.
 DE Bacterial polypeptide #19004.
 PN US2003233675-A1.
 PD 18-DEC-2003.
 PA (CAOY/) CAO Y.
 PA (HINK/) HINKLE G J.
 PA (SLAT/) SLATER S C.
 PA (CHEN/) CHEN X.
 PA (GOLD/) GOLDMAN B S.
 Query Match 4.2%; Score 71; DB 8; Length 751;
 Best Local Similarity 22.3%; Pred. No. 1e+03;
 RESULT 1320
 ID ABB48512 standard; protein; 765 AA.
 DE Listeria monocytogenes protein #1216.
 PN WO200177335-A2.
 PD 18-OCT-2001.
 PA (INSP-) INST. PASTEUR.
 Query Match 4.2%; Score 71; DB 5; Length 765;
 Best Local Similarity 21.3%; Pred. No. 1e+03;
 RESULT 1321
 ID ABB91316 standard; protein; 776 AA.
 DE Hericidially active polypeptide SEQ ID NO 527.
 PN WO200210210-A2.
 PD 07-FEB-2002.
 PA (FARB-) BAYER AG.
 Query Match 4.2%; Score 71; DB 5; Length 776;
 Best Local Similarity 19.7%; Pred. No. 1.1e+03;
 RESULT 1322
 ID ABB93377 standard; protein; 794 AA.
 DE Hericidially active polypeptide SEQ ID NO 2588.
 PN WO200210210-A2.
 PD 07-FEB-2002.
 PA (FARB-) BAYER AG.
 Query Match 4.2%; Score 71; DB 5; Length 794;
 Best Local Similarity 19.5%; Pred. No. 1.1e+03;
 RESULT 1323
 ID AAR41869 standard; protein; 836 AA.
 DE Human OSF-2.
 PN EP562508-A2.
 PD 29-SEP-1993.
 PA (FARB-) HOECHST JAPAN LTD.
 Query Match 4.2%; Score 71; DB 2; Length 836;

Best Local Similarity 20.3%; Pred. No. 1.2e+03;
RESULT 1324
ID AAE06520 standard; protein; 836 AA.
DE Human OSF-2 (perlestin) protein.
PN WO200157062-A1.
PD 09-AUG-2001.
PA (GENE-) GENE LOGIC INC.
Query Match 4.2%; Score 71; DB 4; Length 836;
Best Local Similarity 20.3%; Pred. No. 1.2e+03;
RESULT 1325
ID AAV79826 standard; protein; 836 AA.
DE OSF-2 protein associated protein #4.
PN WO200220055-A1.
PD 14-MAR-2002.
PA (SUNR) SUNTORY LTD.
Query Match 4.2%; Score 71; DB 5; Length 836;
Best Local Similarity 20.3%; Pred. No. 1.2e+03;
RESULT 1326
ID ABJ05566 standard; protein; 836 AA.
DE Breast cancer-associated protein 31.
PN WO200259377-A2.
PD 01-AUG-2002.
PA (EOSB-) EOS BIOTECHNOLOGY INC.
Query Match 4.2%; Score 71; DB 5; Length 836;
Best Local Similarity 20.3%; Pred. No. 1.2e+03;
RESULT 1327
ID AAO21726 standard; protein; 836 AA.
DE Human allergy-associated protein SEQ ID NO 33.
PN WO200252006-A1.
PD 04-JUL-2002.
PA (GENO-) GENOX RES INC.
Query Match 4.2%; Score 71; DB 5; Length 836;
Best Local Similarity 20.3%; Pred. No. 1.2e+03;
RESULT 1328
ID ABR48235 standard; protein; 836 AA.
DE Human bladder cancer associated protein sequence SEQ ID NO:191.
PN WO2003003906-A2.
PD 16-JAN-2003.
PA (EOSB-) EOS BIOTECHNOLOGY INC.
Query Match 4.2%; Score 71; DB 6; Length 836;
Best Local Similarity 20.3%; Pred. No. 1.2e+03;
RESULT 1329
ID ABUS6601 standard; protein; 836 AA.
DE Lung cancer-associated polypeptide #194.
PN WO200286443-A2.
PD 31-OCT-2002.
PA (EOSB-) EOS BIOTECHNOLOGY INC.
Query Match 4.2%; Score 71; DB 6; Length 836;
Best Local Similarity 20.3%; Pred. No. 1.2e+03;
RESULT 1330
ID ABR47552 standard; protein; 836 AA.
DE Breast cancer associated protein sequence SEQ ID NO:342.
PN WO2003004989-A2.
PD 16-JAN-2003.
PA (MILL-) MILLENIUM PHARM INC.
Query Match 4.2%; Score 71; DB 6; Length 836;
Best Local Similarity 20.3%; Pred. No. 1.2e+03;
RESULT 1331
ID ABP96201 standard; protein; 836 AA.
DE Human osteoblast-specific factor-2 (OSF-2) protein SEQ ID NO:2.
PN WO2003016471-A2.
PD 27-FEB-2003.
PA (DAND) DNA PARBER CANCER INST INC.
Query Match 4.2%; Score 71; DB 6; Length 836;
Best Local Similarity 20.3%; Pred. No. 1.2e+03;
RESULT 1332
ID ABR92134 standard; protein; 836 AA.
DE Human cervical cancer cell marker protein SEQ ID NO:178.
PN WO2002101075-A2.
PD 19-DEC-2002.
PA (MILL-) MILLENIUM PHARM INC.
Query Match 4.2%; Score 71; DB 6; Length 836;

Best Local Similarity 20.3%; Pred. No. 1.2e+03;
RESULT 1333
ID ABB80502 standard; protein; 836 AA.
DE Ovarian cancer-associated protein #33.
PN WO2002102235-A2.
PD 27-DEC-2002.
PA (EOSB-) EOS BIOTECHNOLOGY INC.
Query Match 4.2%; Score 71; DB 7; Length 836;
Best Local Similarity 20.3%; Pred. No. 1.2e+03;
RESULT 1334
ID ADN38718 standard; protein; 836 AA.
DE Cancer/angiogenesis/fibrosis-related polypeptide, SEQ ID NO:36.
PN WO2003042661-A2.
PD 22-MAY-2003.
PA (EOSB-) EOS BIOTECHNOLOGY INC.
Query Match 4.2%; Score 71; DB 7; Length 836;
Best Local Similarity 20.3%; Pred. No. 1.2e+03;
RESULT 1335
ID ADP65282 standard; protein; 836 AA.
DE Human osteoblast specific factor 2 (fasciclin I-like).
PN WO2003072827-A1.
PD 04-SEP-2003.
PA (CHIL-) CHILDREN'S HOSPITAL MEDICAL CENT.
Query Match 4.2%; Score 71; DB 7; Length 836;
Best Local Similarity 20.3%; Pred. No. 1.2e+03;
RESULT 1336
ID ADJ75297 standard; protein; 836 AA.
DE Marker gene related amino acid sequence SEQ ID NO:549.
PN EP1394274-A2.
PD 03-MAR-2004.
PA (GENO-) GENOX RES INC.
Query Match 4.2%; Score 71; DB 8; Length 836;
Best Local Similarity 20.3%; Pred. No. 1.2e+03;
RESULT 1337
ID ADN04500 standard; protein; 836 AA.
DE Antiproliferative protein sequence #443.
PN WO2004028479-A2.
PD 08-APR-2004.
PA (GERTH) GENENTECH INC.
Query Match 4.2%; Score 71; DB 8; Length 836;
Best Local Similarity 20.3%; Pred. No. 1.2e+03;
RESULT 1338
ID ADO19060 standard; protein; 836 AA.
DE Human soft tissue sarcoma-upregulated protein - SEQ ID 1879.
PN WO2004048938-A2.
PD 10-JUN-2004.
PA (PROT-) PROTEIN DESIGN LABS INC.
Query Match 4.2%; Score 71; DB 8; Length 836;
Best Local Similarity 20.3%; Pred. No. 1.2e+03;
RESULT 1339
ID ADQ30566 standard; protein; 836 AA.
DE Pancreas cancer marker - osteoblast specific factor 2 precursor.
PN WO2004055519-A2.
PD 01-JUL-2004.
PA (HOEF) HOFMANN LA ROCHER & CO AG F.
Query Match 4.2%; Score 71; DB 8; Length 836;
Best Local Similarity 20.3%; Pred. No. 1.2e+03;
RESULT 1340
ID ADQ29664 standard; protein; 836 AA.
DE Human colorectal cancer-associated protein #19.
PN EP1439393-A2.
PD 21-JUL-2004.
PA (FARB) BAYER HEALTHCARE LLC.
Query Match 4.2%; Score 71; DB 8; Length 836;
Best Local Similarity 20.3%; Pred. No. 1.2e+03;
RESULT 1341
ID ADC00978 standard; protein; 943 AA.
DE Enterohaemorrhagic E. coli O157:H7-specific protein SEQ ID NO: 1022.
PD 10-DEC-2002.
PA (UUTS-) UNIV TSUKUBA.

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Query Match
Best Local Similarity 4.2%; Score 71; DB 7; Length 943;
RESULT 1342
ID ABO70459 standard; protein; 1021 AA.
DE Pseudomonas aeruginosa polypeptide #2634.
PN US6551795-B1.
PD 22-APR-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match
Best Local Similarity 4.2%; Score 71; DB 7; Length 1021;
RESULT 1343
ID ABG28598 standard; protein; 1038 AA.
DE Novel human diagnostic protein #28589.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match
Best Local Similarity 4.2%; Score 71; DB 4; Length 1038;
RESULT 1344
ID ABB63423 standard; protein; 1345 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 17061.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match
Best Local Similarity 4.2%; Score 71; DB 4; Length 1345;
RESULT 1345
ID ADO29116 standard; protein; 1379 AA.
DE Mouse novel GPCR LEC1, SEQ ID NO:215.
PN WO2004040000-A2.
PD 13-MAY-2004.
PA (PRIM-) PRIMAL INC.
Query Match
Best Local Similarity 4.2%; Score 71; DB 8; Length 1379;
RESULT 1346
ID ABP69142 standard; protein; 1759 AA.
DE Human polypeptide SEQ ID NO 1189.
PN WO200270539-A2.
PD 12-SEP-2002.
PA (HYSE-) HYSEQ INC.
Query Match
Best Local Similarity 4.2%; Score 71; DB 5; Length 1759;
RESULT 1347
ID ABG15511 standard; protein; 1907 AA.
DE Novel human diagnostic protein #15502.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match
Best Local Similarity 4.2%; Score 71; DB 4; Length 1907;
RESULT 1348
ID ADE56175 standard; protein; 2842 AA.
DE Rat protein P70478, SEQ ID NO 2024.
PN WO2003016475-A2.
PD 27-FEB-2003.
PA (GENO-) GEN HOSPITAL CORP.
PA (FARB) BAYER AG.
Query Match
Best Local Similarity 4.2%; Score 71; DB 7; Length 2842;
RESULT 1349
ID AAG81395 standard; protein; 276 AA.
DE Human AFP protein sequence SEQ ID NO:308.
PN WO200129221-A2.
PD 26-APR-2001.
PA (ZYMO) ZYMOGENETICS INC.
Query Match
Best Local Similarity 4.2%; Score 70.5; DB 4; Length 276;
RESULT 1350
ID AD719859 standard; protein; 282 AA.
DE Murine AKO78523 (310) partial sequence/betacellulin antibody SEQ ID NO:66.
PN WO2004083241-A2.
PD 30-SEP-2004.
PA (TAKE) TAKEIDA CHEM IND LTD.

Query Match
Best Local Similarity 4.2%; Score 70.5; DB 8; Length 282;
RESULT 1351
ID ADA55092 standard; protein; 293 AA.
DE Human protein, SEQ ID 2660.
PN EP1293569-A2.
PD 19-MAR-2003.
PA (HELI-) HELIX RES INST.
PA (REMS-) RES ASSOC BIOTECHNOLOGY.
Query Match
Best Local Similarity 4.2%; Score 70.5; DB 6; Length 293;
RESULT 1352
ID ADH09610 standard; protein; 293 AA.
DE Human host factor protein, SEQ ID NO 138.
PN WO2003094847-A2.
PD 20-NOV-2003.
PA (UYEM-) UNIV EMORY.
Query Match
Best Local Similarity 4.2%; Score 70.5; DB 8; Length 293;
RESULT 1353
ID AAB58346 standard; protein; 301 AA.
DE Lung cancer associated polypeptide sequence SEQ ID 684.
PN WO200055180-A2.
PD 21-SEP-2000.
PA (HUMA-) HUMAN GENOME SCI INC.
PA (ROSE-) ROSEN C A.
Query Match
Best Local Similarity 4.2%; Score 70.5; DB 3; Length 301;
RESULT 1354
ID ABG08171 standard; protein; 301 AA.
DE Novel human diagnostic protein #8162.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match
Best Local Similarity 4.2%; Score 70.5; DB 4; Length 301;
RESULT 1355
ID AAU39100 standard; protein; 361 AA.
DE Frog potassium-chloride cotransporter KCC.
PN WO200179525-A2.
PD 25-OCT-2001.
PA (UYVA-) UNIV VANDERBILT.
PA (GAMB/) GAMBA G.
Query Match
Best Local Similarity 4.2%; Score 70.5; DB 4; Length 361;
RESULT 1356
ID ADQ95860 standard; protein; 432 AA.
DE T cell activation associated protein #19.
PN WO2004058805-A2.
PD 15-JUL-2004.
PA (ASAH-) ASAH KASEI PHARMA CORP.
Query Match
Best Local Similarity 4.2%; Score 70.5; DB 8; Length 432;
RESULT 1357
ID ADC46743 standard; protein; 451 AA.
DE Thalecress transcription factor-like protein G513.
PN US2003093837-A1.
PD 15-MAY-2003.
PA (KEDD/) KEDDIE J.
PA (RIEC/) RIECHMANN J L.
PA (RATC/) RATCLIFFE O.
PA (ZHAN/) ZHANG J.
PA (JIAN/) JIANG C.
PA (PLNE/) PINEDA O.
PA (HEAR/) HEARD J.
PA (YUGG/) YU G.
PA (ADAM/) ADAM L.
PA (BROU/) BROUD P.
PA (REUB/) REUBER L.
PA (PLIG/) PILGRIM M.
PA (SAMA/) SAMARA R.
Query Match
Best Local Similarity 4.2%; Score 70.5; DB 7; Length 451;
RESULT 1358
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RESULT 1358
 ID ADO01911 standard; protein; 451 AA.
 DE Thalecress transcription factor protein #162.
 PN US2004045049-A1.
 PD 04-MAR-2004.
 PA (ZHAN)/ ZHANG J.
 PA (FROM)/ FROM M E.
 PA (HEAR)/ HEARD J E.
 PA (RIEC)/ RIECHMANN J L.
 PA (ADAM)/ ADAM L J.
 PA (BROU)/ BROUN P E.
 PA (PINE)/ PINEA O.
 PA (REUB)/ REUBER T L.
 PA (KEDD)/ KEDDIE J S.
 PA (YUGG)/ YU G.
 PA (UTAN)/ UTANG C.
 PA (SAMA)/ SAMAH R S.
 PA (PIIG)/ PILGRIM M L.
 PA (CREE)/ CREELMAN R A.
 PA (DUBE)/ DUBELL A N.
 PA (RATC)/ RATCLIFFE O.
 PA (KUMI)/ KUMIMOTO R.
 PA (SHER)/ SHERMAN B K.
 Query Match
 Best Local Similarity 22.5%; Score 70.5; DB 8; Length 451;
 RESULT 1359
 ID ADO95862 standard; protein; 451 AA.
 DE T cell activation associated protein #20.
 PN WO2004058805-A2.
 PD 15-JUL-2004.
 PA (ASAH)/ ASAH KASEI PHARMA CORP.
 Query Match
 Best Local Similarity 20.8%; Score 70.5; DB 8; Length 451;
 RESULT 1360
 ID AAY35457 standard; protein; 453 AA.
 DE Chlamydia pneumoniae involved in the secretory system.
 PN WO9927105-A2.
 PD 03-JUN-1999.
 PA (GERS)/ GENSER.
 Query Match
 Best Local Similarity 4.2%; Score 70.5; DB 2; Length 453;
 RESULT 1361
 ID AAB85574 standard; protein; 496 AA.
 DE C. pneumoniae general secretion pathway protein E polypeptide.
 PN WO200121805-A1.
 PD 29-MAR-2001.
 PA (AVET)/ AVENTIS PASTEUR LTD.
 Query Match
 Best Local Similarity 4.2%; Score 70.5; DB 4; Length 496;
 RESULT 1362
 ID AAB54776 standard; protein; 517 AA.
 DE Lactococcus lactis protein kimb.
 PN FR280746-A1.
 PD 12-OCT-2001.
 PA (INRG)/ INRA INST NAT RECH AGRONOMIQUE.
 Query Match
 Best Local Similarity 18.4%; Score 70.5; DB 5; Length 517;
 RESULT 1363
 ID AAY20011 standard; protein; 524 AA.
 DE B. burgdorferi antigenic protein, c301.aa.
 PN WO9859071-A1.
 PD 30-DEC-1998.
 PA (HUMA)/ HUMAN GENOME SCI INC.
 PA (MEDI)/ MEDIMUNE INC.
 Query Match
 Best Local Similarity 4.2%; Score 70.5; DB 2; Length 524;
 RESULT 1364
 ID ADD14175 standard; protein; 525 AA.
 DE Human src biomarker polypeptide SEQ ID NO:364.
 PN WO2003062395-A2.
 PD 31-JUL-2003.
 PA (BRIM)/ BRISTOL-MYERS SQUIBB CO.
 Query Match
 Best Local Similarity 4.2%; Score 70.5; DB 7; Length 525;

Best Local Similarity 22.6%; Pred. No. 6.7e+02;
 RESULT 1365
 ID ABB47270 standard; protein; 543 AA.
 DE Enterococcus faecalis polypeptide Abc8.
 PN WO200179257-A2.
 PD 25-OCT-2001.
 PA (PHYT)/ PHYTERA INC.
 Query Match
 Best Local Similarity 4.2%; Score 70.5; DB 4; Length 543;
 RESULT 1366
 ID AAM50094 standard; protein; 547 AA.
 DE Artemisia-4,11-diene synthase associated protein #2.
 PN KR2001084864-A.
 PD 06-SEP-2001.
 PA (KIMS)/ KIM S U.
 Query Match
 Best Local Similarity 4.2%; Score 70.5; DB 5; Length 547;
 RESULT 1367
 ID ADI82350 standard; protein; 551 AA.
 DE Artemisia annua epi-cedrol synthase protein sequence SeqID40.
 PN US2004005678-A1.
 PD 08-JAN-2004.
 PA (KEAS)/ KEASLING J.
 PA (MART)/ MARTIN V.
 PA (PIRE)/ PITERA D.
 PA (WITR)/ WITHERS S T.
 PA (NEMM)/ NEMMAN J.
 Query Match
 Best Local Similarity 4.2%; Score 70.5; DB 8; Length 551;
 RESULT 1368
 ID AAY20010 standard; protein; 553 AA.
 DE B. burgdorferi antigenic protein, f301.aa.
 PN WO9859071-A1.
 PD 30-DEC-1998.
 PA (HUMA)/ HUMAN GENOME SCI INC.
 PA (MEDI)/ MEDIMUNE INC.
 Query Match
 Best Local Similarity 4.2%; Score 70.5; DB 2; Length 553;
 RESULT 1369
 ID ADH86572 standard; protein; 575 AA.
 DE Enterococcus faecalis polypeptide #1052.
 PN US6617156-B1.
 PD 09-SEP-2003.
 PA (DOUC)/ DOUCETTE-STAMM L A.
 PA (BUSH)/ BUSH D.
 Query Match
 Best Local Similarity 4.2%; Score 70.5; DB 7; Length 575;
 RESULT 1370
 ID AAR85888 standard; protein; 605 AA.
 DE WD-40 domain-contg. insulin-like growth factor binding protein.
 PN WO9521252-A2.
 PD 10-AUG-1995.
 PA (STRD)/ UNIV LELAND STANFORD JUNIOR.
 Query Match
 Best Local Similarity 4.2%; Score 70.5; DB 2; Length 605;
 RESULT 1371
 ID AAO23109 standard; protein; 605 AA.
 DE IGFALS 'human modifier of p53 pathway' protein.
 PN WO2003035833-A2.
 PD 01-MAY-2003.
 PA (EXEL)/ EXELIXIS INC.
 Query Match
 Best Local Similarity 4.2%; Score 70.5; DB 6; Length 605;
 RESULT 1372
 ID ADD48887 standard; protein; 605 AA.
 DE Human Protein P35858, SEQ ID NO 14598.
 PN WO2003016475-A2.
 PD 27-FEB-2003.
 PA (GERO)/ GEN HOSPITAL CORP.
 PA (FARB)/ BAYER AG.
 Query Match
 Best Local Similarity 4.2%; Score 70.5; DB 7; Length 605;
 RESULT 1373
 ID AAY20010 standard; protein; 553 AA.
 DE B. burgdorferi antigenic protein, f301.aa.
 PN WO9859071-A1.
 PD 30-DEC-1998.
 PA (HUMA)/ HUMAN GENOME SCI INC.
 PA (MEDI)/ MEDIMUNE INC.
 Query Match
 Best Local Similarity 4.2%; Score 70.5; DB 2; Length 553;

ID ADD47835 standard; protein; 605 AA.
DE Human Protein P35858, SEQ ID NO 13531.
PD WO2003016475-A2.
PA (GEHO) GEN HOSPITAL CORP.
PA (FARB) BAYER AG.
Query Match
Best Local Similarity 4.2%; Score 70.5; DB 7; Length 605;
RESULT 1374
ID ADE61677 standard; protein; 605 AA.
DE Human Protein P35858, SEQ ID NO 7599.
PD WO2003016475-A2.
PD 27-FEB-2003.
PA (GEHO) GEN HOSPITAL CORP.
PA (FARB) BAYER AG.
Query Match
Best Local Similarity 4.2%; Score 70.5; DB 7; Length 605;
RESULT 1375
ID ADU68826 standard; protein; 605 AA.
DE Human heat mitochondrial protein as a therapeutic target SeqID632.
PD 23-OCT-2003.
PA (MITO-) MITOKOR.
PA (BUCK-) BUCK INST AGE RES.
Query Match
Best Local Similarity 4.2%; Score 70.5; DB 7; Length 605;
RESULT 1376
ID ABB54535 standard; protein; 665 AA.
DE Lactococcus lactis protein ymch.
PD FR2807446-A1.
PD 12-OCT-2001.
PA (INRG) INRA INST NAT RECH AGRONOMIQUE.
Query Match
Best Local Similarity 4.2%; Score 70.5; DB 5; Length 665;
RESULT 1377
ID ABO76825 standard; protein; 677 AA.
DE Pseudomonas aeruginosa polypeptide #9000.
PD US6551795-B1.
PD 22-APR-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match
Best Local Similarity 4.2%; Score 70.5; DB 7; Length 677;
RESULT 1378
ID AAR34445 standard; protein; 680 AA.
DE Sequence encoded by a cDNA clone contg. the ADMIX gene associated with X-linked Kallmann Syndrome (KS).
PD WO9307267-A1.
PD 15-APR-1993.
PA (INSP) INST PASTEUR.
PA (USSH) US DEPT HEALTH & HUMAN SERVICE.
Query Match
Best Local Similarity 4.2%; Score 70.5; DB 2; Length 680;
RESULT 1379
ID AAM49015 standard; protein; 680 AA.
DE Human KAL protein.
PD WO9824898-A2.
PD 11-JUN-1998.
PA (INSP) INST PASTEUR.
PA (CNRS) CNRS CENT NAT RECH SCI.
Query Match
Best Local Similarity 4.2%; Score 70.5; DB 2; Length 680;
RESULT 1380
ID ADQ18482 standard; protein; 680 AA.
DE Human soft tissue sarcoma-upregulated protein - SEQ ID 1301.
PD 10-JUN-2004.
PA (PROT-) PROTEIN DESIGN LABS INC.
Query Match
Best Local Similarity 4.2%; Score 70.5; DB 8; Length 680;
RESULT 1381
ID ADR09060 standard; protein; 726 AA.
DE Human protein useful for treating neurological disease Seq 2566.
PD EP1447413-A2.

PD 18-AUG-2004.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
Query Match
Best Local Similarity 4.2%; Score 70.5; DB 8; Length 726;
RESULT 1382
ID AAB68952 standard; peptide; 728 AA.
DE Arabidopsis thaliana CDC27A1 protein.
PD WO200102430-A2.
PD 11-JAN-2001.
PA (CROP-) CROPPESIGN NV.
PA (UYRI-) UNIV RIO DE JANEIRO.
Query Match
Best Local Similarity 4.2%; Score 70.5; DB 4; Length 728;
RESULT 1383
ID ADM97327 standard; protein; 728 AA.
DE A thaliana cdc27 allele 1 encoded protein.
PD WO2004029257-A1.
PD 08-APR-2004.
PA (CROP-) CROPPESIGN NV.
PA (UYRI-) UNIV RIO DE JANEIRO.
PA (HEME/) HEMERLY A S.
Query Match
Best Local Similarity 4.2%; Score 70.5; DB 8; Length 728;
RESULT 1384
ID ADR87282 standard; protein; 755 AA.
DE Liv-1 mutant BCR4M1 protein sequence.
PD WO2004067564-A2.
PD 12-AUG-2004.
PA (PROT-) PROTEIN DESIGN LABS INC.
Query Match
Best Local Similarity 4.2%; Score 70.5; DB 8; Length 755;
RESULT 1385
ID ADG39856 standard; protein; 847 AA.
DE Protein similar to human NOV12 #2.
PD US2003203843-A1.
PD 30-OCT-2003.
PA (PENNA/) PENNA C E A.
PA (GUOX/) GUO X.
PA (SHIM/) SHIMKETS R A.
PA (PAD1/) PADIGARU M.
PA (KERU/) KERODA R.
PA (SPYT/) SPYTEK K A.
PA (MEHR/) MEHRABAN F.
PA (TOPP/) TOPPER J N.
PA (MALY/) MALYANKAR U M.
PA (VASS/) VASSERMAN S M.
PA (EDIN/) EDINGER S R.
PA (SMIT/) SMITHSON G.
PA (GUNT/) GUNTHER E.
PA (KOMU/) KOMIVES L.
Query Match
Best Local Similarity 4.2%; Score 70.5; DB 7; Length 847;
RESULT 1386
ID ABU36130 standard; protein; 893 AA.
DE Disease treating protein encoded by prokaryotic essential gene #21657.
PD WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match
Best Local Similarity 4.2%; Score 70.5; DB 6; Length 893;
RESULT 1387
ID AAK64818 standard; protein; 944 AA.
DE Disease treating protein complex-derived protein #1607.
PD EP1338608-A2.
PD 27-AUG-2003.
PA (CELL-) CELLZOME AG.
Query Match
Best Local Similarity 4.2%; Score 70.5; DB 7; Length 944;
RESULT 1388
ID AAP97052 standard; protein; 1095 AA.
DE Sequence encoded by insecticide gene from Bacillus thuringiensis DE israelensis strain.
PD JF01080294-A.

PD 27-MAR-1989.
PA (SUMO) SUMITOMO CHEM IND KK.
PA (MARU-) MARUBENI KK.
Query Match 4.2%; Score 70.5; DB 1; Length 1095;
Best Local Similarity 21.5%; Pred. No. 1.9e+03;
RESULT 1389
ID AAP82314 standard; protein; 1136 AA.
DE Bacillus thuringiensis 8 protein.
PN MO8806631-A.
PD 07-SEP-1988.
PA (UNMS) UNIV MICHIGAN STATE.
PA (PLAN-) PLANT GENETIC SVST.
PA (UNMI) UNIV MICHIGAN.
Query Match 4.2%; Score 70.5; DB 1; Length 1136;
Best Local Similarity 21.5%; Pred. No. 2e+03;
RESULT 1390
ID AAP93341 standard; protein; 1136 AA.
DE Sequence encoded by toxin gene derived from a Bacillus thuringiensis var.
DE tseraelensis (B.t.i.) microbe identified as strain HD567.
PN EP308199-A.
PD 22-MAR-1989.
PA (MYCO) MYCOGEN CORP.
Query Match 4.2%; Score 70.5; DB 1; Length 1136;
Best Local Similarity 21.5%; Pred. No. 2e+03;
RESULT 1391
ID AAU76029 standard; protein; 1136 AA.
DE Bacillus thuringiensis variant tseraelensis toxin (Bt8) protein sequence.
PN US6335008-B1.
PD 01-JAN-2002.
PA (UNMS) UNIV MICHIGAN STATE.
Query Match 4.2%; Score 70.5; DB 5; Length 1136;
Best Local Similarity 21.5%; Pred. No. 2e+03;
RESULT 1392
ID ADR89427 standard; protein; 1136 AA.
DE CRY4Ba.
PN WO2004074462-A2.
PD 02-SEP-2004.
PA (ATHE-) ATHENIX CORP.
Query Match 4.2%; Score 70.5; DB 8; Length 1136;
Best Local Similarity 21.5%; Pred. No. 2e+03;
RESULT 1393
ID AAP82589 standard; protein; 1180 AA.
DE Insecticidal (Diptera) protein (exon 2).
PN JP63230090-A.
PD 26-SEP-1988.
PA (SUMO) SUMITOMO CHEM IND KK.
Query Match 4.2%; Score 70.5; DB 1; Length 1180;
Best Local Similarity 21.5%; Pred. No. 2.2e+03;
RESULT 1394
ID ADR89426 standard; protein; 1180 AA.
DE CRY4Aa.
PN WO2004074462-A2.
PD 02-SEP-2004.
PA (ATHE-) ATHENIX CORP.
Query Match 4.2%; Score 70.5; DB 8; Length 1180;
Best Local Similarity 21.5%; Pred. No. 2.2e+03;
RESULT 1395
ID ABW81850 standard; protein; 1193 AA.
DE Tumour-associated antigenic target (TAT) polypeptide PRO82709, SEQ:4766.
PN WO2004030615-A2.
PD 15-APR-2004.
PA (GERTH) GENENTECH INC.
Query Match 4.2%; Score 70.5; DB 8; Length 1193;
Best Local Similarity 22.8%; Pred. No. 2.2e+03;
RESULT 1396
ID AAW98761 standard; protein; 1279 AA.
DE H. pylori GHP0 1090 protein.
PN WO9843478-A1.
PD 08-OCT-1998.
PA (INMR) MERIEUX ORAVAX PASTEUR MERIEUX SERUMS.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 4.2%; Score 70.5; DB 2; Length 1279;
Best Local Similarity 19.8%; Pred. No. 2.4e+03;

RESULT 1397
ID ABU07385 standard; protein; 1706 AA.
DE Human protein NOV16.
PN WO200285922-A2.
PD 31-OCT-2002.
PA (CURA-) CURAGEN CORP.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 4.2%; Score 70.5; DB 6; Length 1706;
Best Local Similarity 20.5%; Pred. No. 3.7e+03;
RESULT 1398
ID ABG91808 standard; protein; 1736 AA.
DE Human intracellular signalling molecule protein INSTIG-10.
PN WO200263008-A2.
PD 15-AUG-2002.
PA (INCY-) INCYTE GENOMICS INC.
Query Match 4.2%; Score 70.5; DB 5; Length 1736;
Best Local Similarity 20.5%; Pred. No. 3.8e+03;
RESULT 1399
ID ABJ35589 standard; protein; 1805 AA.
DE Protein encoded by Prokaryotic essential gene #21116.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 4.2%; Score 70.5; DB 6; Length 1805;
Best Local Similarity 24.0%; Pred. No. 4e+03;
RESULT 1400
ID ABO23572 standard; protein; 1805 AA.
DE Mycoplasma genitalium outlier protein #3.
PN US2003039963-A1.
PD 27-FEB-2003.
PA (BRAH/) BRAHMACHARI S K.
PA (RAMA/) RAMACHANDRAN S.
PA (NAND/) NANDI T.
PA (BHIM/) BHIMARAO C.
Query Match 4.2%; Score 70.5; DB 7; Length 1805;
Best Local Similarity 24.0%; Pred. No. 4e+03;
RESULT 1401
ID AAB23012 standard; protein; 2742 AA.
DE Human APC protein (splice variant 2).
PN US6114124-A.
PD 05-SEP-2000.
PA (ICIL) IMPERIAL CHEM IND PLC.
PA (UYJO) UNIV JOHNS HOPKINS.
PA (UTAH) UNIV UTAH.
PA (CANC-) CANCER INST.
Query Match 4.2%; Score 70.5; DB 3; Length 2742;
Best Local Similarity 21.8%; Pred. No. 7.3e+03;
RESULT 1402
ID AAR63508 standard; protein; 2842 AA.
DE Adenomatous polyposis coli tumour repressor.
PN US5352775-A.
PD 04-OCT-1994.
PA (ICIL) IMPERIAL CHEM IND.
PA (CANC-) CANCER INST.
PA (UYJO) UNIV JOHNS HOPKINS.
PA (UTAH) UNIV UTAH.
Query Match 4.2%; Score 70.5; DB 2; Length 2842;
Best Local Similarity 21.8%; Pred. No. 7.7e+03;
RESULT 1403
ID ABG90968 standard; peptide; 2842 AA.
DE Human APC protein.
PN US6413727-B1.
PD 02-JUL-2002.
PA (UYJO) UNIV JOHNS HOPKINS.
PA (UTAH) UNIV UTAH.
PA (NICA-) JAPANESE FOUND CANCER RES.
PA (ZENB) ZENECA LTD.
Query Match 4.2%; Score 70.5; DB 5; Length 2842;
Best Local Similarity 21.8%; Pred. No. 7.7e+03;
RESULT 1404
ID AAR26052 standard; protein; 2843 AA.
DE APC gene product in familial adenomatous polyposis.
PN WO9213103-A1.

PD 06-AUG-1992.
PA (UYJO) UNIV JOHNS HOPKINS.
PA (ICIL) IMPERIAL CHEM IND PLC.
PA (UTAH) UNIV UTAH.
PA (CANC-) CANCER INST.
Query Match 4.2%; Score 70.5; DB 2; length 2843;
Best Local Similarity 21.8%; Pred. No. 7.7e+03;
RESULT 1405
ID AAR58634 standard; protein; 2843 AA.
DE Adenomatous polyposis coli protein (APC).
PN W09421814-A1.
PD 29-SEP-1994.
PA (UYJO) UNIV JOHNS HOPKINS.
Query Match 4.2%; Score 70.5; DB 2; length 2843;
Best Local Similarity 21.8%; Pred. No. 7.7e+03;
RESULT 1406
ID AAW11922 standard; protein; 2843 AA.
DE Adenomatous polyposis coli protein.
PN JP06347459-A.
PD 22-DEC-1994.
PA (SANK-) SANKO JUNKYAKU CO LTD.
Query Match 4.2%; Score 70.5; DB 2; length 2843;
Best Local Similarity 21.8%; Pred. No. 7.7e+03;
RESULT 1407
ID AAW35392 standard; protein; 2843 AA.
DE Human adenomatous polyposis coli gene product.
PN US5648212-A.
PD 15-JUL-1997.
PA (NICA-) JAPANESE FOUND CANCER RES.
PA (UTAH) UNIV UTAH.
PA (UYJO) UNIV JOHNS HOPKINS.
PA (ZENE) ZENECA LTD.
Query Match 4.2%; Score 70.5; DB 2; length 2843;
Best Local Similarity 21.8%; Pred. No. 7.7e+03;
RESULT 1408
ID AAW8370 standard; protein; 2843 AA.
DE Human adenomatous polyposis coli gene product.
PN US5691454-A.
PD 25-NOV-1997.
PA (CANC-) CANCER INST.
PA (UYJO) UNIV JOHNS HOPKINS.
PA (ICIL) IMPERIAL CHEM IND PLC.
PA (UTAH) UNIV UTAH.
Query Match 4.2%; Score 70.5; DB 2; length 2843;
Best Local Similarity 21.8%; Pred. No. 7.7e+03;
RESULT 1409
ID AAW76140 standard; protein; 2843 AA.
DE Human APC protein #1.
PN US5783666-A.
PD 21-JUL-1998.
PA (CANC-) CANCER INST.
PA (UYJO) UNIV JOHNS HOPKINS.
PA (UTAH) UNIV UTAH.
PA (ZENE) ZENECA PHARM.
Query Match 4.2%; Score 70.5; DB 2; length 2843;
Best Local Similarity 21.8%; Pred. No. 7.7e+03;
RESULT 1410
ID AAW76144 standard; protein; 2843 AA.
DE Human APC protein #2.
PN US5783666-A.
PD 21-JUL-1998.
PA (CANC-) CANCER INST.
PA (UYJO) UNIV JOHNS HOPKINS.
PA (UTAH) UNIV UTAH.
PA (ZENE) ZENECA PHARM.
Query Match 4.2%; Score 70.5; DB 2; length 2843;
Best Local Similarity 21.8%; Pred. No. 7.7e+03;
RESULT 1411
ID AAW33011 standard; protein; 2843 AA.
DE Human APC protein (splice variant 1).
PN US6114124-A.
PD 05-SEP-2000.
PA (ICIL) IMPERIAL CHEM IND PLC.

PA (UYJO) UNIV JOHNS HOPKINS.
PA (UTAH) UNIV UTAH.
PA (CANC-) CANCER INST.
Query Match 4.2%; Score 70.5; DB 3; length 2843;
Best Local Similarity 21.8%; Pred. No. 7.7e+03;
RESULT 1412
ID ABG90964 standard; protein; 2843 AA.
DE Human adenomatous polyposis coli (APC) protein #1.
PN US6413727-B1.
PD 02-JUL-2002.
PA (UYJO) UNIV JOHNS HOPKINS.
PA (UTAH) UNIV UTAH.
PA (NICA-) JAPANESE FOUND CANCER RES.
PA (ZENE) ZENECA LTD.
Query Match 4.2%; Score 70.5; DB 5; length 2843;
Best Local Similarity 21.8%; Pred. No. 7.7e+03;
RESULT 1413
ID ABG71105 standard; protein; 2843 AA.
DE Human adenomatous polyposis coli (APC) protein.
PN EP1243646-A2.
PD 25-SEP-2002.
PA (COUL) COUNCIL SCI & IND RES.
Query Match 4.2%; Score 70.5; DB 5; length 2843;
Best Local Similarity 21.8%; Pred. No. 7.7e+03;
RESULT 1414
ID ADE65846 standard; protein; 2843 AA.
DE Human adenomatous polyposis coli protein.
PN US2003170723-A1.
PD 11-SEP-2003.
PA (SAVO/) SATO T.
Query Match 4.2%; Score 70.5; DB 7; length 2843;
Best Local Similarity 21.8%; Pred. No. 7.7e+03;
RESULT 1415
ID ADJ70164 standard; protein; 2843 AA.
DE Human heat mitochondrial protein as a therapeutic target SegID1970.
PN W02003087768-A2.
PD 23-OCT-2003.
PA (MITO-) MITOKOR.
PA (BUCK-) BUCK INST AGE RES.
Query Match 4.2%; Score 70.5; DB 7; length 2843;
Best Local Similarity 21.8%; Pred. No. 7.7e+03;
RESULT 1416
ID ADJ32540 standard; protein; 2843 AA.
DE Human adenomatous polyposis coli protein.
PN US20032493-A1.
PD 04-DEC-2003.
PA (LAND/) LAND H.
PA (DELE/) DELEU L.
Query Match 4.2%; Score 70.5; DB 8; length 2843;
Best Local Similarity 21.8%; Pred. No. 7.7e+03;
RESULT 1417
ID ADO08044 standard; protein; 2844 AA.
DE Human polypeptide #45.
PN US2004071700-A1.
PD 15-APR-2004.
PA (LIFE-) LIFE SCI DEV CORP.
Query Match 4.2%; Score 70.5; DB 8; length 2844;
Best Local Similarity 21.8%; Pred. No. 7.7e+03;
RESULT 1418
ID AAR63507 standard; protein; 2860 AA.
DE Adenomatous polyposis coli tumour repressor.
PN US5352775-A.
PD 04-OCT-1994.
PA (ICIL) IMPERIAL CHEM IND.
PA (CANC-) CANCER INST.
PA (UYJO) UNIV JOHNS HOPKINS.
PA (UTAH) UNIV UTAH.
Query Match 4.2%; Score 70.5; DB 2; length 2860;
Best Local Similarity 21.8%; Pred. No. 7.7e+03;
RESULT 1419
ID AAW76821 standard; protein; 2973 AA.
DE Human APC protein.
PN W09841631-A2.

PD 24-SEP-1998.
PA (UYJO) UNIV JOHNS HOPKINS.
PA (UYUT-) RIJKSUNIV UTRECHT.
Query Match 4.2%; Score 70.5; DB 2; Length 2973;
RESULT 1420
ID AAY70304 standard; protein; 2973 AA.
DE Protein used in cancer diagnosis associated with APC/beta-catenin.
PN WO200011195-A1.
PD 02-MAR-2000.
PA (UYJO) UNIV JOHNS HOPKINS SCHOOL MEDICINE.
Query Match 4.2%; Score 70.5; DB 3; Length 2973;
RESULT 1421
ID AAY72762 standard; protein; 2973 AA.
DE Transcriptional activation protein #1 related to the invention.
PN WO200116167-A2.
PD 08-MAR-2001.
PA (UYJO) UNIV JOHNS HOPKINS.
Query Match 4.2%; Score 70.5; DB 4; Length 2973;
RESULT 1422
ID AB863663 standard; protein; 3688 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 17781.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PKEK) PE CORP NY.
Query Match 4.2%; Score 70.5; DB 4; Length 3868;
RESULT 1423
ID ADL99351 standard; protein; 3917 AA.
DE Nanostructure assembly protein #2.
PN US200315903-A1.
PD 20-NOV-2003.
PA (HYMA/) HYMAN P L.
PA (GOLD/) GOLDBERG E B.
Query Match 4.2%; Score 70.5; DB 8; Length 3917;
RESULT 1424
ID AAG09240 standard; protein; 182 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 7094.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 4.1%; Score 70; DB 3; Length 182;
RESULT 1425
ID AAG52842 standard; protein; 182 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 67215.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 4.1%; Score 70; DB 3; Length 182;
RESULT 1426
ID AAY76622 standard; protein; 196 AA.
DE Human ovarian tumor EST fragment encoded protein 118.
PN DE19817557-A1.
PD 21-OCT-1999.
PA (METR-) METAGEN GES GENOMFORSCHUNG MEH.
Query Match 4.1%; Score 70; DB 2; Length 196;
RESULT 1427
ID AD448115 standard; protein; 229 AA.
DE Polypeptide sequence #165 useful in producing transgenic plants.
PN US2003233670-A1.
PD 18-DEC-2003.
PA (EDGE/) EDGERTON M D.
PA (CHOM/) CHOMET P S.
PA (LACC/) LACCETTI L B.
Query Match 4.1%; Score 70; DB 8; Length 229;
RESULT 1428
ID AD448130 standard; protein; 229 AA.
DE Polypeptide sequence #180 useful in producing transgenic plants.

PN US2003233670-A1.
PD 18-DEC-2003.
PA (EDGE/) EDGERTON M D.
PA (CHOM/) CHOMET P S.
PA (LACC/) LACCETTI L B.
Query Match 4.1%; Score 70; DB 8; Length 229;
RESULT 1429
ID ADJ95198 standard; protein; 232 AA.
DE Novel NOVX protein sequence #213.
PN WO2003040325-A2.
PD 15-MAY-2003.
PA (CURA-) CURAGEN CORP.
Query Match 4.1%; Score 70; DB 7; Length 232;
RESULT 1430
ID ADJ95190 standard; protein; 236 AA.
DE Novel NOVX protein sequence #209.
PN WO2003040325-A2.
PD 15-MAY-2003.
PA (CURA-) CURAGEN CORP.
Query Match 4.1%; Score 70; DB 7; Length 236;
RESULT 1431
ID AAG52841 standard; protein; 245 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 67214.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 4.1%; Score 70; DB 3; Length 245;
RESULT 1432
ID AAG09239 standard; protein; 245 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 7093.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 4.1%; Score 70; DB 3; Length 245;
RESULT 1433
ID ABG00390 standard; protein; 253 AA.
DE Novel human diagnostic protein #381.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match 4.1%; Score 70; DB 4; Length 253;
RESULT 1434
ID ABU44361 standard; protein; 260 AA.
DE Protein encoded by Prokaryotic essential gene #29888.
PN WO20027183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 4.1%; Score 70; DB 6; Length 260;
RESULT 1435
ID AAG52840 standard; protein; 271 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 67213.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 4.1%; Score 70; DB 3; Length 271;
RESULT 1436
ID AAG09238 standard; protein; 271 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 7092.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 4.1%; Score 70; DB 3; Length 271;
RESULT 1437
ID AB222933 standard; protein; 271 AA.
DE Protein encoded by Prokaryotic essential gene #8460.
PN WO20027183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.

Query Match
Best Local Similarity 4.1%; Score 70; DB 6; Length 271;
RESULT 1438
ID ADH45301 standard; protein; 306 AA.
DE Human enzyme (ENZM) polypeptide, SEQ ID NO 25.
PN WO2003104410-A2.
PD 18-DEC-2003.
PA (INCY-) INCYTE CORP.
Query Match
Best Local Similarity 4.1%; Score 70; DB 8; Length 306;
RESULT 1439
ID AAG81589 standard; protein; 308 AA.
DE S. epidermidis open reading frame protein sequence SEQ ID NO:272.
PN WO200134809-A2.
PD 17-MAY-2001.
PA (GLAX) GLAXO GROUP LTD.
Query Match
Best Local Similarity 4.1%; Score 70; DB 4; Length 308;
RESULT 1440
ID ABP40326 standard; protein; 311 AA.
DE Staphylococcus epidermidis ORF amino acid sequence SEQ ID NO:5171.
PN US6380370-B1.
PD 30-APR-2002.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match
Best Local Similarity 4.1%; Score 70; DB 5; Length 311;
RESULT 1441
ID ADS07667 standard; protein; 311 AA.
DE Staphylococcus epidermis polypeptide seqid 6962.
PN US2004147734-A1.
PD 29-JUL-2004.
PA (DOUC/) DOUCETTE-STAMM L.
Query Match
Best Local Similarity 4.1%; Score 70; DB 8; Length 311;
RESULT 1442
ID ABR71390 standard; protein; 366 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 40962.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match
Best Local Similarity 4.1%; Score 70; DB 4; Length 366;
RESULT 1443
ID ADJ37979 standard; protein; 366 AA.
DE D melanogaster malichromosome inheritance-related protein Seqid96.
PN US2003134278-A1.
PD 17-JUL-2003.
PA (KARP/) KARPEN G H.
PA (DOBI/) DOBIE K W.
PA (COOK/) COOK K R.
PA (MDRP/) MDRPHY T D.
Query Match
Best Local Similarity 4.1%; Score 70; DB 7; Length 366;
RESULT 1444
ID AAG09500 standard; protein; 386 AA.
DE Novel human diagnostic protein #9491.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match
Best Local Similarity 4.1%; Score 70; DB 4; Length 386;
RESULT 1445
ID ADA55093 standard; protein; 397 AA.
DE Human protein, SEQ ID 2661.
PN EP1293569-A2.
PD 19-MAR-2003.
PA (HELI-) HELIX RES INST.
PA (RRAS-) RES ASSOC BIOTECHNOLOGY.
Query Match
Best Local Similarity 4.1%; Score 70; DB 6; Length 397;
RESULT 1446
ID AAR83414 standard; protein; 402 AA.

DE Humicola insolens endoglucanase variant K217A + K218T.
PN WO9524471-A1.
PD 14-SEP-1995.
PA (NOVO) NOVO-NORDISK AS.
Query Match
Best Local Similarity 4.1%; Score 70; DB 2; Length 402;
RESULT 1447
ID ADH35290 standard; protein; 417 AA.
DE ENZM protein #4.
PN WO2004003162-A2.
PD 08-JAN-2004.
PA (INCY-) INCYTE CORP.
Query Match
Best Local Similarity 4.1%; Score 70; DB 8; Length 417;
RESULT 1448
ID AAU91336 standard; protein; 423 AA.
DE Human novel secreted protein LP255(a).
PN WO200214358-A2.
PD 21-FEB-2002.
PA (BILI) LILLY & CO ELI.
Query Match
Best Local Similarity 4.1%; Score 70; DB 5; Length 423;
RESULT 1449
ID ABG18976 standard; protein; 444 AA.
DE Novel human diagnostic protein #18967.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match
Best Local Similarity 4.1%; Score 70; DB 4; Length 444;
RESULT 1450
ID AAR73668 standard; protein; 468 AA.
DE Human oxidoreductase protein ORP-1.
PN WO200144448-A2.
PD 21-JUN-2001.
PA (INCY-) INCYTE GENOMICS INC.
Query Match
Best Local Similarity 4.1%; Score 70; DB 4; Length 468;
RESULT 1451
ID ADG69432 standard; protein; 468 AA.
DE Human heat mitochondrial protein as a therapeutic target Seqid1238.
PN WO2003087768-A2.
PD 23-OCT-2003.
PA (MITO-) MITOKOR.
PA (BUCK-) BUCK INST AGE RES.
Query Match
Best Local Similarity 4.1%; Score 70; DB 7; Length 468;
RESULT 1452
ID AAM23525 standard; protein; 473 AA.
DE Rabbit EST encoded protein SEQ ID NO: 1050.
PN WO200154477-A2.
PD 02-AUG-2001.
PA (HYSE-) HYSEQ INC.
Query Match
Best Local Similarity 4.1%; Score 70; DB 4; Length 473;
RESULT 1453
ID ABP69510 standard; protein; 473 AA.
DE Human polypeptide SEQ ID NO 1557.
PN WO200270539-A2.
PD 12-SEP-2002.
PA (HYSE-) HYSEQ INC.
Query Match
Best Local Similarity 4.1%; Score 70; DB 5; Length 473;
RESULT 1454
ID AA017865 standard; protein; 504 AA.
DE Pryn domain containing protein MALP10/Py14.
PN WO200240668-A2.
PD 23-MAY-2002.
PA (APOT-) APOTEC RES & DEV LTD.
Query Match
Best Local Similarity 4.1%; Score 70; DB 5; Length 504;
RESULT 1455
ID ADB36415 standard; protein; 504 AA.

DE Human PAAD and nucleotide binding protein PANS.
PN US200307699-A1.
PD 24-APR-2003.
PA (REED/) REED J C.
PA (GODZ/) GODZIK A.
PA (CHUZ/) CHU Z.
PA (PAWL/) PAWLOWSKI K.
PA (FIOR/) FIORENTINO L.
PA (ARIZ/) ARIZA M E.
PA (STEH/) STEHLIK C.
Query Match 4.1%; Score 70; DB 5; Length 504;
Best Local Similarity 21.8%; Pred. No. 7.2e+02;
RESULT 1456
ID ADJ19337 standard; protein; 504 AA.
DE Human PANS PAAD domain-containing full-length protein.
PN US2004002593-A1.
PD 01-JAN-2004.
PA (REED/) REED J C.
PA (GODZ/) GODZIK A.
Query Match 4.1%; Score 70; DB 8; Length 504;
Best Local Similarity 21.8%; Pred. No. 7.2e+02;
RESULT 1457
ID ADH72096 standard; protein; 579 AA.
DE Human protein of the invention NOV42k SEQ ID NO:992.
PN WO2003102155-A2.
PD 11-DEC-2003.
PA (CURA-) CURAGEN CORP.
Query Match 4.1%; Score 70; DB 8; Length 579;
Best Local Similarity 19.3%; Pred. No. 8.8e+02;
RESULT 1458
ID ADJ19403 standard; protein; 590 AA.
DE Human PANS PAAD/NAOHT/AREO domain-containing protein - SEQ ID 94.
PN US2004002593-A1.
PD 01-JAN-2004.
PA (REED/) REED J C.
PA (GODZ/) GODZIK A.
Query Match 4.1%; Score 70; DB 8; Length 590;
Best Local Similarity 21.8%; Pred. No. 9e+02;
RESULT 1459
ID ADQ97102 standard; protein; 631 AA.
DE Human cancer associated sequence HPI-10-006, SEQ ID 78.
PN WO2004060304-A2.
PD 22-JUL-2004.
PA (SAGR-) SAGRES DISCOVERY INC.
Query Match 4.1%; Score 70; DB 8; Length 631;
Best Local Similarity 20.0%; Pred. No. 9.9e+02;
RESULT 1460
ID ABB63926 standard; protein; 633 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 18570.
PN WO2001171042-A2.
PD 27-SEP-2001.
PA (PEKE-) PE CORP NY.
Query Match 4.1%; Score 70; DB 4; Length 633;
Best Local Similarity 19.0%; Pred. No. 9.9e+02;
RESULT 1461
ID AAM39589 standard; protein; 639 AA.
DE Human polypeptide SEQ ID NO 2734.
PN WO200153312-A1.
PD 26-JUN-2001.
PA (HYSE-) HYSEQ INC.
Query Match 4.1%; Score 70; DB 4; Length 639;
Best Local Similarity 19.5%; Pred. No. 1e+03;
RESULT 1462
ID ADP04701 standard; protein; 639 AA.
DE Sea squirt protein with tissue specific expression in development Seq296.
PN JP2004057129-A.
PD 26-FEB-2004.
PA (KAGA-) KAGAKU GIYUSU SHINKO JIGYODAN.
Query Match 4.1%; Score 70; DB 8; Length 639;
Best Local Similarity 22.9%; Pred. No. 1e+03;
RESULT 1463
ID ADS21109 standard; protein; 700 AA.
DE Bacterial polypeptide #10142.

PN US2003233675-A1.
PD 18-DEC-2003.
PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
Query Match 4.1%; Score 70; DB 8; Length 700;
Best Local Similarity 21.7%; Pred. No. 1.2e+03;
RESULT 1464
ID ABP97757 standard; protein; 712 AA.
DE Amino acid sequence of a murine ACDK3 polypeptide.
PN WO2003008557-A2.
PD 30-JAN-2003.
PA (UYFL-) UNIV FLORIDA.
Query Match 4.1%; Score 70; DB 6; Length 712;
Best Local Similarity 23.1%; Pred. No. 1.2e+03;
RESULT 1465
ID AAB41943 standard; protein; 723 AA.
DE Human ORF1707 polypeptide sequence SEQ ID NO:3414.
PN WO200058473-A2.
PD 05-OCT-2000.
PA (CURA-) CURAGEN CORP.
Query Match 4.1%; Score 70; DB 3; Length 723;
Best Local Similarity 19.9%; Pred. No. 1.2e+03;
RESULT 1466
ID AAG31404 standard; protein; 727 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 37707.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 4.1%; Score 70; DB 3; Length 727;
Best Local Similarity 17.2%; Pred. No. 1.2e+03;
RESULT 1467
ID ABB93080 standard; protein; 727 AA.
DE Herbicidially active polypeptide SEQ ID NO 2291.
PN WO200210210-A2.
PD 07-FEB-2002.
PA (FARB-) BAYER AG.
Query Match 4.1%; Score 70; DB 5; Length 727;
Best Local Similarity 17.2%; Pred. No. 1.2e+03;
RESULT 1468
ID AAG31683 standard; protein; 770 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 38090.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 4.1%; Score 70; DB 3; Length 770;
Best Local Similarity 17.2%; Pred. No. 1.3e+03;
RESULT 1469
ID ABM85165 standard; protein; 777 AA.
DE Human diagnostic and therapeutic pprotein SEQ ID NO:5414.
PN WO2004023973-A2.
PD 25-MAR-2004.
PA (INCY-) INCYTE CORP.
Query Match 4.1%; Score 70; DB 8; Length 777;
Best Local Similarity 20.0%; Pred. No. 1.3e+03;
RESULT 1470
ID ABU08709 standard; protein; 786 AA.
DE Alzheimer's disease associated gene screening related Notch1 protein.
PN WO2003012141-A1.
PD 13-FEB-2003.
PA (TAKE-) TAKEDA CHEM IND LTD.
PA (NICH-) JAPAN SEC CHUBU NAT HOSPITAL.
PA (KOMA/) KOMANO H.
Query Match 4.1%; Score 70; DB 6; Length 786;
Best Local Similarity 22.7%; Pred. No. 1.4e+03;
RESULT 1471
ID ADP61453 standard; protein; 786 AA.
DE Amyloid beta related 786 amino acid protein.
PN WO2003048204-A1.
PD 12-JUN-2003.
PA (TAKE-) TAKEDA CHEM IND LTD.
PA (NICH-) JAPAN SEC CHUBU NAT HOSPITAL.
PA (KOMA/) KOMANO H.

Query Match
Best Local Similarity 22.7%; Pred. No. 1.4e+03; Length 786;
RESULT 1472
ID ADF53262 standard; protein; 786 AA.
DE Mouse Notch1 NCID intracellular domain.
PN JP2003289881-A.
PD 14-OCT-2003.
PA (KOKU-) KOKURITSU RYOYOJO CHUBU BYOINCHO.
PA (KOMA/) KOMANO H.
PA (TAKE) TAKEDA CHEM IND LTD.
Query Match
Best Local Similarity 22.7%; Pred. No. 1.4e+03; Length 786;
RESULT 1473
ID ADQ82206 standard; protein; 786 AA.
DE Mouse Notch 1 protein intracellular domain - NICD.
PN JP2004215517-A.
PD 05-AUG-2004.
PA (KOKU-) KOKURITSU RYOYOJO CHUBU BYOINCHO.
PA (KOMA/) KOMANO H.
PA (TAKE) TAKEDA CHEM IND LTD.
Query Match
Best Local Similarity 22.7%; Pred. No. 1.4e+03; Length 786;
RESULT 1474
ID ABB61944 standard; protein; 878 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 12624.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match
Best Local Similarity 18.3%; Pred. No. 1.6e+03; Length 878;
RESULT 1475
ID AAE06695 standard; protein; 888 AA.
DE Arabidopsis thaliana ethylene-overproducer1 (ETOL1)-like protein 1 (EOL1).
PN WO200157063-A1.
PD 09-AUG-2001.
PA (UNVE-) UNIV PENNSYLVANIA.
Query Match
Best Local Similarity 4.1%; Score 70; DB 4; Length 888;
RESULT 1476
ID ADN72911 standard; protein; 888 AA.
DE Thale cress protein upregulated in E2Fa/Dpa expressing plants Segid 806.
PN WO2004035798-A2.
PD 29-APR-2004.
PA (CROP-) CROPDDESIGN NV.
Query Match
Best Local Similarity 4.1%; Score 70; DB 8; Length 888;
RESULT 1477
ID ADN73171 standard; protein; 888 AA.
DE Thale cress protein upregulated in E2Fa/Dpa expressing plants Segid 1066.
PN WO2004035798-A2.
PD 29-APR-2004.
PA (CROP-) CROPDDESIGN NV.
Query Match
Best Local Similarity 4.1%; Score 70; DB 8; Length 888;
RESULT 1478
ID ADU22728 standard; protein; 938 AA.
DE Human disease detection and treatment (MDDT) protein - SEQ ID 177.
PN WO2003062379-A2.
PD 31-JUL-2003.
PA (INCY-) INCYTE GENOMICS INC.
Query Match
Best Local Similarity 4.1%; Score 70; DB 7; Length 938;
RESULT 1479
ID ADO6760 standard; protein; 978 AA.
DE Novel human protein sequence #1733.
PN EP1440981-A2.
PD 28-JUL-2004.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
Query Match
Best Local Similarity 4.1%; Score 70; DB 8; Length 978;
RESULT 1480
ID ABM83330 standard; protein; 1002 AA.
DE Human diagnostic and therapeutic pproteins SEQ ID NO:3579.

PN WO2004023973-A2.
PD 25-MAR-2004.
PA (INCY-) INCYTE CORP.
Query Match
Best Local Similarity 4.1%; Score 70; DB 8; Length 1002;
RESULT 1481
ID ABB63556 standard; protein; 1006 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 17460.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match
Best Local Similarity 4.1%; Score 70; DB 4; Length 1006;
RESULT 1482
ID ADO6747 standard; protein; 1012 AA.
DE Novel human protein sequence #1720.
PN EP1440981-A2.
PD 28-JUL-2004.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
Query Match
Best Local Similarity 4.1%; Score 70; DB 8; Length 1012;
RESULT 1483
ID ABM84874 standard; protein; 1025 AA.
DE Human diagnostic and therapeutic pproteins SEQ ID NO:5123.
PN WO2004023973-A2.
PD 25-MAR-2004.
PA (INCY-) INCYTE CORP.
Query Match
Best Local Similarity 4.1%; Score 70; DB 8; Length 1025;
RESULT 1484
ID ADB62760 standard; protein; 1085 AA.
DE Rat Protein AAC52634, SEQ ID NO 8693.
PN WO2003016475-A2.
PD 27-FEB-2003.
PA (GEHO) GEN HOSPITAL CORP.
PA (FARB) BAYER AG.
Query Match
Best Local Similarity 4.1%; Score 70; DB 7; Length 1085;
RESULT 1485
ID ADB62756 standard; protein; 1085 AA.
DE Rat Protein AAC52634, SEQ ID NO 8689.
PN WO2003016475-A2.
PD 27-FEB-2003.
PA (GEHO) GEN HOSPITAL CORP.
PA (FARB) BAYER AG.
Query Match
Best Local Similarity 4.1%; Score 70; DB 7; Length 1085;
RESULT 1486
ID ADB62752 standard; protein; 1085 AA.
DE Rat Protein AAC52634, SEQ ID NO 8685.
PN WO2003016475-A2.
PD 27-FEB-2003.
PA (GEHO) GEN HOSPITAL CORP.
PA (FARB) BAYER AG.
Query Match
Best Local Similarity 4.1%; Score 70; DB 7; Length 1085;
RESULT 1487
ID ABU09232 standard; protein; 1167 AA.
DE Rat neuropathic pain gene 4, NP64, polypeptide.
PN US2003003538-A1.
PD 02-JAN-2003.
PA (DIET/) DIETRICH P S.
PA (HUAN/) HUANG C.
PA (JOHN/) JOHNSON C D.
PA (SANG/) SANGMESMARAN L.
Query Match
Best Local Similarity 4.1%; Score 70; DB 6; Length 1167;
RESULT 1488
ID ABR53027 standard; protein; 1358 AA.
DE Protein sequence #SEQ ID 919.
PN EP1258494-A1.
PD 20-NOV-2002.
PA (CELL-) CELLZONE AG.

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Query Match
Best Local Similarity 18.0%; Score 70; DB 6; Length 1358;
RESULT 1489
ID ADK62848 standard; protein; 1358 AA.
DE Disease treating protein complex-derived protein #550.
PN EPI338608-A2.
PD 27-AUG-2003.
PA (CELL-) CELLZOME AG.
Query Match
Best Local Similarity 18.0%; Score 70; DB 7; Length 1358;
RESULT 1490
ID ADN19005 standard; protein; 1358 AA.
DE Bacterial polypeptide #1658.
PN US2003233675-A1.
PD 18-DEC-2003.
PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
Query Match
Best Local Similarity 18.0%; Score 70; DB 8; Length 1358;
RESULT 1491
ID ABR52895 standard; protein; 1748 AA.
DE Protein sequence #SEQ ID 655.
PN EPI258494-A1.
PD 20-NOV-2002.
PA (CELL-) CELLZOME AG.
Query Match
Best Local Similarity 23.3%; Score 70; DB 6; Length 1748;
RESULT 1492
ID ADK62418 standard; protein; 1748 AA.
DE Disease treating protein complex-derived protein #335.
PN EPI338608-A2.
PD 27-AUG-2003.
PA (CELL-) CELLZOME AG.
Query Match
Best Local Similarity 23.3%; Score 70; DB 7; Length 1748;
RESULT 1493
ID ADN19312 standard; protein; 1748 AA.
DE Bacterial polypeptide #1965.
PN US2003233675-A1.
PD 18-DEC-2003.
PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
Query Match
Best Local Similarity 23.3%; Score 70; DB 8; Length 1748;
RESULT 1494
ID ADN24076 standard; protein; 1956 AA.
DE Bacterial polypeptide #6729.
PN US2003233675-A1.
PD 18-DEC-2003.
PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
Query Match
Best Local Similarity 20.8%; Score 70; DB 8; Length 1956;
RESULT 1495
ID ABR53118 standard; protein; 2000 AA.
DE Protein sequence #SEQ ID 1101.
PN EPI258494-A1.
PD 20-NOV-2002.
PA (CELL-) CELLZOME AG.
Query Match
Best Local Similarity 22.7%; Score 70; DB 6; Length 2000;
RESULT 1496
ID ADK62826 standard; protein; 2000 AA.
DE Disease treating protein complex-derived protein #539.

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PN EPI338608-A2.
PD 27-AUG-2003.
PA (CELL-) CELLZOME AG.
Query Match
Best Local Similarity 22.7%; Score 70; DB 7; Length 2000;
RESULT 1497
ID ADN72303 standard; protein; 2009 AA.
DE Thale cress protein upregulated in E2Fa/Dpa expressing plants SeqID 198.
PN W02004035798-A2.
PD 29-APR-2004.
PA (CROP-) CROPDDESIGN NV.
Query Match
Best Local Similarity 20.8%; Score 70; DB 8; Length 2009;
RESULT 1498
ID ADO58587 standard; protein; 2531 AA.
DE Mouse Notch-1 protein, SEQ ID NO:5.
PN W02004048578-A1.
PD 10-JUN-2004.
PA (PHAR) PHARMACIA & UPJOHN CO.
Query Match
Best Local Similarity 22.7%; Score 70; DB 8; Length 2531;
RESULT 1499
ID ABR48232 standard; protein; 152 AA.
DE Listeria monocytogenes protein #936.
PN W0200177335-A2.
PD 18-OCT-2001.
PA (INSP) INST PASTEUR.
Query Match
Best Local Similarity 24.7%; Score 69.5; DB 5; Length 152;
RESULT 1500
ID ABG05308 standard; protein; 204 AA.
DE Novel human diagnostic protein #5299.
PN W0200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match
Best Local Similarity 20.5%; Score 69.5; DB 4; Length 204;

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